

GenCore version 5.1.1.6
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CM protein - protein search, using sw model

Run on: February 13, 2004, 13:06:37 ; Search time 17 Seconds
(without alignments)
2309.841 Million cell updates/sec

Title: US-09-934-323-2

Perfect score: 4508
Sequence: 1 MWLLALCLVLAGAQRGGG.....PPTATSHNTLPHPHSTTRV 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4508	100.0	835	1 NLG2 HUMAN	Q8nfz4 homo sapien
2	4415.5	97.9	836	1 NLG2 RAT	Q62888 rattus norv
3	2876	63.8	840	1 NLG1 MOUSE	Q8n2q7 homo sapien
4	2809	62.3	843	1 NLG1 MOUSE	Q99k10 mus musculus
5	2773.5	61.5	825	1 NLG3 MOUSE	Q8b5m5 mus musculus
6	2771	61.5	843	1 NLG3 RAT	Q62765 rattus norv
7	2750	61.0	848	1 NLG3 HUMAN	Q9n294 homo sapien
8	2746	60.9	848	1 NLG3 RAT	Q62889 rattus norv
9	2713.5	60.2	816	1 NLG4 HUMAN	Q8n0w4 homo sapien
10	2678.5	59.4	816	1 NLG4 HUMAN	Q8nfz3 homo sapien
11	859	19.1	574	1 CHLE HORSE	P81908 equus cabal
12	858	19.0	581	1 CHLE RAT	P21927 oryctolagus
13	855	19.0	602	1 CHLE HUMAN	P06276 homo sapien
14	852	18.9	614	1 ACES MOUSE	P21836 mus musculus
15	846.5	18.8	614	1 ACES RAT	F37136 rattus norv
16	841.5	18.7	613	1 ACES BOVIN	P23795 bos taurus
17	841	18.6	611	1 ACES FELICA	Q62763 felis silve
18	837	18.6	603	1 CHLE MOUSE	Q03311 mus musculus
19	836.5	18.6	566	1 EST1 PIG	Q29550 sus scrofa
20	830	18.4	557	1 SASE ANAPL	Q04791 anas platyr
21	830	18.4	581	1 ACES BUNFA	Q92035 bungarus fa
22	828.5	18.4	742	1 BAL HUMAN	P19835 homo sapien
23	827.5	18.4	614	1 ACES HUMAN	P22303 homo sapien
24	823.5	18.3	562	1 ES22 MOUSE	Q64176 mus musculus
25	819	18.2	561	1 EST3 RAT	Q63108 rattus norv
26	819	18.2	612	1 BAL RAT	P23141 homo sapien
27	817	18.1	567	1 EST1 HUMAN	P23141 homo sapien
28	812.5	18.0	586	1 ACES TORCA	P04058 torpeda cal
29	807	17.9	584	1 ACES BRAT	Q99499 oryctolagus
30	804.5	17.8	634	1 ACES BRARE	Q9dd63 brachydanio
31	800.5	17.8	590	1 ACES TORMA	P07692 torpeda mar
32	797	17.7	549	1 EST1 RAT	P10959 rattus norv
33	793.5	17.6	561	1 EST4 RAT	Q64573 rattus norv

34	792	17.6	561	1 EST5 RAT	Q63010 rattus norv
35	792	17.6	599	1 BAL MOUSE	Q64285 mus musculus
36	790	17.5	565	1 ES10 RAT	P16303 rattus norv
37	787	17.5	633	1 ACES ELEEL	O42275 electrophor
38	781.5	17.3	597	1 BAL BOVIN	P30122 bos taurus
39	772.5	17.1	554	1 ESTN MOUSE	P23953 mus musculus
40	768	17.0	561	1 EST1 MESAU	O64419 mesocricetu
41	757.5	16.8	532	1 EST2 RABIT	P14943 oryctolagus
42	740	16.4	554	1 ESTM MOUSE	Q63880 mus musculus
43	717.5	15.9	767	1 ACES CHICK	P36196 gallus gall
44	715.5	15.9	539	1 EST1 RABIT	P12337 oryctolagus
45	704	15.6	202	1 NLG3 MACMU	Q8wmh2 macaca mula

ALIGNMENTS

RESULT 1	NLG2_HUMAN	STANDARD;	PRT;	835 AA.
ID	Q8NPZ4; Q9P211;			
AC	15-SEP-2003 (Rel. 42, Created)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DE	Neurologin 2 precursor.			
GN	Neurologin 2 precursor.			
OS	Neurologin 2 precursor.			
OC	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RP	SEQUENCE FROM N.A.			
RX	PubMed=12669065;			
RA	Jamain S., Quach H., Betancur C., Rastam M., Colineaux C.,			
RA	Gillberg I.C., Soderstrom H., Giros B., Leboyer M., Gillberg C.,			
RA	Bourgeron T., Nyden A., Philippe A., Cohen D., Chabane N.,			
RA	Mourren-Simeoni M.C., Brice A., Sponheim E., Spurkland I.,			
RA	Skjeldal O.H., Coleman M., Pearl P.L., Cohen I.L., Tsouris J.,			
RA	Zappella M., Menchetti G., Pompella A., Aschauer H., Van Maldergem L.,			
RT	"Mutations of the X-linked genes encoding neurologins NLGN3 and NLGN4			
RT	are associated with autism";			
Nat. Genet.	34:27-29 (2003)			
[2]				
RP	SEQUENCE OF 286-835 FROM N.A.			
RX	Medline=20181126; PubMed=10718198;			
RA	Tissue=Brain;			
RA	Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.,			
RT	"Prediction of the coding sequences of unidentified human genes. XVI.			
RT	The complete sequences of 150 new cDNA clones from brain which code			
RT	for large proteins in vitro."			
RL	DNA Res. 7:65-73 (2000).			
[3]				
RP	INTERACTION WITH DLG4.			
RX	PubMed=9278515;			
RA	Irie M., Hata Y., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,			
RA	Takai Y., Rosahl T.W., Suedhof T.C.;			
RT	"Binding of neurologins to PSD-95";			
RL	Science 277:1511-1515 (1997).			
[4]				
RP	FUNCTION.			
RX	PubMed=10892652;			
RA	Scheiffele P., Fan J., Choih J., Fetter R., Serafini T.;			
RT	"Neurologin expressed in nonneuronal cells triggers presynaptic			
RT	development in contacting axons";			
RL	Cell 101:657-669 (2000).			
CC	1- FUNCTION: Neuronal cell surface protein thought to be involved in			
CC	cell-cell interactions by forming intercellular junctions through			
CC	binding to beta-neurexins. Seems to play role in formation or			
CC	maintenance of synaptic junctions. In vitro, triggers the de novo			
CC	formation of presynaptic structures			
CC	-!- SUBUNIT: Interacts with neuroligin 1-beta, neuroligin 2-beta and			
CC	neuroligin 3-beta (By similarity). Probably interacts through its C-			
CC	terminus with DLG4/PSD-95 third PDZ domain.			

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF376802; AA045111.1; --
DR EMBL: AB037787; BA092604.1; --
DR HSSP: P21836; 1MAA.
DR GenSeq: HGNC:14290; NLGN2.
DR MIM: 606479; --
DR InterPro: IPR002018; Carbesterease.
DR InterPro: IPR000460; Neuroligin.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR01090; NEUROLIGIN.
DR PROSITE: PS00941; CARBOXYLESTERASE B_2; 1.
KW Cell adhesion; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 14
FT CHAIN 15 835
FT DOMAIN 15 677
FT TRANSMEM 678 698
FT DOMAIN 699 835
FT DISULFID 106 141
FT DISULFID 317 328
FT DISULFID 487 521
FT CARBOHYD 98 98
FT CARBOHYD 136 136
FT CARBOHYD 522 522
SQ SEQUENCE 835 AA; 90819 MW; 359938630193EF87 CRC64;

Query Match 100.0%; Score 4508; DB 1; Length 835;
Best Local Similarity 100.0%; Pred. No. 9.6e-244;
Matches 835; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLLALCLVLGAGAGCGGGGPGGAGPGGGLGSLGSEERFPVNTAYGRVGRVRELN 60
DB 1 MWLLALCLVLGAGAGCGGGGPGGAGPGGGLGSLGSEERFPVNTAYGRVGRVRELN 60

QY 61 ELIGPVQVPLGVYATPPLIGARRFQPEAPASWPGVRNATLTPACPNLHGALPAIMLP 120
DB 61 ELIGPVQVPLGVYATPPLIGARRFQPEAPASWPGVRNATLTPACPNLHGALPAIMLP 120

QY 121 VWFTDNLEAAATVYVQSEDCLYLNLVYPTEDGPLTKKRDEATLNPPTDIRDPKXPVM 180
DB 121 VWFTDNLEAAATVYVQSEDCLYLNLVYPTEDGPLTKKRDEATLNPPTDIRDPKXPVM 180

QY 181 LFLHGSYMEGTGNMFDGSLAAYGNVATLNLVGLVGLSTGDAQAKNGYGLDQIQ 240
DB 181 LFLHGSYMEGTGNMFDGSLAAYGNVATLNLVGLVGLSTGDAQAKNGYGLDQIQ 240

QY 241 ALRWLSENIAHFGGPPERITIFSGAGASCYNLLILSHHSEGLFQKALQAGSTAISNSV 300
DB 241 ALRWLSENIAHFGGPPERITIFSGAGASCYNLLILSHHSEGLFQKALQAGSTAISNSV 300

QY 301 NYQPLKYTRLAAKVGCDREDSABAEVCLRRKPSRELVDQVQPARHYAIGPVVDGDDV 360
DB 301 NYQPLKYTRLAAKVGCDREDSABAEVCLRRKPSRELVDQVQPARHYAIGPVVDGDDV 360

QY 361 PDPEILMQCGEFLNVDMLIGNVQCEGLKFVEDSAESDGVSAFDTVSNFVDNLGY 420
DB 361 PDPEILMQCGEFLNVDMLIGNVQCEGLKFVEDSAESDGVSAFDTVSNFVDNLGY 420

QY 421 PGKDVLRITIKFMYTDWADRNNGEMRRKTLALFTDQWVAPAVATAKLHADYQSPYVF 480
DB 421 PGKDVLRITIKFMYTDWADRNNGEMRRKTLALFTDQWVAPAVATAKLHADYQSPYVF 480

QY 481 YTFYHHCQAEGRPEWADAAGDELPLYFGVPMVGATDLFPNFSKNDVWLSAVVMTYTN 540

DB 481 YTFYHHCQAEGRPEWADAAGDELPLYFGVPMVGATDLFPNFSKNDVWLSAVVMTYTN 540
QY 541 FAKTGDNPQVQDQKFTHTKRNREEVVSWKFNSEKQYLIHGLKPRVDNRANKVAF 600
DB 541 FAKTGDNPQVQDQKFTHTKRNREEVVSWKFNSEKQYLIHGLKPRVDNRANKVAF 600
QY 601 WLELPHLNLHNLTELTFTTTRLPYPYATRWPPPPAGAGTGRPPPPATLPPPEPEPGR 660
DB 601 WLELPHLNLHNLTELTFTTTRLPYPYATRWPPPPAGAGTGRPPPPATLPPPEPEPGR 660
QY 661 AYDRPQDSRDYSTELSVTVAGSILFLNLIILAFALYVYKRROROLRCRRLSPGSGS 720
DB 661 AYDRPQDSRDYSTELSVTVAGSILFLNLIILAFALYVYKRROROLRCRRLSPGSGS 720
QY 721 GVFGGGLLPAAAGRELPPPEELVSLQKRGCGVGADPAEALPACPPDYTLALRAPDDV 780
DB 721 GVFGGGLLPAAAGRELPPPEELVSLQKRGCGVGADPAEALPACPPDYTLALRAPDDV 780
QY 781 PLLAPGALTLLPSGLGPPPPPPPSLHPGPPPPPPPTATSHNNTLPHPHSTTRV 835
DB 781 PLLAPGALTLLPSGLGPPPPPPPSLHPGPPPPPPPTATSHNNTLPHPHSTTRV 835

RESULT 2
NLG2 RAT STANDARD; PRT; 836 AA.
AC Q62888;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuroligin 2 precursor.
GN NLGN2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RX NCBI_TaxID=101116;
[1]
RP SEQUENCE FROM N.A. (ISOPFORMS 1 AND 2). SEQUENCE OF N-TERMINUS, TISSUE
RP SPECIFICITY, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN 2-BETA AND
RP NEUREXIN 3-BETA.
RC TISSUE=Forebrain;
RX MEDLINE-96162010; PubMed-8576240;
RA Ichtchenko K., Nguyen T., Suedhof T.C.;
RT "Structures, alternative splicing, and neuroligin binding of multiple
RT neuroligins";
RL J. Biol. Chem. 274:2676-2682 (1996)
[2]
RP TISSUE SPECIFICITY.
RX PubMed-11329178;
RA Gilbert M., Smith J., Roskams A.J., Auld V.J.;
RT "Neuroligin 3 is a vertebrate gliotactin expressed in the olfactory
RT ensheathing glia, a growth-promoting class of macroglia";
RL Glia 34:151-164 (2001).
CC -!- FUNCTION: Neuronal cell surface protein thought to be involved in
CC cell-cell interactions by forming intercellular junctions through
CC binding to beta-neurexins. Seems to play role in formation or
CC maintenance of synaptic junctions. In vitro, triggers the de novo
CC formation of presynaptic structures (By similarity).
CC -!- SUBUNIT: Interacts with neuroligin 1-beta isoforms 3/Beta 4B5A and
CC 4/Beta 4B5B. Interacts with neuroligin 2-beta isoforms 3/Beta 4B5A and
CC 4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with
CC neuroligin 3-beta. Probably interacts through its C-terminus with
CC DLG4/PSD-95 third PDZ domain (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q62888-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q62888-2; Sequence=VSP_007533;
CC -!- TISSUE SPECIFICITY: Expressed in brain, spinal chord and dorsal
CC root ganglion.

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CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U41662; AAA97870.1; --
CC DR HSP; P37967; 1053.
CC DR InterPro; IPR002018; CarboxylesteraseB.
CC DR InterPro; IPR000460; Neurotrophin.
CC DR InterPro; IPR000379; Ser esterase site.
CC DR Pfam; PF00135; Coesterase_1.
CC DR PRINTS; PR01090; NEUROLOGIN.
CC DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC KW Cell adhesion; Glycoprotein; Signal; Transmembrane;
CC Alternative splicing.
CC FT SIGNAL 1 14 PROBABLE.
CC FT CHAIN 15 836 NEUROLOGIN 2.
CC FT DOMAIN 15 678 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 679 699 POTENTIAL.
CC FT DOMAIN 700 836 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 106 141 BY SIMILARITY.
CC FT DISULFID 317 328 BY SIMILARITY.
CC FT CARBOHYD 487 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARSPLIC 153 169 Missing (in isoform 2).
CC FT FTID; VSP_007533.
CC SEQUENCE 836 AA; 90961 MW; 1AD51CB1E4BF9CF CRC64;
CC -----
Query March 97.98; Score 4415.5; DB 1; Length 836;
Best Local Similarity 98.38; Pred No. 1.4e-238;
Matches 822; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
QY 1 MWLLALCLVLGAGQRRGGGPGGAPGGGLGSLGSEGRFPVNTAYGRVGRRLNN 60
DB 1 MWLLALCLVLGAGQRRGGGPGGAPGGGLGSLGSEGRFPVNTAYGRVGRRLNN 60
QY 61 EILGPVVOFLGVPVATPLGARFPQPEAPASPGVGNATLTPACPNLHGLPALMLP 120
DB 61 EILGPVVOFLGVPVATPLGARFPQPEAPASPGVGNATLTPACPNLHGLPALMLP 120
QY 121 VWFDTNLEAAATVYQNSDCLYLNLYVPTDGLTKRDEATLNPPDTRDGGKPYM 180
DB 121 VWFDTNLEAAATVYQNSDCLYLNLYVPTDGLTKRDEATLNPPDTRDGGKPYM 180
QY 181 LFLHGGSYMEGTGNMFGSVLAAYGNVIVATLYRVLGFLSTGQAAKGYLLDQIQ 240
DB 181 LFLHGGSYMEGTGNMFGSVLAAYGNVIVATLYRVLGFLSTGQAAKGYLLDQIQ 240
QY 241 ALRWLSNIAHFGDPERITIFSGAGASCNLLILSHHSEGLFQKALQSGTAISSW 300
DB 241 ALRWLSNIAHFGDPERITIFSGAGASCNLLILSHHSEGLFQKALQSGTAISSW 300
QY 301 NYQPLKVTLLAAKVGQRDESAVCLRLKRSRELVDDQVOPARYHIAFGVWDGVV 360
DB 301 NYQPLKVTLLAAKVGQRDESAVCLRLKRSRELVDDQVOPARYHIAFGVWDGVV 360
QY 361 PDDPEILMQCEFLNYDMLIGNOGEGIKFVEDSAESDGVSAFDTVSNFVDNLGY 420
DB 361 PDDPEILMQCEFLNYDMLIGNOGEGIKFVEDSAESDGVSAFDTVSNFVDNLGY 420
QY 421 PEGKDVLRITIKMYTDWADRNGEMRKTLALFTDQHWAPAVATAKLHAYQSPVYF 480
DB 421 PEGKDVLRITIKMYTDWADRNGEMRKTLALFTDQHWAPAVATAKLHAYQSPVYF 480
QY 481 YTFYHHCQAEGRPEWADAAGDELPLYVGVPMVGATDLFFCNFSKNDVMSAVVMTWTN 540

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Db 481 YTFYHHCQAEGRPEWADAAGDELPLYVGVPMVGATDLFFCNFSKNDVMSAVVMTWTN 540
QY 541 FAKTGDNDQVPQDTKFIHTKPNRFEVWVSKNSKEQVYLHGLKPRVDNRYANKVAF 600
Db 541 FAKTGDNDQVPQDTKFIHTKPNRFEVWVSKNSKEQVYLHGLKPRVDNRYANKVAF 600
QY 601 WLELVPHLNLHTELTFTTTLRLPPYATRWPRPPA-GAPOTRRPPPPATLPPPEPEPGP 659
Db 601 WLELVPHLNLHTELTFTTTLRLPPYATRWPRPPA-GAPOTRRPPPPATLPPPEPEPGP 660
QY 660 RAYDRFQDSDRSTELSVTVAVGASLLEINILAFALYYKRRRQELRCRLSPPGSG 719
Db 661 RAYDRFQDSDRSTELSVTVAVGASLLEINILAFALYYKRRRQELRCRLSPPGSG 720
QY 720 SGVPGGGPLPAAGRELPPPEELVSLQKRGVGGADPAEALPACPPDYTLARRAPDD 779
Db 721 SGVPGGGPLPAAGRELPPPEELVSLQKRGVGGADPAEALPACPPDYTLARRAPDD 780
QY 780 VPLLAPGALTLLPSGLGPPPPPPPSLHPGPPPPPPPTATSHNNTLPHPHSTTRV 835
Db 781 VPLLAPGALTLLPSGLGPPPPPPPSLHPGPPPPPPPTATSHNNTLPHPHSTTRV 836

RESULT 3
NLG1_HUMAN STANDARD; PRT; 840 AA.
ID NLG1_HUMAN Q90UPT2;
AC Q90UPT2; Q90UPT2;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurotrophin 1 precursor.
GN NLGN1 OR KIAA1070.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=99397452; PubMed=10470851;
RA Kikuno R., Negase T., Ishikawa K.-I., Hirose M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 6:197-205 (1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Ductenium;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE OF 315-823 FROM N.A.
RC TISSUE=Embryo;

```

RA Isogai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project";
RN Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CONCEPTUAL TRANSLATION (ISOFORM 1).
RA Roehrborn B.;
RL Unpublished observations (MAY-2003).
RN [5]
RP INTERACTION WITH DLG4.
RX PubMed:9278515;
RA Irie M., Hata Y., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,
RA Takai Y., Rosahl T.W., Suedhof T.C.;
RT "Binding of neurotrophins to PSD-95";
RN Science 277:1511-1515(1997).
RN [6]
RP FUNCTION
RX PubMed:10892652;
RA Scheiffele P., Fan J., Choih J., Fetter R., Serafini T.;
RT "Neurotrophin expressed in nonneuronal cells triggers presynaptic
RT development in contacting axons";
RN Cell 101:657-669(2000).
CC -!- FUNCTION: Neuronal cell surface protein thought to be involved in
CC cell-cell interactions by forming intercellular junctions through
CC binding to beta-neurexins. Seems to play role in formation or
CC maintenance of synaptic junctions. In vitro, triggers the de novo
CC formation of presynaptic structures. May be involved in
CC specification of excitatory synapses.
CC -!- SUBUNIT: Interacts with neuroligin 1-beta, neuroligin 2-beta and
CC neuroligin 3-beta [By similarity]. Interacts through its C-terminus
CC with DLG4/PSD-95 third PDZ domain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Enriched in
CC synaptic plasma membranes and clustered in synaptic clefts and
CC postsynaptic densities [By similarity].
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8N2Q7-1; Sequence=Displayed;
CC Note=No experimental confirmation available;
CC Name=2;
CC IsoId=Q8N2Q7-2; Sequence=VSP_007527;
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AB028993; BAA83022.1; --
CC EMBL; BC032555; AAH32555.1;
CC EMBL; AK074522; BAC11039.1; ALT_INIT.
CC HSP; P21836; 1MAA.
CC Genew; HGNC:14291; NLGN1.
CC MIM; 600568; --
CC InterPro; IPR002018; Carboxylesterase.
CC InterPro; IPR000460; Neurotrophin.
CC InterPro; IPR000379; Ser esterase.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR01090; NEUROLOGIN.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Cell adhesion; Glycoprotein; Signal; Transmembrane;
KW Alternative splicing.
KW SIGNAL 1 45 POTENTIAL.
FT CHAIN 46 840 NEUROLOGIN 1.
FT DOMAIN 46 694 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 695 715 POTENTIAL.
FT

FT DOMAIN 716 840 CYTOPLASMIC (POTENTIAL).
FT DISULFID 117 153 BY SIMILARITY.
FT DISULFID 339 350 BY SIMILARITY.
FT DISULFID 509 543 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 544 544 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 165 181 Missing (in isoform 2).
FT FTId=VSP_007527.
FT CONFLICT 711 711 F -> L (IN REF. 3).
SQ SEQUENCE 840 AA; 93835 MW; A3FB21716F62DE29 CRC64;
Query Match 63.8%; Score 2876; DB 1; Length 840;
Best Local Similarity 63.5%; Pred. No. 6.6e-153;
Matches 556; Conservative 98; Mismatches 134; Indels 88; Gaps 16;
QY 1 MWLLAL-CLVLAGAORGGGPGGAGPGGGLGSLG-----LTLMLGCLLQAGHVLSQLDDVDLVAL 46
DB 12 VWRVAVACLV-----HRLGAP-----LTLMLGCLLQAGHVLSQLDDVDLVAL 57
QY 47 AYGRVGRVRELNNEILGPVVFGLVPPYATPPIGARRFQPPPEAPASWPGVNRNATLPPAC 106
DB 58 NFGKIRGIRKELNNEILGPVVFGLVPPYATPPIGARRFQPPPEAPASWPGVNRNATLPPAC 117
QY 107 PON-LHGALPAIMLPVWFTDNLLEAATYVQNOSEDCLYLNLYVPTEDGPLTKKRDATLN 165
DB 118 PQNIIDRLPEVWMLPVWFTDNLVSVYQDQSEDCLYLNLYVPTEDGPLTKKRDATLN 177
QY 166 PPDTDIRDP-GKKPVMLFLHGGSYMEGTGMFGSVLAAYGNVIVATLNYRLGVGLFLST 224
DB 178 PPDTDIRDSGPKFPMVYIHGGSYMEGTGMFGSVLAAYGNVIVATLNYRLGVGLFLST 237
QY 225 GDQAAGKNGYLLDQIQALRWLSENIAHFGDDPRITIFSGAGASCNLLILSHHE--- 281
DB 238 GDQAAGKNGYLLDQIQALRWLSENIAHFGDDPRITIFSGAGASCNLLILSHHE--- 297
QY 282 -----GLFOKAIAGSGTAISMSVNVQPLKYTRLLAAKVGCDREDSAAVECLRKPSR 335
DB 298 WSNSTKGLFQRAIAQSGTALSSWAVSFQAKYARMLATKVCNVDVELVECLKPKYK 357
QY 336 ELVDQDVQARYHIAFGPVVDGVDVDPDPEILMQGSEFLNYDMLGNOGEGKLFVEDSA 395
DB 358 ELVDQDVQARYHIAFGPVVDGVDVDPDPEILMQGSEFLNYDMLGNOGEGKLFVENIV 417
QY 396 ESDGYSASAFDTVSNFVDNLGYPEGKDVLRETIKEMVTDWADRGEMREKTLALF 455
DB 418 DSDDGISASDFDFAVSNFVDNLGYPEGKDVLRETIKEMVTDWADRGEMREKTLALF 477
QY 456 TDHQWAPAVATAKLHAYQSPVYFTFYHHCQAGRPWADAAGDELFPYFVGPMVGA 515
DB 478 TDHQWAPAVATAKLHAYQSPVYFTFYHHCQAGRPWADAAGDELFPYFVGPMVGA 537
QY 516 TDLPPCNFSKNDVMSAVMYTNFAKTDGDPNQVPQDTKFIHTKPNRFEFVWMSKFS 575
DB 538 TDLPPCNFSKNDVMSAVMYTNFAKTDGDPNQVPQDTKFIHTKPNRFEFVWMSKFS 597
QY 576 KEQQLYHLGLKPRVRDNRANKVAFLELVPHLNLH--TELFTTTTTLPPFYATRWPPRP 633
DB 598 KDQLYHLGLKPRVKEHVRANKVNLVPHLNLHNDISQYTSITTTKVPSTDTIRPTR 657
QY 634 PAGAGTTRPPPPATLPPPEPEPGPRAYDRPFGDSRDYSTELSVTVAVGASLLFNILA 693
DB 658 KNSVPVTSAPPTAKQDDPKQQSP-----FSDQORDYSTELSVTVAVGASLLFNILA 710
QY 694 FAALYVKRDRERQELRCRRRLSPGSGSGVPGGGLLPAAGRELPPPEELVSLQKRGGV 753
DB 711 FAALYVKRDRERQELRCRRRLSPGSGSGVPGGGLLPAAGRELPPPEELVSLQKRGGV 755
QY 754 GAD-----PAE-ALRPACPPDYTLARRAPDDVELLAPGALTLPGLGPPPPPPPPS 805
DB 756 DLQHECESIHPHEVLRACPPDYTLARRAPDDVELLAPGALTLPGLGPPPPPPPPS 810


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Db 233 GVLGFLSTGDQAQKNGYGLLDLIQALRWTSNENIFPGDPLRITVFGAGGSCVNLITL 292
Qy 277 SHSE-----GLFQKAIASQGTASSVNVYQPLKYTRLLAAKVCGRDSEAEAVE 327
Db 293 SHYSEGNRRNSNTKGLFORAIAQSQTALSSWAFQPAKYARILATKVCNVSDTVLVE 352
Qy 328 CLRKRPSRELVDQVQPARHYAFAGVVDGDDPEILMOGGEFLNMLIGVNOGEG 387
Db 353 CLOKPEYKELVDQVQPARHYAFAGVVDGDDPEILMOGGEFLNMLIGVNOGEG 412
Qy 388 LKFVEDSAESDGVSAFDFTVSNFVNDLYGPEGKVLRETIFKMTYTDWADRNGEMR 447
Db 413 LKFVENIVSDGVSAFDFTVSNFVNDLYGPEGKVLRETIFKMTYTDWADRNPETR 472
Qy 448 RKTLLALFTDQHWAPAVATAKLHADYQSPVYTFYHHQCBGEPWADAAGDELPIV 507
Db 473 RKTLLALFTDQHWAPAVATAKLHNSFGSTFYFAPHHCQTDQVPAWADAAGDEVPYV 532
Qy 508 FGVPVMGATDLPFCNFKNDVMSLVAVMTYTNFNAKTGPNQVQDQTKFIHTKPNREE 567
Db 533 LGIPMIGTELPFCNFKNDVMSLVAVMTYTNFNAKTGPNQVQDQTKFIHTKPNREE 592
Qy 568 VVWSKENSKEQYHLIGLPRVDNRANKYAFWELVPHLNLH--TELFTTTRLPDPY 625
Db 593 VAWTRYSQDQLYHLIGLPRVKHYRANKVNLVLELPHLNLNDISQYSTTKVP-- 650
Qy 626 ATRWPPRPAGAGTTRPPPPAT-----LPPEPEPGPRAYDRFPDGSRDYSSTELSVT 679
Db 651 STDITILRP-----TKNSTPTVSAPPAKQDDPKQOSP-----FSDVDQDYSSTELSVT 699
Qy 680 VAVGASLLFLNTLFAALYKDRQELRCLRSLPFGSGGSGVPGGGLLPAAGRELPE 739
Db 700 IAVGASLLFLNTLFAALYKDRQELRCLRSLPFGSGGSGVPGGGLLPAAGRELPE 747
Qy 740 ELVLSQLXRGGVGAD-----PAB-ALRPACSPDYTLALRAPDDVPILLACALTL 791
Db 748 EELMSQMKH-----TDLHCEHSIHHEVVRITACPDYTLAWRSPDDIPLMTNTIMI 804
Qy 792 PSLGOLPPPPPPSLHFGFPFPPPTATSHNTLPHP-----HSTTRV 835
Db 805 PNTI-----PGIQLTFTNTF-----TGGQNNTLPHPHPHSHSTRV 843

RESULT 5
NLG3_MOUSE
ID NLG3_MOUSE
AC Q8BYM5; Q8BXK4;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuroigin 3 precursor (Gliotactin homolog).
GN NLG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus, and Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogani A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Garioldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
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RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX PubMed=11329178;
RA Gilbert M., Smith J., Roakams A.J., Auld V.J.;
RT "Neuroigin 3 is a vertebrate gliotactin expressed in the olfactory
RT ensheathing glia, a growth-promoting class of macroglia.";
RL Glia 34:151-164 (2001).
CC -|- FUNCTION: Neuronal cell surface protein thought to be involved in
CC cell-cell interactions by forming intercellular junctions through
CC binding to beta-neurexins. May play a role in formation or
CC maintenance of synaptic junctions. May also play a role in glia-
CC glia or glia-neuron interactions in the developing peripheral
CC nervous system.
CC -|- SUBUNIT: Interacts with neuroligin 1-beta, neuroligin 2-beta and
CC neuroligin 3-beta, and probably through its C-terminus with
CC DLG4/PSD-95 third PDZ domain (by similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -|- TISSUE SPECIFICITY: Expressed in olfactory bulb and olfactory
CC epithelium. Found in olfactory ensheathing glia but not in
CC olfactory neurons, and in developing peripheral glia.
CC -|- DEVELOPMENTAL STAGE: Detected at embryonic day E17 and postnatal
CC day P1 in retinal astrocytes, spinal chord astrocytes and Schwann
CC cells of the dorsal root ganglion.
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC
CC -----
CC ENBL; AK039018; BAC30207.1; -
CC ENBL; AK044438; BAC31918.1; -
CC MGD; MGI:2444609; A230085M13Rik.
CC InterPro; IPR002018; CarboxylesteraseB.
CC InterPro; IPR000379; Ser_estrases.
CC Pfam; PF00135; Coesterase; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Cell adhesion; Glycoprotein; Signal; Transmembrane.
CC SIGNAL 1 34
CC CHAIN 35 825
CC FT DOMAIN 35 686 NEUROLIGIN 3.
CC FT DOMAIN 687 707 POTENTIAL.
CC FT TRANSMEM 687 707 POTENTIAL.
CC FT DOMAIN 708 825 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 103 138 BY SIMILARITY.
CC FT DISULFID 317 328 BY SIMILARITY.
CC FT DISULFID 487 521 BY SIMILARITY.
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 459 459 O -> K (IN REF. 1; BAC31918).
CC SQ SEQUENCE 825 AA; 31175 MW; 3BF17F889B0A44CE CRC64;
CC
CC Query Match 61.5%; Score 2773.5; DB 1; Length 825;
CC Best Local Similarity 64.8%; Pred.No. 3.3e-147;
CC Matches 531; Conservative 98; Mismatches 132; Indels 59; Gaps 14;
```

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QY 42 PVNTAYVRGVRRELNNEILGVVQFLGVPVATPPLGARRFOPPEAPASPGVVRNATT 101
DB 39 PTNTWTFEGLRGARVPLPSELGLGVQYQYVAAAPPEKFLPEPPPPSSGSGRNATH 98
QY 102 LPACQNLHGLALPALMPWFNTDNLAAATVYQVQNSDCLVNLVYPPEDGFLPKRDE 161
DB 99 FPPVCPQNIHTAVFVNLVPLVWFNTANLDIVATIQEENEDCLVNLVYPTDGGAKKQGE 158
QY 162 ATLN---PPDTRDRGKPKVMLFLGGSGMGTGNGMFGSVLAAYGNVIVATLVNRLGV 218
DB 159 DLADNDGDEDEDIRDSGAKPVWYIIHGGSGMGTGNGMIDGSLVLAGNVIVITLVNRLGV 218
QY 219 LGFLSTGDAQAKNGYGLLDQIQALRWLSENIAHFQGGDPERITIFGSGAGASCVNLLISH 278
DB 219 LGFLSTGDAQAKNGYGLLDQIQALRWLSENIAHFQGGDPERITIFGSGAGASCVNLLISH 278
QY 279 HSEGLFKQALQAGSTALSSVNYQPKYKTRLLAAKVGCDREDSAFAYECLARKPSREL 338
DB 279 HSEGLFKQALQAGSTALSSVNYQPKYKTRLLAAKVGCDREDSAFAYECLARKPSREL 338
QY 339 DQDVQPARVHIAFGPVVGDVDPDDPEILMQQGEFLNYDMLGVNQEGELKFVEDSAESE 398
DB 339 EQIQIPARVHVAFGPVVDGVIDDPEILMQQGEFLNYDMLGVNQEGELKFVEDSAESE 398
QY 399 DGVSAGAFDTVNFVNLGYPEGKDVLRRETIKFWYTDWADRDNGEMRKILLALFTDH 458
DB 399 DGVSAGAFDTVNFVNLGYPEGKDVLRRETIKFWYTDWADRDNGEMRKILLALFTDH 458
QY 459 QWVAPAVATAKLHADYQSPVYFTVYHHCQAEGRPEWADAAGDELPPYVFGVPMVGCATDL 518
DB 459 QWVAPAVATAKLHADYQSPVYFTVYHHCQAEGRPEWADAAGDELPPYVFGVPMVGCATDL 518
QY 519 FPCNFKNDVMSAVVMTYWNFAKTGDPNQPVQDTKFIHTKPNRFEVWVSKNSKEK 578
DB 519 FPCNFKNDVMSAVVMTYWNFAKTGDPNQPVQDTKFIHTKPNRFEVWVSKNSKEK 578
QY 579 QYHLGLKPRVRNRYANKVAFWELVPHLNLHTELF---TTTTLPP-----YATRWPP 631
DB 579 LYHLGLKPRVRNRYANKVAFWELVPHLNLHTELF---TTTTLPP-----YATRWPP 631
QY 632 RPPAGAGTRRRPPPPATLPPPEPEPEPRAYDRFPQDS-----RDYSTELSVTVA 681
DB 632 RPPAGAGTRRRPPPPATLPPPEPEPEPRAYDRFPQDS-----RDYSTELSVTVA 681
QY 682 VGASLLFLNLTAALYALYKRDQERLRLSPGSGSGVPGGGPLLPAAARELPPEE 741
DB 682 VGASLLFLNLTAALYALYKRDQERLRLSPGSGSGVPGGGPLLPAAARELPPEE 741
QY 691 VGASLLFLNLTAALYALYKRDQERLRLSPGSGSGVPGGGPLLPAAARELPPEE 739
DB 691 VGASLLFLNLTAALYALYKRDQERLRLSPGSGSGVPGGGPLLPAAARELPPEE 739
QY 742 LVSLQLKRGSGV-----GADPAALRAPCPDPDTLALRAPDVPVLLAPGALTLPGLG 796
DB 742 LVSLQLKRGSGV-----GADPAALRAPCPDPDTLALRAPDVPVLLAPGALTLPGLG 796
QY 797 PPPPPPPSPHFGPPPPPPPTATSHNNT-LPHPHSHSTRV 835
DB 797 PPPPPPPSPHFGPPPPPPPTATSHNNT-LPHPHSHSTRV 835
QY 796 ---VGLQTLHPYNTF-----AAGENSTGLPHSHSTRV 825
DB 796 ---VGLQTLHPYNTF-----AAGENSTGLPHSHSTRV 825
```

RESULT 6

NLG1 RAT

ID NLG1 RAT

AC Q62765

DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Neurotrophin 1 precursor (Neurotrophin 1)

GN NLG1

OS Rattus norvegicus (Rat)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), PARTIAL SEQUENCE.

CHARACTERIZATION, AND INTERACTION WITH NEUREXIN 1-BETA.

TISSUE=Brain;

MEDLINE=95254653; PubMed=7736595;

Ichchenko K., Hata Y., Nguyen T., Ullrich B., Missler M., Moonaw C., Suedhof T.C.;

"Neurotrophin 1: a splice site-specific ligand for beta-neurexins.";

Cell 81:435-443(1995).

[2]

INTERACTION WITH NEUREXIN 1-BETA, AND FUNCTION.

MEDLINE=97467410; PubMed=9325340;

Nguyen T., Suedhof T.C.;

"Binding properties of neurotrophin 1 and neurexin 1beta reveal function as heterophilic cell adhesion molecules.";

J. Biol. Chem. 272:26032-26039(1997).

[3]

BLOCKAGE OF N-TERMINUS, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN 2-BETA AND NEUREXIN 3-BETA.

MEDLINE=96162010; PubMed=8576240;

Ichchenko K., Nguyen T., Suedhof T.C.;

"Structures, alternative splicing, and neurexin binding of multiple neurotrophins.";

J. Biol. Chem. 271:2676-2682(1996).

[4]

TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.

PubMed=9927700;

Song J.-Y., Ichchenko K., Suedhof T.C., Brose N.;

"Neurotrophin 1 is a postsynaptic cell-adhesion molecule of excitatory synapses.";

Proc. Natl. Acad. Sci. U.S.A. 96:1100-1105(1999).

[5]

TISSUE SPECIFICITY.

PubMed=11329178;

Gilbert M., Smith J., Roskams A.J., Auld V.J.;

"Neurotrophin 3 is a vertebrate gliotactin expressed in the olfactory ensheathing glia, a growth-promoting class of macroglia.";

Glia 34:151-164(2001).

CC -!- FUNCTION: Neuronal cell surface protein thought to be involved in cell-cell-interactions by forming intercellular junctions through binding to beta-neurexins. Seems to play role in formation or maintenance of synaptic junctions. In vitro, triggers the de novo formation of presynaptic structures (By similarity). May be involved in specification of excitatory synapses.

CC -!- SUBUNIT: Interacts with neurexin 1-beta isoforms 3/Beta 4B5A and 4/Beta 4B5B. Interacts with neurexin 2-beta isoforms 3/Beta 4B5A, 4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with corresponding neurexin 3-beta isoforms. Interacts through its C-terminus with DLG4/PSD-95 third PDZ domain (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Enriched in synaptic plasma membranes and clustered in synaptic clefts and postsynaptic densities. Colocalized with DLG4/PSD-95 and NMDAR1/glutamate (NMDA) receptor subunit zeta 1.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;

CC Name=1;

CC IsoId=Q62765-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q62765-2; Sequence=VSP_007531, VSP_007532;

CC Note=No experimental confirmation available;

CC Name=3;

CC IsoId=Q62765-3; Sequence=VSP_007532;

CC Name=4;

CC IsoId=Q62765-4; Sequence=VSP_007531;

CC -!- TISSUE SPECIFICITY: Expressed in brain, almost exclusively in neurons, and spinal chord.

CC -!- DEVELOPMENTAL STAGE: Expression is low in embryonic brains (E12-E16) but increases dramatically after birth (postnatal days P0-P3) and reaches a plateau during the period when most synapses are formed (P5-P8).

CC -!- PTM: N- and O-glycosylated.

CC -!- PTM: The N-terminus is blocked.

CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

CC -----

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U22952; AAA85720.1; --
DR HSP; P37967; 10E3
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000460; Neurotrophin.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLOGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Cell adhesion; Glycoprotein; Signal; Transmembrane;
KW Alternative splicing.
FT SIGNAL 1 45
FT CHAIN 46 843
FT DOMAIN 46 697
FT TRANSMEM 698 718
FT DOMAIN 719 843
FT DISULFID 117 153
FT DISULFID 172 181
FT DISULFID 342 353
FT DISULFID 512 546
FT CARBOHYD 109 109
FT CARBOHYD 303 303
FT CARBOHYD 343 343
FT CARBOHYD 547 547
FT VARSPLIC 165 184
FT VARSPLIC 298 306
FT SEQUENCE 843 AA; 94294 MW; 90A18540245B789D CRC64;
SQ
Query Match 61.5%; Score 2771; DB 1; Length 843;
Best Local Similarity 61.1%; Pred. No. 4.6e-147;
Matches 546; Conservative 100; Mismatches 133; Indels 114; Gaps 21;
QY 1 MW-----LLALCLVLGAGAQGGGPGGPGGLGLGSLG-----LTLCLGLCLQTFHVLSQLDQD 52
DB 7 MWENYVRAMACVV-----HKGSGAP-----LTLCLGLCLQTFHVLSQLDQD 52
QY 42 PVNTAYGRVGRVRELNELIPVQVQFVGYATPTTGARFQPEAPASGPGVGRNAT 101
DB 53 PLVTTFNGKIRGKIKELNELLGPVQVQFVGYATPTTGARFQPEAPASGPGVGRNAT 112
QY 102 LPPACPN-LHGALPALMLPVMTDLNLEAAATVQNSDCILNLYVPTDGPITKED 160
DB 113 FAPVCPQNIIDGLPEVMLPVMTDLNLEAAATVQNSDCILNLYVPTDGPITKED 169
QY 161 EATLNPPDT-----DIRDP-GKKPMLFHGSGYMEGTGNMFDGSLVLAAYGNVIVATLN 213
DB 170 KECARPGKIKRKGIDRSDGGPKPVWYIHGSGYMEGTGNMFDGSLVLAAYGNVIVATLN 229
QY 214 YRLGVLFSTGDAKNGNYGLDQALRWLSENIAHFGDPERITFGSAGASCVNL 273
DB 230 YRLGVLFSTGDAKNGNYGLDQALRWLSENIAHFGDPERITFGSAGASCVNL 289
QY 274 LILSHSE-----GLFQKAIQSGTAISWSVNTQPLKYLRLAAYGCCREDSDAE 324
DB 290 LTLSHYSEGNRWSNPKGLFQALQSGTALSMWVSPQAKYARILATKVCNVSDIVE 349
QY 325 AVECLARKESRELVDQVPARYHIAFGVVDGVDVDDPEILMQGSEFLNMDLIGNVQ 384
DB 350 LVECLQKPEYKELVDQVPARYHIAFGVVDGVDVDDPEILMQGSEFLNMDLIGNVQ 409
QY 385 GEGLEKVEDSDGVSASAFDFTVSNFVDNLYGYPEGKVLRETIKFMVTDNDRNG 444
DB 410 GEGLEKVENIVSDGVSASAFDFTVSNFVDNLYGYPEGKVLRETIKFMVTDNDRNG 469
QY 445 EMRRKTLALFTDHWAPAVATAKLHADYQSVVYFTYTHHCOAEGRPWADAAGDEL 504

DB 470 ETRKTKLALFTDHWAPAVATAKLHADYQSVVYFTYTHHCOAEGRPWADAAGDEL 529
QY 505 PYFVGVMVATDLPFCNFKNDVMSAVVMTYNTFAKTGDPNQVPQDTKFIHKPNR 564
DB 530 PYVLGIPMIGTLPFCNFKNDVMSAVVMTYNTFAKTGDPNQVPQDTKFIHKPNR 589
QY 565 PEEVWSKFNSEKQYLIHGLKPRVDRNRYANKVAFWLELVPHLNLH--TELFTTTTREL 622
DB 590 FEEVATRYSKQQLYLIHGLKPRVKEHYRANKVNLWLELVPHLNLNDISQVSTTTTKV 649
QY 623 PPYATRWPPPPACAGCTRRPPPPAT-----LPPEPEPPGPRAYDRFPDGRDYSTEL 676
DB 650 P--STDITLAP-----TRKNSIPVTSAPFAKQDDPKQSP-----FVSDQEDYSTEL 696
QY 677 SVTVAGASLLFLNLAFALYKRRDRRQELRRLSPGSGSGVGGGGLLPAGREL 736
DB 697 SVTVAGASLLFLNLAFALYKRRDRRQELRRLSPGSGSGVGGGGLLPAGREL 745
QY 737 PPEELVSLQKRGGVGAD-----PAB-ALRPACPPDYTLALRRAPDDVPLAPGAL 788
DB 746 -PEEINSLQKH---TDLDECESIHPHEVVLRTACPPDYTLARRSPDDVPLMTPTNTI 801
QY 789 TLLPSGGLGPPPPPPSLHPFGPPPPPTATSHNNTLPHP-----HSTRV 835
DB 802 TMIPTNTI-----PGIQPLHTFNTF-----TGGQNTLPHPHPHSHSTRV 843

RESULT 7
ID NLG3 HUMAN STANDARD; PRT; 848 AA.
AC Q9NZ94; Q9NZ94; Q9NZ94; Q9NZ94; Q9NZ94; Q9NZ94;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurotrophin 3 precursor (Glycocalyx homolog)
GN NLG3 OR NL3 OR KIAA1480.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
EN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=2021756; PubMed=10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Ginns E.I.;
RT "The structure and expression of the human neurotrophin-3 gene."
RL Gene 246:303-310(2000).
EN [2]
RP SEQUENCE OF 12-848 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirotsawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 7:143-150(2000).
EN [3]
RP SEQUENCE OF 410-848 FROM N.A.
RA Isogai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Maehuo Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EN [4]
RP INTERACTION WITH DLG4.
RX PubMed=9278515;
RA Irie M., Hata Y., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,
RA Takai Y., Rosahl T.W., Suedhof T.C.;
RT "Binding of neurotrophins to PSD-95."
RL Science 277:1511-1515(1997).
EN [5]

NLG3_RAT
 ID NLG3_RAT STANDARD; PRT; 848 AA.
 AC Q62889;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuroligin 3 precursor (Glycactin homolog).
 GN NLGN3.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID:10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4). BLOCKAGE OF N-TERMINUS,
 RP TISSUE SPECIFICITY, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN
 RP 2-BETA AND NEUREXIN 3-BETA.
 RC TISSUE=Forebrain;
 RX MEDLINE=96162010; PubMed=8576240;
 RA Ichchenko K., Nguyen T., Suedhof T.C.;
 RT "Structures, alternative splicing, and neurexin binding of multiple
 RT neuroligins."; J. Biol. Chem. 271:2676-2682(1996).
 RL J. Biol. Chem. 271:2676-2682(1996).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX PubMed=1329178;
 RA Gilbert M., Smith J., Roskams A.J., Auld V.J.;
 RT "Neuroligin 3 is a vertebrate gliotactin expressed in the olfactory
 RT ensheathing glia, a growth-promoting class of macroglia."; Glia
 RL Glia 34:151-164(2001).
 CC -!- FUNCTION: Neuronal cell surface protein thought to be involved in
 CC cell-cell interactions by forming intercellular junctions through
 CC binding to beta-neurexins. May play a role in formation or
 CC maintenance of synaptic junctions. May also play a role in glia-
 CC glia or glia-neuron interactions in the developing peripheral
 CC nervous system.
 CC -!- SUBUNIT: Interacts with neurexin 1-beta isoforms 3/Beta 4B5A and
 CC 4/Beta 4B5B. Interacts with neurexin 2-beta isoforms 3/Beta 4B5A,
 CC 4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with
 CC corresponding neurexin 3-beta isoforms. Probably interacts through
 CC its C-terminus with DLG4/PSD-95 third PDZ domain (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoID=Q62889-1; Sequence=Displayed;
 CC Name=2;
 CC IsoID=Q62889-2; Sequence=VSP_007535; VSP_007536;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoID=Q62889-3; Sequence=VSP_007536;
 CC Name=4;
 CC IsoID=Q62889-4; Sequence=VSP_007535;
 CC -!- TISSUE SPECIFICITY: Expressed in brain, spinal cord and dorsal
 CC root ganglion.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U41663; AAA9781.1; -;
 CC HSSP; P21836; 1MAA.
 CC InterPro; IPR002018; CarboxylesteraseB.
 CC InterPro; IPR000460; Neuroligin.
 CC Pfam; PF00135; COesterase; 1.
 CC PRINTS; PR01090; NEUROLIGIN.
 CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

KW Cell adhesion; Glycoprotein; Signal; Transmembrane;
 KW Alternative splicing.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 848 NEUROLIGIN 3.
 FT DOMAIN 38 709 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 710 730 POTENTIAL.
 FT DOMAIN 731 848 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 141 BY SIMILARITY.
 FT DISULFID 340 351 BY SIMILARITY.
 FT DISULFID 510 544 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 153 172 Missing (in isoform 2 and isoform 4).
 FT VARSPLIC 173 192 Missing (in isoform 2 and isoform 3).
 FT VARSPLIC 192 192 Missing (in isoform 2 and isoform 3).
 FT VARSPLIC 192 192 Missing (in isoform 2 and isoform 3).
 SQ SEQUENCE 848 AA; 93888 MW; 7520653B3253E750 CRC64;
 Query Match 60.9%; Score 2746; DB 1; Length 848;
 Best Local Similarity 61.1%; Pred. No. 1,le-145;
 Matches 538; Conservative 101; Mismatches 138; Indels 104; Gaps 18;
 QY 1 MWLLALCLVGLAGAQRGGGGPGGAPGGGLGLGLGSEERFPVNTAYQVRGVRRLNN 60
 DB 26 LWFSLVL--RASTQ-----APA-----FTVNTFFGLRGARVPLES 60
 QY 61 EILGPPVQFLGVPTATPLGARRFQPEAPASPGVVRNATTLPPACPNLHGALPAIMLP 120
 DB 61 EILGPPVQFLGVPTATPLGARRFQPEAPASPGVVRNATTLPPACPNLHGALPAIMLP 120
 QY 121 VFTDNLAAATVYQNSDCLYLNLYPTD-----GPTFKKD 160
 DB 121 VFTANLDIVATYIQPNEDCLYLVYPTDVKRISKECARPKKKICRGKSGAKQK 180
 QY 161 EATLN--SPDITRDPGKPKVWFLHGSGYEGTGMEDGSLAAYGNVIVATLNRYLG 217
 DB 181 EDLADNDGEDEDIRSGAKPVWYIHGSGYEGTGMIDGSLAAYGNVIVATLNRYLG 240
 QY 218 VLGFSLTGDAKNGYGLLDQALRWLSENIAHFGDPERITIFGSGAGASCVNLLIS 277
 DB 241 VLGFSLTGDAKNGYGLLDQALRWLSENIAHFGDPERITIFGSGAGASCVNLLIS 300
 QY 278 HHSEGLFQKAIQSGTAISSWSVNYQPLKYTRLLAAKVCGRDSDSAEVECLRRKESREL 337
 DB 301 HHSEGLFQKAIQSGTAISSWSVNYQPLKYTRLLAAKVCGRDSDSAEVECLRRKESREL 360
 QY 338 VDQDVOPARVHIAFGPVVDGDDPEILMQGFEPLNDMLGVNQGLKPFVEDSAES 397
 DB 361 VEQDIQPARVHIAFGPVVDGDDPEILMQGFEPLNDMLGVNQGLKPFVEDSAES 420
 QY 398 EDGVSASAFDTVSNFVNDLYGYPEGKDVLRITKPMYTDWADRDNGEMRRTLLALFTD 457
 DB 421 EDGVSAGTDFYSVSNFVNDLYGYPEGKDVLRITKPMYTDWADRDNGEMRRTLLALFTD 480
 QY 458 HQWVAFAVATAKLHADYQSPVYFVTHHCQAEGRPEWADAAGDELVYVFGVPMVGATD 517
 DB 481 HQWVEFSVTVADLHARYGFTFYFAYFHCQSLMKPWSADAAGDEVYVFGVPMVGPTD 540
 QY 518 LFFCNFSKNDVMSLAVVMTYTNFAKTGDPNFPQDTKFIHTKPNRFEVYVMSKFSKE 577
 DB 541 LFFCNFSKNDVMSLAVVMTYTNFAKTGDPNFPQDTKFIHTKPNRFEVYVMSKFSKE 600
 QY 578 KQYLHGLKPRVDNTRANKVAFWLEVLPHNLHTELP---TTTTLRPP---YATRNP 630
 DB 601 QLYLHGLKPRVDNTRANKVAFWLEVLPHNLHTELP---TTTTLRPP---YATRNP 659
 QY 631 PRPPAGAGTRRPPPPATLPPRPEPEPGPRAYDRFPDGS-----RDYSTELSVTV 680
 DB 660 RRPNGKTWSTKRP-----AISPAYSINENAFSGWN---GDQDAGFLLVENPRDSTELSVTV 712
 QY 681 AVGASLLFLNLIAFAALYYKRRRQELCRRLRSLPPGSGSGVGGGLLPAGARELPPEE 740
 DB 713 AVGASLLFLNLIAFAALYYKRRRQELCRRLRSLPPGSGSGVGGGLLPAGARELPPEE 761

Takai Y., Rosahl T.W., Suedhof T.C.;
"Binding of neuroilgins to PSD-95.";
Science 277:1511-1515(1997).
[5]
INTERACTION WITH DLG4, AND TISSUE SPECIFICITY.
PubMed=11368789;
Bolliger M.F., Frei K., Winterhalter K.H., Gloor S.M.;
"Identification of a novel neuroilgin in humans which binds to PSD-95
and has a widespread expression.";
Biochem. J. 355:581-588(2001).
-1- FUNCTION: Putative neuronal cell surface protein involved in cell-
cell-interactions.
-1- SUBUNIT: Interacts through its C-terminus with Dlg4/PSD-95 third
PDZ domain.
-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-1- TISSUE SPECIFICITY: Expressed at highest levels in heart.
Expressed at lower levels in liver, skeletal muscle and pancreas
and at very low levels in brain.
-1- DISEASE: Defects in NLGN4 may be the cause of X-linked autism
[MIM:300425]; a pervasive developmental disorder (PDD),
prototypically characterized by impairments in reciprocal social
interaction and communication, restricted and stereotyped patterns
of interests and activities, and the presence of developmental
abnormalities by 3 years of age.
-1- DISEASE: Defects in NLGN4 may be the cause of Asperger syndrome
(AS), a form of childhood autism.
-1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

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or send an email to license@isb-sib.ch.

EMBL; AF376803; AAM46112.1; -;
EMBL; AB033086; BAA86574.1; ALT_INIT.
EMBL; BC034018; AAH34018.1; -;
HSP; P21836; IMAA.
Genew; HGNC:14287; NLGN4.
MIM; 300427; -;
MIM; 300425; -;
InterPro; IPR002018; Carboxesterase.
InterPro; IPR000460; Neuroilgin.
InterPro; IPR000379; Ser estrs_site.
Pfam; PF00135; Coesterase; 1.
PRINTS; PR01090; NEUROILGIN
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
Cell adhesion; Glycoprotein; Signal; Transmembrane.
SIGNAL 1 43
CHAIN 44 816
DOMAIN 44 676
TRANSMEM 677 697
DOMAIN 698 816
DOMAIN 110 146
DISULFID 306 317
DISULFID 476 510
CARBOHYD 102 102
CARBOHYD 511 511
SEQUENCE 816 AA; 91915 MW; EAL320D690F76BBD CRC64;
Query Match 60.2%; Score 2713.5; DB 1; Length 816;
Best Local Similarity 63.6%; Pred. No. 7e-144;
Matches 520; Conservative 96; Mismatches 139; Indels 63; Gaps 13;
38 EERFPVVNTAYGKVGVRRELNNELIGLWQVFLGVPVATPPLGARRQPPEAFASWPGVR 97
42 QAQYFVVNTYNGKIGRLTFLPNEILGVFEQYLGVPVATPPTGRRQPPEPSSWTGIR 101
98 NATTLPPACPQML-HGALPAIMLPVFTNDILEAATVYQNOSEDCLYLNIVPTDGLPT 156
102 NTPQFAAVCPQHLDRSLIHDMLPFTWFTANLDTLMTVYQDQNECLYNIYVPTD --- 157

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QY 157 KKEDENTLNPPTDIRDP-GKPVMLFLHGSGYMEGTGNMFDGSLVLAAYGNVIVATLNYR 215
Db 158 -----DHDQNSKKPVNVYIHGSGYMEGTGNMFDGSLVLAAYGNVIVATLNYR 204
QY 216 LGVLGFLSTGDAQAAGNYGLLQICQALRWLSNIAHFGGDPERITIFGSGAGASCWLLI 275
Db 205 LGILGFLSTGDAQAAGNYGLLQICQALRWLSNIAHFGGDPERITIFGSGAGASCWLLI 264
QY 276 LSHHSEGLFQKAIASGTAISSWVNYQPLKTRLLAAKVGCDREDSAEAVECLRRKPSR 335
Db 265 LSHYSEGFLQKAIISGTAISSWVNYQPAKTRILADKVGCMMLDITDYMVECLRNKNYK 324
QY 336 ELVDQDVQPARVHIAFGVPVGDGVDDPEILLMOQGEFLNMDLGVNQGSLGFVEDSA 395
Db 325 ELIQTITPATVHIAFGVVDGVDVDPDPOILMEQGEFLNMDLGVNQGSLGFVEDGIV 384
QY 396 ESDGVSAFDTVSNFVNDLVYGPBGKVLRETIFKMYTDMADRDNGEMRKTLLALF 455
Db 385 DNEGDGVTNDFSVSNFVNDLVYGPBGKVLRETIFKMYTDMADRDNGEMRKTLLALF 444
QY 456 TDHOMVAPAVATAKLHADYQSPVYEVTVHHCOAGREPEWADAAGDELPTVFGVPMUGA 515
Db 445 TDHOMVAPAVATAKLHADYQSPVYEVTVHHCOAGREPEWADAAGDELPTVFGVPMUGA 504
QY 516 TDLFFCNFSKNDVMSAVVMTYNTFAKTGDPNPQVQDTKFIHTKPNRFEVVWSKFN 575
Db 505 TELFCNFSKNDVMSAVVMTYNTFAKTGDPNPQVQDTKFIHTKPNRFEVVWSKFN 564
QY 576 KEKQVHLGLKPRVDNRYANKVAFWELVPLHLNHLTELF-----TTTTRLP 625
Db 565 KDQLYLHLGLKPRVDNRYANKVAFWELVPLHLNHLN-EIFQYVSTTTKVPDPMTSFF 623
QY 626 ATRWPPPPAGG-POTRPPPPATLPPPEPEP-----GPRVDRFPDGRSDYSTLSVTVA 681
Db 624 GTR-----RSPAKWPTTKPATPANPKSKDPKHTGPDVTVLIEKXDYSTLSVTIA 680
QY 682 VGASLLFLNLAFAALYKRRDRQELRCRLSPGGSGGVGGPGLLPAAAGRELPEEE 741
Db 681 VGASLLFLNLAFAALYKRRDRQELRCRLSPGGSGGVGGPGLLPAAAGRELPEEE 728
QY 742 LVSLOLQK-----GGGVGADPAELRFPACPDYTLALRAPDDVPLAPGALTLPGLSP 797
Db 729 LMSLOKLEHDEHCESELAQHTLRLTCTPDYTLRLRSPDDIFLMTPTNITMPTLTG 788
QY 798 PPPPPPLHFGPPPPPPPTATSHNNTLPHPHSTTRV 835
Db 789 MQP-----LHTFNTF-----SGGQNSTLPHGHSTTRV 816

RESULT 10
NLGY HUMAN
ID NLGY HUMAN STANDARD; PRT; 816 AA.
AC Q8NFZ3; Q9Y2F8;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuroigin 4, y linked precursor (Neuroigin y).
GN NLGN4Y OR KIAA0951.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX PubMed=12669065;
RA Jamin S., Quach H., Betancur C., Rastam M., Colineaux C.,
RA Gillberg I.C., Soderstrom H., Gjos B., Leboyer M., Gillberg C.,
RA Bourgeron T., Nyden A., Philippe A., Cohen D., Chabane N.,
RA Mourén-Simeoni M.C., Brice A., Sponheim E., Spurkland I.,
RA Skjeldal O.H., Coleman M., Pearl P.L., Cohen I.L., Teisuris J.,
RA Zappella M., Menchetti G., Pompella A., Aschauer H., Van Maldergem L.;
RT "Mutations of the X-linked genes encoding neuroiggins NLGN3 and NLGN4
```

```
RT are associated with autism.";
RL Nat. Genet. 34:27-29(2003).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=99246063; PubMed=10231032;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hiroseawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
CC -I- FUNCTION: Putative neuronal cell surface protein involved in cell-
CC cell-interactions.
CC -I- SUBUNIT: Interacts through its C-terminus with DLG4/PSD-95 third
CC PDZ domain (by similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8NFZ3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8NFZ3-2; Sequence=VSP_007537;
CC Note=No experimental confirmation available;
CC -I- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF376804; AAM46113.1; --
CC EMBL; AS023168; BAA76795.1; --
CC InterPro; IPR002018; Carboxylesterase.
CC InterPro; IPR000460; Neuroigin.
CC InterPro; IPR000379; Ser esterase site.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR01090; NEUROIGIN.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Cell adhesion; Glycoprotein; Signal; Transmembrane;
KW Alternative splicing.
FT SIGNAL 1 43
FT CHAIN 44 816
FT DOMAIN 44 676
FT TEASSEM 677 697
FT DOMAIN 698 816
FT DISULFID 110 146
FT DISULFID 306 317
FT DISULFID 476 510
FT CARBOHYD 511 511
FT VARSPIC 1 168
SQ SEQUENCE 816 AA; 92020 MW; FB68910773B1BBF6 CRC64;

Query Match 59.4%; Score 2678.5; DB 1; Length 816;
Best Local Similarity 62.7%; Pred. No. 6.2e-142;
Matches 513; Conservative 101; Mismatches 141; Indels 63; Gaps 13;

QY 38 ERFVNTAYGRVGRVRELNNEILGPVQPLGVYATPPLGARRFQPPAPASWPGVR 97
Db 42 QAYFVNTYKIQGLRTPLESEILGPVQYLVYASPTTGERFQPPSPSSWTGIR 101
QY 98 NATTLPPACQNL-HGALPALMPVWTDNLEAAATVYQNOSEDCLNLYVPTDGLT 156
Db 102 NATQSAVCPQHLDERFLHMLPFWFTSLDTLMTYVQDQDCLNLYVPMED---- 157
QY 157 KKRDEATLNPPTDIRDP-GKPVMLFLHGSGYMEGTGNMFDGSLVLAAYGNVIVATLNYR 215
Db 158 -----DIHEQNSKKPVNVYIHGSGYMEGTGNMFDGSLVLAAYGNVIVATLNYR 204
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Qy 216 LGVIGLSTGDAAGNKGILLDQIQALRWLSENIAHFGGDPERITIFGSGAGASCNLLI 275
 Db 205 LGILGFLSTGDAAGNKGILLDQIQALRWLSENIAHFGGDPKRVITIFGSGAGASCNLLI 264
 Qy 276 LSHHSGFLGKATAQSGTALSSVSNVQPLKYTRLLAAKVGCDREDSAAVECLARKPSR 335
 Db 265 LSHYSEGLFQKALIQSGTALSSVSNVQPYFRIILADKVGCMNLTDTMDVCLXKNYK 324
 Qy 336 ELVDQVQPARYHIAFGPVVDGWDVDDPEILMQGFEFLNMDLIGVNOGEGELKFVEDSA 395
 Db 325 ELTCQITPATYHIAFGPVVDGWDVDDPEILMQGFEFLNMDLIGVNOGEGELKFVDGIV 384
 Qy 396 ESDGVSASAFDTVSNFVNLVYEGEGKDVJRETIKFMYTOWADNCGEMRKLLALF 455
 Db 385 DNEBGTVPNDFDSVSNFVNLVYEGEGKDVJRETIKFMYTOWADNCGEMRKLLALF 444
 Qy 456 TDHGWAPAVATAKLHADYQSPVYFVYHHCQAEGRPEWADAAGDELPPYVFGPMVGA 515
 Db 445 TDHGWAPAVATAKLHADYQSPVYFVYHHCQAEGRPEWADAAGDELPPYVFGPMVGA 504
 Qy 516 TDLFPNCFKNDYMLSAVMTYTNFAKTGDPNPQVPODTKFIHTKPNRFEVVMKNS 575
 Db 505 TELFSCNFSKNDYMLSAVMTYTNFAKTGDPNPQVPODTKFIHTKPNRFEVVMKNS 564
 Qy 576 KEQYLIHGLKPRVDRYRANKVAFWLELPHLNLHTELF---TTTTLP-----PY 625
 Db 565 KDQLYLHGLKPRVDRYRANKVAFWLELPHLNLHTELF---TTTTLP-----PY 623
 Qy 626 ATWRPFRPPAGA-PGTRRRPPPPATLPPEPEPEP---GPRAYDRFPDGRDYSDELSTVVA 681
 Db 624 GTR---RSPAKIWTYTKRAITANNPKSKDHKTGPEDTIVTLTKDYDELSTVVA 680
 Qy 682 VGASLFLNLFAALYKXDRQELRCRLSPGGSGVPGGGLPPLPAGRELPPEE 741
 Db 681 VGASLFLNLFAALYKXDRQELRCRLSPGGSGVPGGGLPPLPAGRELPPEE 728
 Qy 742 LVSLQKLR---GGVGADPAEALRACPDYTLALRRAPDVLAPCALTLPSGLP 797
 Db 729 IMSLQKLEHDECSLQNHDLRLTCTPDYTLALRRAPDVLAPCALTLPSGLP 788
 Qy 798 PPPPPPLPHFGFPFPPPTATSHNLTLPHPHSTTV 835
 Db 789 MQP-----LHTKFTF-----SGGQSNLPHGSHSTTV 816

RESULT 11
 CHLE HORSE
 ID CHLE HORSE STANDARD; PRT; 574 AA.
 AC P81908;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cholinesterase (EC 3.1.1.8) (Acetylcholine acylhydrolase) (Choline
 esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (EQ-
 3N BCHE).
 DE 3N BCHE.
 CS Equis caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CX NCBI_TaxID=9796;
 RN [1]
 RN SEQUENCE.
 RC TISSUE=Plasma;
 RA Moorad D.R., Luo C., Garcia G.E., Doctor B.P.;
 RT "Amino acid sequence of horse serum butyrylcholinesterase.";
 RL (In) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.I., Gentry M.K.
 RL (eds.);
 RL Structure and function of cholinesterases and related proteins,
 RL pp.145-146, Plenum Press, New York and London (1998).
 CC -i- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -i- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO DIMERS. THE

CC TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.
 CC -i- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
 CC -i- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
 CC ORGANOPHOSPHATE ESTERS.
 CC -i- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR HSP2; P21836; IMAA.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser_estra_site.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS0094; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase; Serine esterase; Glycoprotein.
 FT ACT SITE 198
 FT ACT SITE 325
 FT ACT SITE 438
 FT ACT SITE 438
 FT DISULFID 65
 FT DISULFID 92
 FT DISULFID 252
 FT DISULFID 263
 FT DISULFID 400
 FT DISULFID 571
 FT DISULFID 571
 FT CARBOHYD 57
 FT CARBOHYD 106
 FT CARBOHYD 241
 FT CARBOHYD 241
 FT CARBOHYD 256
 FT CARBOHYD 341
 FT CARBOHYD 341
 FT CARBOHYD 455
 FT CARBOHYD 481
 FT CARBOHYD 486
 FT CARBOHYD 486
 SQ SEQUENCE 574 AA; 65641 MW; 07755EE9FB9CB33E CRC64;
 Query Match 19.18; Score 859; DB 1; Length 574;
 Best Local Similarity 33.4%; Pred. No. 7.6e-41;
 Matches 203; Conservative 100; Mismatches 229; Indels 76; Gaps 15;
 Qy 43 VNTAYGRVRRELNNEIL-GEVQVGLGVVATPPGLARRFQPPAPAPSGVNRATT 101
 Db 5 IITTKNGKVRG---MNLPLVGLGTVTAFLGIPYAAQPLGLRFRKPKQSLTKWSNINWATK 60
 Qy 102 LPPACPNLHGLPAIMLPVWFDTNLEAAATYVQNSQEDCLYLNLYVPTEDGFLTKRDE 161
 Db 61 YANSCYQNTQSPFGLGSEMNPTEL-----SEDCLYLNWIPAP----- 102
 Qy 162 ATLNPPTDIRDPKPKVPLFLHGGSVMEGTGMN--FDGSLVLAAYGNVIVATLYRLGLVL 219
 Db 103 -----KPKNAVMIWYGGGFQGTGTSLSPLVYDGFARVERVIVSNRYRGAL 151
 Qy 220 GFLSTGDPQ-AAKNYGLLDQIQALRWLSENIAHFGGDPERITIFGSGAGASCNLLILSH 278
 Db 152 GFLALSENPEAPGNMGLFDQQLALQWQKNIAAFGGNPRSVTLFGESAGAASVSLHLLSP 211
 Qy 279 HSEGLFQKATAQSGTALSSVSNV--YQPLKYTRLLAAKVGCDREDSAAVECLARKPSRE 336
 Db 212 RSQPLFTFRLIQSGSNAPWAVTSLYEARVNTTLAKRMCGSRDNETEMTKLRDKDQPE 271
 Qy 337 LVDDQVQPARY---HIAFGPVVDGWDVDDPEILMQGFEFLNMDLIGVNOGEGELKFVE 392
 Db 272 ILLNEVFWPVYDTLLSVNFGPTVDGFLTDMPDTLLQGLQKTKQILVGNKDEGTAFV 331
 Qy 393 DSAB--SEDGVSASAFDTVSNFVNLVYEGEGKDVJRETIKFMYTOWADNCGEMRK 449
 Db 332 YGAFGFSKDNNSI-----ITRKEFQEGELKIFPFRVSEFGRESILFYHMDWLDQDAENYRE 387
 Qy 450 TLLALFTDHWAPAVATAKLHADYQSPVYFVYHHCQAEGRPEWADAAGDELPPYVFG 509
 Db 388 ALDDVGDYNIICPALEFTRKFSLELGNDAFFYFEHRSTKLPHPEWGMVHGVEIEBFVG 447
 Qy 510 VPMVGATDLFPNCFKNDYMLSAVMTYTNFAKTGDPNPQVPODTKFIHTKPNRFEV 569
 Db 448 LPLERRV-----NYTRAEEILSRIMKRWANFAKYGPNPGTQNNSTR----- 489
 Qy 570 WSKNSKSEKQYLIHGLK-PRVDRYRANKVAFW-----LELVPHLNLHTELF----- 621

DE (Choline esterase II) (Butyrylcholine esterase)
 GN (Pseudocholinesterase).
 GN BCHE OR CHEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=90212557; PubMed=2325535;
 RX Arpagaus M., Kott M., Varsis K.P., Bartels C.F., la Du B.N.,
 RA Lockridge O.;
 RA "Structure of the gene for human butyrylcholinesterase. Evidence for
 RT a single copy";
 RL Biochemistry 29:124-131(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Fetal;
 RC TISSUE=Fetal;
 RX MEDLINE=87231856; PubMed=3035536;
 RA Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreq H.;
 RT "Isolation and characterization of full-length cDNA clones coding for
 RT cholinesterase from fetal human tissues";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC TISSUE=Brain;
 RX MEDLINE=88016155; PubMed=3477799;
 RA McTiernan C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,
 RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.;
 RT "Brain cDNA clone for human cholinesterase";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Skin;
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Hopkins R.F., Zeeb B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN SEQUENCE OF 29-602.
 RP TISSUE=Plasma;
 RC TISSUE=Plasma;
 RX MEDLINE=87109144; PubMed=3542989;
 RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
 RA Johnson L.L.;
 RA "Complete amino acid sequence of human serum cholinesterase";
 RL J. Biol. Chem. 262:549-557(1987).
 RN [6]
 RN DISULFIDE BONDS.
 RP MEDLINE=88007487; PubMed=3115973;
 RX Lockridge O., Adkins S., la Du B.N.;
 RA "Location of disulfide bonds within the sequence of human serum
 RT cholinesterase";
 RL J. Biol. Chem. 262:12945-12952(1987).
 RN [7]
 RN REVIEW.
 RP MEDLINE=89149759; PubMed=3067729;

RA Lockridge O.;
 RT "Structure of human serum cholinesterase";
 RL Bioessays 9:125-128(1988).
 RN [8]
 RN VARIANT ATYPICAL GLY-98.
 RP MEDLINE=89128896; PubMed=2915989;
 RX McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
 RA van der Spek A.F.L., Lockridge O., la Du B.N.;
 RA "Identification of the structural mutation responsible for the
 RT dibucaine-resistant (atypical) variant form of human serum
 RT cholinesterase";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
 RN [9]
 RN VARIANT ILE-358.
 RP MEDLINE=96287386; PubMed=8680411;
 RX Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
 RA Moriaki K.;
 RT "Mutations of human butyrylcholinesterase gene in a family with
 RT hypocholinesterasemia";
 RL Hum. Mutat. 6:349-351(1995).
 CC -|- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC -|- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED
 CC OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A
 CC DISULFIDE BOND.
 CC -|- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
 CC -|- DISEASE: MUTANT ALLELES OF CHE1 ARE RESPONSIBLE FOR
 CC HYPOCHOLINESTERASEMIA RESULTING IN SUXAMETHONIUM SENSITIVITY.
 CC HOMOCYGOTUS PERSONS SUSTAIN PROLONGED APNEA AFTER ADMINISTRATION
 CC OF THE MUSCLE RELAXANT SUXAMETHONIUM IN CONNECTION WITH SURGICAL
 CC ANESTHESIA.
 CC -|- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
 CC ORGANOPHOSPHATE ESTERS.
 CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC
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 CC
 CC EMBL; M32391; AAA99296.1; -;
 CC EMBL; M32389; AAA99296.1; JOINED.
 CC EMBL; M32390; AAA99296.1; JOINED.
 CC EMBL; M16541; AAA98113.1; -;
 CC EMBL; M16474; AAA52015.1; -;
 CC EMBL; BC018141; AAH18141.1; -;
 CC PIR; A33769; ACU.
 CC PDB; IEHQ; 08-AUG-01.
 CC PDB; IEHQ; 08-AUG-01.
 CC Genew; HGNC:983; BCHE.
 CC MIM; 177400; -;
 CC GO; GO:0004104; F:cholinesterase activity; TAS.
 CC InterPro; IPR002018; CarboxylesteraseB.
 CC InterPro; IPR000997; Cholinesterase.
 CC InterPro; IPR000379; Ser_setra_site.
 CC Pfam; PF00135; Coesterase; 1.
 CC PRINTS; PR00878; CHOLINESTERASE.
 CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 CC Hydrolase; Serine esterase; Glycoprotein; Signal; Disease mutation;
 CC Polymorphism; 3D-structure.
 CC SIGNAL 1 28
 FT CHAIN 29 602 CHOLINESTERASE.
 FT ACT SITE 226 226 BY SIMILARITY.
 FT ACT SITE 353 353 BY SIMILARITY.
 FT ACT SITE 466 466 BY SIMILARITY.
 FT DISULFID 93 120
 FT DISULFID 280 291
 FT DISULFID 428 547
 FT DISULFID 599 599 INTERCHAIN.

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EMBL; X56518; CAA39867.1; -.
EMBL; AF312033; AAK28816.1; -.
PIR; JH0314; JH0314.
PDB; 1MAH; 03-APR-96.
PDB; 1MAA; 20-APR-99.
PDB; 1C28; 29-DEC-99.
PDB; 1C20; 19-JAN-00.
PDB; 1J06; 04-FEB-03.
PDB; 1J07; 04-FEB-03.
PDB; 1NEM; 04-FEB-03.
PDB; 1NSR; 04-FEB-03.
MGD; MGI:87876; Ache.
GO; GO:0045202; C:synaptic junction; IDA.
InterPro; IPR002018; Carboxylesterase.
InterPro; IPR000937; Cholinesterase.
InterPro; IPR000379; Ser esterase site.
Pfam; PF00135; Coesterase; 1.
PRINTS; PR00878; CHOLINESTERASE.
PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00441; CARBOXYLESTERASE_B_2; 1.
Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
Neurotransmitter degradation; Glycoprotein; Alternative splicing;
3D-structure.
1 31
2 CHAIN 32 614
3 ACT_SITE 234 234 ACETYLCHOLINESTERASE.
4 ACT_SITE 365 365
5 ACT_SITE 478 478
6 DISULFID 100 127
7 DISULFID 288 303
8 DISULFID 440 560
9 DISULFID 611 611
10 CARBOHYD 286 286
11 CARBOHYD 381 381
12 CARBOHYD 495 495
13 HELIX 37 39 INTERCHAIN (BY SIMILARITY).
14 STRAND 40 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
15 TURN 44 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
16 STRAND 46 49
17 TURN 51 55
18 STRAND 56 57
19 STRAND 58 67
20 STRAND 69 69
21 HELIX 74 76
22 TURN 77 78
23 STRAND 83 83
24 STRAND 90 92
25 STRAND 94 94
26 STRAND 99 100
27 TURN 109 110
28 HELIX 112 115
29 TURN 116 117
30 STRAND 123 124
31 STRAND 129 135
32 STRAND 143 149
33 TURN 153 155
34 TURN 159 160
35 HELIX 162 164
36 HELIX 166 173
37 STRAND 176 180
38 HELIX 185 189
39 TURN 193 194
40 HELIX 202 217
41 HELIX 218 221
42 TURN 222 222

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FT STRAND 223 233
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FT HELIX 557 564
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FT TURN 574 576
SQ SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;

Query Match 18.9%; Score 852; DB 1; Length 614;
Best Local Similarity 33.3%; Pred. No. 2e-40;
Matches 207; Conservative 96; Mismatches 235; Indels 83; Gaps 17;

Qy 31 LGGLSLGEERFP---VNTAYGEVGVRELNNEILGPVVQELGVPEYATPEPLGAREFQPP 87
Db 25 LGGGARAREGREDPQLLVVRGGQLRGLKAPG---GPVSAFLGIPFAEPFVGSRFPNP 81
Qy 88 EAPASWPGVRNATLPPACPNQLHGPALPAIMLPWFPTDNLAAATYVQNSDCLYLNLY 147
Db 82 EPKRPMWGVLDATTFQNVCVQYVDTLPGFEGTEWMPNREL-----SEDCLYLVNW 133
Qy 148 VPTDGLTKRDEATLNPPDITRDPKPKVMLFLHGSYMEGTGNM--FDGSVLAAVG 205
Db 134 TTPY-----RPASPTPLVIWYGGFGYSGAASLDVYDGRFLAQVE 173
Qy 206 NVIVATLNRYRLGVIGFLS-TGDOAAKNTGLLDQIOALRWLSENTIAHFGGDPERITIFGS 264
Db 174 GAVLSMNYRVGCTFGFLALPGSREAPGNVGLDQRLALQWQENIAAFGGDDPMSVTLFGE 233
Qy 265 GAGACVNLILLSHHSEGLFQKAIAGSGTAISWSV--NYQPLKYTRLLAAKVGCD----- 318
Db 234 SAGAAASVGMHILSLPSRSLFHRVAVLQSGTPNGPWATVSAGARRRATLLARLVGCPGGA 293
Qy 319 REDSAEAECLRKPSRELVDQD-----VQPARVHIAFGFVWDGVDVDPDPEILMQQGEFL 374

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Db 294 GNDTELIACTRAQDLVDHEWHLVQESIFRFSFVVDGDFSLSTPEALINTGDFQ 353
QY 375 NYDMLIGNVQSGELKFV-----EDSAESEDGVSASAFDTYSNFVDNLYGYPEGKDVLR 429
Db 354 DLQVLGVGVKDEGSYFLVGVGFSKDNESLISRAQFLAGVR-----IGVPGASDLAAE 407
QY 430 TIKFWYTOWADRDNGEMERKILLALFTDHWVAPAVATAKLHADYQSPVYTYTHHCQA 489
Db 408 AVLHYITDWHPEEDTHURDAMSAVGVHNVVCPVQAQLAGLAAQAGARVAYIIEHRAST 467
QY 490 EGRPEWADAADDELYFVGVGPMVGATDLFCNFSKNDVMSLVAVMTYWTNFAKTGDPNQ 549
Db 468 LTMPLMWGVPHGYEYEFGLPLDPS-----LNYTTERIIRAQLMKYWTNFAKTGDPND 522
QY 550 PVPQTKIHTKPNRPFVEVWSKFSKQYLHGLKP-RVVDNVRANKVAFWELVPHL 608
Db 523 --PRDSK-----SPQ-----WPPYTTAAQQYVSLMLKPLEVRGLRAQTCAFMNRFLP-- 568
QY 609 HNLHTELETTTTRLPYPATRW 629
Db 569 -----KLISATDTLDEAEQW 584

RESULT 15
ACES_RAT
ID ACES_RAT STANDARD, PRT; 614 AA.
AC P37136;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN ACHE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM T).
RX MEDLINE=93107932; PubMed=8417155;
RA Legay C., Bon S., Vernier P., Coussein F., Massoulie J.;
RT "Cloning and expression of a rat acetylcholinesterase subunit;
RT generation of multiple molecular forms and complementarity with a
RT Torpedo collogenec subunit.";
RL J. Neurochem. 60:337-346 (1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS H AND R).
RX MEDLINE=93114454; PubMed=8417973;
RA Legay C., Bon S., Massoulie J.;
RT "Expression of a cDNA encoding the glycolipid-anchored form of rat
RT acetylcholinesterase.";
RL FEBS Lett. 315:163-166 (1993).
CC -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-
CC TAILED), WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES
CC OF KNOWN ACHE FORMS.
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=3;
CC Name=T;
CC Name=H;
CC IsoId=P37136-1; Sequence=Displayed;
CC IsoId=P37136-2; Sequence=VSP_001458;
CC Name=R;
CC IsoId=P37136-3; Sequence=VSP_001459;
CC Note=May be not functional;
CC -!- TISSUE SPECIFICITY: HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND
CC MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT
CC LIVER.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S50879; AAB24586.1; -
CC EMBL; X70140; CAA49717.1; -
CC EMBL; X70141; CAA49718.1; -
CC PIR; JH0811; JH0811.
CC HSP; P21836; 1MAA.
CC InterPro; IPR002018; Carboxylesterase.
CC InterPro; IPR000997; Cholinesterase.
CC InterPro; IPR000379; Ser esters_site.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR00878; CHOLNESTRASE.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
CC Neurotransmitter degradation; Glycoprotein; Alternative splicing.
CC SIGNAL 1 31 POTENTIAL.
CC CHAIN 32 614 ACETYLCHOLINESTERASE.
CC ACT_SITE 234 234 BY SIMILARITY.
CC ACT_SITE 365 365 BY SIMILARITY.
CC ACT_SITE 478 478 BY SIMILARITY.
CC DISULFID 100 127 BY SIMILARITY.
CC DISULFID 288 303 BY SIMILARITY.
CC DISULFID 440 560 BY SIMILARITY.
CC DISULFID 611 611 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 296 296 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 381 381 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 495 495 N-LINKED (GLCNAC...) (POTENTIAL).
CC VARSPIC 575 614 DTLDEARQWKAERFRWSSYVHWKQFDHSHKQRCSDL
CC -> ATEVPCTCPAAGHGAAPRGPALSLDLFLFLHSG
CC LRM (in isoform H).
CC /FTIC-VSP_001458.
CC FT VARSPLIC 575 614
CC DTLDEARQWKAERFRWSSYVHWKQFDHSHKQRCSDL
CC isoform R)
CC /FTIC-VSP_001459.
CC SEQUENCE 614 AA; 68196 MW; 2EDAE7D46292E7C0 CRC64;
Query Match 18.8%; Score 846.5; DB 1; Length 614;
Best Local Similarity 33.0%; Pred. No. 4.1e-40;
Matches 205; Conservative 98; Mismatches 235; Indels 83; Gaps 17;
QY 31 LGLSLGEERFP---VVNTAYGRVGVRELNELILGPVQFLGVYATPPLGARFQPP 87
Db 25 LGGGAAREGDPQLLVVRVGGQLRGIRLKAPG---GPVSAPLGIPIFAEPVPSRRFPP 81
QY 88 EAPASWPGVRNATLPPACPQMLHGALPAIMLPVWFTDNLAAATVQNSDCLYLNLY 147
Db 82 EPKRPSGLDATTQNVCYQVVDLYPGFEGTEMWPNREL-----SEDCLYLNW 133
QY 148 VTEOPLTKGDEATLPPDITDIDPKKPVMLFHGGSYMEGTGM--PDGSLVLAAYG 205
Db 134 TYP-----RPTSPTPLIWIYGGFGYSGASSLDVVDGRLAQVE 173
QY 206 NVIVATLNYRLGVGLFS-TGDOAAKNGVGLDQALRWLSENIAHFQGPERRITFGS 264
Db 174 GTVLVSMYRVGTGFLALPGSREAPGVNGLDQRLALQWQENIAAEGDPMSTLGE 233
QY 265 GAGACVNLILSHSEGLFQKAIQSGTAISSMSV--NYQPLKYTRLLAAKVGCD---- 318
Db 234 SAGAAVGMHILSPRSILFRAVLQSGTPNGPNWATVSAGEARRATLLARLVGPPGA 293
QY 319 REDSAEAECELRKPSRELVDQD---VQPARYHTAFGVVDGVVDVDDPEILMQGSEFL 374
Db 294 GGNDELISCLNTRPAQLVDHEWHLVQESIFRFSFVVDGDFSLSTPEALINTGDFQ 353
QY 375 NYDMLIGNVQSGELKFV-----EDSAESEDGVSASAFDTYSNFVDNLYGYPEGKDVLR 429

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Db	354	DLOVLGVWVDEGSYFLVYGVPGFSKDNEISRAQFLAGVR-----ICVPOASDLAAE	407
Qy	430	TIKEMYTDWADRDNGEMRRKTLALFTDHOVAPAVATAKLHADYQSPVYFYTFYHHCOA	489
Db	408	AVLHYTDWLHPEDPAHLRDAMSAVVGDHNVCPVAQLAGRLAAQGARVYAYIFEHRAS	467
Qy	490	EGRPEWADAAHGDELPHYGVPMVGATDLEPCNFSKNDVMSAVVMYTNFAKTGDPNQ	549
Db	468	LTWPLMWGVPHGYEIEFIFGLPLDPS-----LNYTVEERIFAQRLAQYWTNFARTGDPND	522
Qy	550	PVPQDTKFIHTKPNRPEEVVWSKFNSKEKOYLHGLKP-RVRDNYRANKVAFWLELVPHL	608
Db	523	--PRDSK-----SPR-----WPPYTTAAQQYVSINLKPLEVRRLRAQTCAFWNRFLP--	568
Qy	609	HNLHLELFTTTTLRPPYATEW	629
Db	569	-----XLSATDTLDEAERQW	584

Search completed: February 13, 2004, 13:12:38
Job time : 19 secs

GenCore version 5.1.1.6
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CM protein - protein search, using sw model

Run on: February 13, 2004, 13:09:47 ; Search time 46 Seconds
(without alignments)
4684.216 Million cell updates/sec

Title: US-09-934-323-2

Perfect score: 4508
Sequence: 1 MWLLALCLVLGLAGAQGGGG.....PPTATSHNNLTLPHPHSTTRV 835

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_virus.*

16: sp_bacteriap.*

17: sp_archesp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4508	100.0	835	4 Q8NFZ4	Q8nfz4 homo sapien
2	4415.5	97.9	836	11 Q62888	Q62888 rattus norv
3	2986	66.2	550	4 Q9P211	Q9p211 homo sapien
4	2773.5	61.5	825	11 Q8BYM5	Q8bym5 mus muscucu
5	2771	61.5	843	11 Q62765	Q62765 rattus norv
6	2770	61.4	828	4 Q9NZ94	Q9nz94 homo sapien
7	2765.5	61.3	823	4 Q9UPT2	Q9upt2 homo sapien
8	2763	61.3	828	4 Q9N297	Q9n297 homo sapien
9	2750	61.0	848	4 Q9NZ95	Q9nz95 homo sapien
10	2746	60.9	848	11 Q62889	Q62889 rattus norv
11	2713.5	60.2	816	4 Q8N0W4	Q8n0w4 homo sapien
12	2713.5	60.2	817	4 Q9ULG0	Q9ulg0 homo sapien
13	2678.5	59.4	816	4 Q8NFZ3	Q8nfz3 homo sapien
14	2344	52.0	682	4 Q9P248	Q9p248 homo sapien
15	2287	50.7	648	4 Q9Y2F8	Q9y2f8 homo sapien
16	1999	44.3	558	4 Q9NZ96	Q9nz96 homo sapien

Q8n2q7 homo sapien
Q8bxr4 mus muscucu
Q8ncd0 homo sapien
Q9ngk5 drosophila
Q9vic5 drosophila
Q9nlh9 equus cabal
Q9vic7 drosophila
Q9nld1 gorilla gor
Q9vdp5 drosophila
Q8row5 mus muscucu
Q46421 macaca fasc
Q9jkc1 rattus norv
Q7540 oryctolagus
Q87582 sus scrofa
Q62760 felis silve
Q8r097 mus muscucu
Q9up41 homo sapien
Q62761 panthera ti
P70104 cavia porce
Q6e88 homo sapien
Q90xk8 gallus gall
Q95n05 canis fami
Q16398 homo sapien
Q64571 rattus norv
Q8i034 felis silve
Q76998 brachiosto
Q8td29 homo sapien
Q9uk77 homo sapien
Q8ism4 anopheles g

ALIGNMENTS

RESULT 1

Q8NFZ4
ID Q8NFZ4 PRELIMINARY; PRT; 835 AA.
AC Q8NFZ4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Neurologin 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jamain S., Quach H., Fellous M., Bourgeron T.,
RT "Evolution and expression of the human neurologin family, including
RT two primate specific members on the X and Y chromosomes.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF376802; AAM46111.1; --
DR InterPro; IPR002018; CarboxesteraseB.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR002965; P rich extensn.
DR InterPro; IPR000379; Ser est:s_site.
DR Pfam; PF00135; Coesterase_1.
DR PRINTS; PR01090; NEUROLIGIN.
DR PRINTS; PR01217; PRICHEXTENSIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 835 AA; 90819 MW; 359938630193EF87 CRC64;

Query Match 100.0%; Score 4508; DB 4; Length 835;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 835; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLLALCLVLGLAGAQGGGGPGGPGGGLGSLGEEFFPVVNTAYGRVGRVRELN 60

Db 1 MWLLALCLVLGLAGAQGGGGPGGPGGGLGSLGEEFFPVVNTAYGRVGRVRELN 60

QY 61 EILGPVVQFLGVPIATPPLGARRFQPEAPASPGVGNATLTPPACPNLHGALPAIMLP 120
 Db 61 EILGPVVQFLGVPIATPPLGARRFQPEAPASPGVGNATLTPPACPNLHGALPAIMLP 120
 QY 121 VFTDNLAAATVYQNSDCLYLNLYVTEDEGLTKKDEATLAPPDTHIDPQKXPM 180
 Db 121 VFTDNLAAATVYQNSDCLYLNLYVTEDEGLTKKDEATLAPPDTHIDPQKXPM 180
 QY 181 LFLHGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSLSTGQAAGNGLDQIQ 240
 Db 181 LFLHGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSLSTGQAAGNGLDQIQ 240
 QY 241 ALRWLSNTAHFGGDPERITIFSGAGASCNVLILSHSEGLFQKAIQAGSTAISSWSV 300
 Db 241 ALRWLSNTAHFGGDPERITIFSGAGASCNVLILSHSEGLFQKAIQAGSTAISSWSV 300
 QY 301 NYOPLKYTRLLAAKVGCDREDSAEAEVCLRRKPSRELVDQVQARYHIAFGPVVDGVDV 360
 Db 301 NYOPLKYTRLLAAKVGCDREDSAEAEVCLRRKPSRELVDQVQARYHIAFGPVVDGVDV 360
 QY 361 PDDPEILMQGGEFLNYDMLIGNVQSGELKFVEDSAESDGVSAFDFTVSNFVNDLYGY 420
 Db 361 PDDPEILMQGGEFLNYDMLIGNVQSGELKFVEDSAESDGVSAFDFTVSNFVNDLYGY 420
 QY 421 PEGKDLVRETIKFMYTDWADRDNGEMRRKTLTLLAFDTHQWAPAVATAKLHADYQSPVYF 480
 Db 421 PEGKDLVRETIKFMYTDWADRDNGEMRRKTLTLLAFDTHQWAPAVATAKLHADYQSPVYF 480
 QY 481 YTFYHHCQAEGRPEWADAAGDELPIYVFGVMVGTDLFPFCNFSKNDVMSAVVMTYTN 540
 Db 481 YTFYHHCQAEGRPEWADAAGDELPIYVFGVMVGTDLFPFCNFSKNDVMSAVVMTYTN 540
 QY 541 FAKTGDNPQVPQDTKFIHTKPNRFEVWVSKFNSKEKQYLHIGLKPRVDNYRANKVAF 600
 Db 541 FAKTGDNPQVPQDTKFIHTKPNRFEVWVSKFNSKEKQYLHIGLKPRVDNYRANKVAF 600
 QY 601 WLELVPHLNLHTELTFTTTLRPPYATRWPPRPPAGAPGTRPPPPATLPPPEPEPEGPR 660
 Db 601 WLELVPHLNLHTELTFTTTLRPPYATRWPPRPPAGAPGTRPPPPATLPPPEPEPEGPR 660
 QY 661 AYDRFPGSDSDYSTELSVTVAVGASLLFNILAFALYKRRRQRELRCRLSPGGSGS 720
 Db 661 AYDRFPGSDSDYSTELSVTVAVGASLLFNILAFALYKRRRQRELRCRLSPGGSGS 720
 QY 721 GVPGGPGLLPAAGRELPPPEELVSLQKGGGVGADPAEALRPACPDYTLALRRAPDDV 780
 Db 721 GVPGGPGLLPAAGRELPPPEELVSLQKGGGVGADPAEALRPACPDYTLALRRAPDDV 780
 QY 781 PLLAPGALTLLPSGLGPPPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV 835
 Db 781 PLLAPGALTLLPSGLGPPPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV 835

RESULT 2

Q62888 PRELIMINARY; PRT; 836 AA.
 ID Q62888
 AC Q62888
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Neurologin 2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=forebrain;
 RX MEDLINE=96162010; PubMed=8576240;
 RA Ichtchenko K., Nguyen T., Sudhof T.C.;
 RT "Structures, alternative splicing, and neurexin binding of multiple
 RT neurologins";
 RL J. Biol. Chem. 271:2676-2682(1996).

CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; U41662; AAA97870.1; --
 DR HSP; P37967; 1OE3.
 DR InterPro; IPR002018; CarboxylesteraseB.
 DR InterPro; IPR000460; Neurologin.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; FRC1090; NEUROLOGIN.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 836 AA; 90961 MW; 1AD51CBI8E4BF9CF CRC64;

Query Match 97.9%; Score 4415.5; DB 11; Length 836;
 Best Local Similarity 98.3%; Pred. No. 8.2e-318;
 Matches 822; Conservative 2; Mismatches 11; Indels 1; Gaps 1;
 QY 1 MWLLALCLVGLAGAQRCGGGPGGAPGPGGLGSLGEERFPVNTAYGVRGVRRELNN 60
 Db 1 MWLLALCLVGLAGAQRCGGGPGGAPGPGGLGSLGEERFPVNTAYGVRGVRRELNN 60
 QY 61 EILGPVVQFLGVPIATPPLGARRFQPEAPASPGVGNATLTPPACPNLHGALPAIMLP 120
 Db 61 EILGPVVQFLGVPIATPPLGARRFQPEAPASPGVGNATLTPPACPNLHGALPAIMLP 120
 QY 121 VFTDNLAAATVYQNSDCLYLNLYVTEDEGLTKKDEATLAPPDTHIDPQKXPM 180
 Db 121 VFTDNLAAATVYQNSDCLYLNLYVTEDEGLTKKDEATLAPPDTHIDPQKXPM 180
 QY 181 LFLHGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSLSTGQAAGNGLDQIQ 240
 Db 181 LFLHGSYMEGTGMFDGSLAAYGNVIVATLNYRLGVLFSLSTGQAAGNGLDQIQ 240
 QY 241 ALRWLSNTAHFGGDPERITIFSGAGASCNVLILSHSEGLFQKAIQAGSTAISSWSV 300
 Db 241 ALRWLSNTAHFGGDPERITIFSGAGASCNVLILSHSEGLFQKAIQAGSTAISSWSV 300
 QY 301 NYOPLKYTRLLAAKVGCDREDSAEAEVCLRRKPSRELVDQVQARYHIAFGPVVDGVDV 360
 Db 301 NYOPLKYTRLLAAKVGCDREDSAEAEVCLRRKPSRELVDQVQARYHIAFGPVVDGVDV 360
 QY 361 PDDPEILMQGGEFLNYDMLIGNVQSGELKFVEDSAESDGVSAFDFTVSNFVNDLYGY 420
 Db 361 PDDPEILMQGGEFLNYDMLIGNVQSGELKFVEDSAESDGVSAFDFTVSNFVNDLYGY 420
 QY 421 PEGKDLVRETIKFMYTDWADRDNGEMRRKTLTLLAFDTHQWAPAVATAKLHADYQSPVYF 480
 Db 421 PEGKDLVRETIKFMYTDWADRDNGEMRRKTLTLLAFDTHQWAPAVATAKLHADYQSPVYF 480
 QY 481 YTFYHHCQAEGRPEWADAAGDELPIYVFGVMVGTDLFPFCNFSKNDVMSAVVMTYTN 540
 Db 481 YTFYHHCQAEGRPEWADAAGDELPIYVFGVMVGTDLFPFCNFSKNDVMSAVVMTYTN 540
 QY 541 FAKTGDNPQVPQDTKFIHTKPNRFEVWVSKFNSKEKQYLHIGLKPRVDNYRANKVAF 600
 Db 541 FAKTGDNPQVPQDTKFIHTKPNRFEVWVSKFNSKEKQYLHIGLKPRVDNYRANKVAF 600
 QY 601 WLELVPHLNLHTELTFTTTLRPPYATRWPPRPPA-GAPGTRPPPPATLPPPEPEPEGPR 659
 Db 601 WLELVPHLNLHTELTFTTTLRPPYATRWPPRPPGPGTSGTRPPPPATLPPESDIDLGP 660
 QY 660 RAYDRFPGSDSDYSTELSVTVAVGASLLFNILAFALYKRRRQRELRCRLSPGGSG 719
 Db 661 RAYDRFPGSDSDYSTELSVTVAVGASLLFNILAFALYKRRRQRELRCRLSPGGSG 720
 QY 720 SGVFGGGPGLLPAAGRELPPPEELVSLQKGGGVGADPAEALRPACPDYTLALRRAPDD 779
 Db 721 SGVFGGGPGLLPAAGRELPPPEELVSLQKGGGVGADPAEALRPACPDYTLALRRAPDD 780
 QY 780 VPLLAPGALTLLPSGLGPPPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV 835
 Db 781 VPLLAPGALTLLPSGLGPPPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV 836

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RESULT 3
Q9P211 Q9P211 PRELIMINARY; PRT; 550 AA.
AC 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Hypothetical protein KIAA1366 (Fragment).
GN KIAA1366.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN 1.
RS SEQUENCE FROM N.A.
RC MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K., Hirotsawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 7:65-73(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AB037787; BA92604.1; -.
DR HSSP; P21836; 1MAA.
DR Genew; HGNC:14290; NLGN2.
DR InterPro; IPR002018; Carboxylase.
DR InterPro; IPR000460; Neurotrophin.
DR InterPro; IPR002965; P-rich_extensn.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLOGIN.
DR PRINTS; PR01217; PRICHEXTENGN.
CW Hypothetical protein; Hydrolase.
CT NON_TER
SEQUENCE 550 AA; 60734 MW; 5B09C3E2323618F1 CRC64;

Query Match 66.2%; Score 2986; DB 4; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.3e-212;
Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 286 KAIAQSGTAISSWSNYQPLKYLTRLLAAKVGCDREDSAEAECLRRKPSRELVDQVQPA 345
b 1 KAIAQSGTAISSWSNYQPLKYLTRLLAAKVGCDREDSAEAECLRRKPSRELVDQVQPA 60

346 RVHIAFGPVVDGVDPPDEILMQQGEFLNYDMLGVNQGEGLKFEVDSAESEDCVSASA 405
b 61 RVHIAFGPVVDGVDPPDEILMQQGEFLNYDMLGVNQGEGLKFEVDSAESEDCVSASA 120

406 FQFTVSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNGEMRKTLLALFTDHWVAPAV 465
b 121 FQFTVSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNGEMRKTLLALFTDHWVAPAV 180

466 ATAKLHADYQSPVYFTFYHHCQAGRPEDWADAAGHDELPLYVFGVPMVGATDLPFCNFSK 525
b 181 ATAKLHADYQSPVYFTFYHHCQAGRPEDWADAAGHDELPLYVFGVPMVGATDLPFCNFSK 240

526 NDVMSAVVMTYNTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSFKNSKEKQYLHIGL 585
b 241 NDVMSAVVMTYNTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSFKNSKEKQYLHIGL 300

586 KPRVRNRYEANKVAFWLELVPHLNLHTELFTTTTLPPYATRWPRPPAGPTRRPP 645
b 301 KPRVRNRYEANKVAFWLELVPHLNLHTELFTTTTLPPYATRWPRPPAGPTRRPP 360

646 PATLPEPEPEGPRAYDFPGDSRDYSTELSVTVAVGASLLFLNLAFALYKDRRQ 705
b 361 PATLPEPEPEGPRAYDFPGDSRDYSTELSVTVAVGASLLFLNLAFALYKDRRQ 420

706 ELRCRLSPFGSGSGVPGGGPLLPAAAGRELPPBELVSLQKRGGGVADPAEALRPAC 765
b 421 ELRCRLSPFGSGSGVPGGGPLLPAAAGRELPPBELVSLQKRGGGVADPAEALRPAC 480

766 PDYTLALRRAPDDVPLAPGALTLLPSGLGPPPPPPPSLHPFGPPPTATSHNNT 825

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Db 481 PPDYTLALRRAPDDVPLAPGALTLLPSGLGPPPPPPPSLHPFGPPPTATSHNNT 540
QY 826 LPHPHSTTRV 835
Db 541 LPHPHSTTRV 550

RESULT 4
Q8BYMS Q8BYMS PRELIMINARY; PRT; 825 AA.
AC Q8BYMS;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE NEUROLOGIN 3 isoform HNL3 homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN 1.
RS SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK039018; BAC30207.1; -.
SQ SEQUENCE 825 AA; 91175 MW; 3BF17F889B0A44CE CRC64;

Query Match 61.5%; Score 2773.5; DB 11; Length 825;
Best Local Similarity 84.8%; Pred. No. 2.2e-196;
Matches 531; Conservative 98; Mismatches 132; Indels 59; Gaps 14;

QY 42 PVNTAYGRVGRVREINNEILGVPVQFLGVPYATPPLGARFPQPEAPASWFGVRNATT 101
Db 39 PTVNTHEKLGARVPLPSSELLGVPVQYLGVPYAAPIGEKRLPPEPPPSWSGIRNATH 98

102 LPACPNLHGAIPALMPLPWFTDNLEAAATYVQNOSEDCLYNLVYPTDGLTKRDE 161
Db 99 FPPVPCQNIHTAVPEVMLPWFTANLDIVATYIQEENEDCLYNLVYPTDGLTKRDE 158

162 ATLN---PPDTRDRDQKPVMLFHHGSGMGTGNMGDGVLLAAYGNVIVATLNYRLGV 218
Db 159 DLADNCGDEDEDIRDSGAKPVVYIHHGSGMGTGNMGDGVLLAAYGNVIVATLNYRLGV 218

219 LGFLSTGDAQAKNGYGLLDQIQALRWLSENIAHFGDPERITIFGSGAGASCYNLLILSH 278
Db 219 LGFLSTGDAQAKNGYGLLDQIQALRWVSENIAPFGDPERITIFGSGIGASCYVSLITLSH 278

279 HSGELFQKATAQSGTAISSWSNYQPLKYLTRLLAAKVGCDREDSAEAECLRRKPSREL 338
Db 279 HSGELFQKATAQSGTAISSWSNYQPLKYLTRLLAAKVGCDREDSAEAECLRRKPSREL 338

339 DQVQPARVHIAFGPVVDGVDPPDEILMQQGEFLNYDMLGVNQGEGLKFEVDSAESE 398
Db 339 EQDIQPARVHIAFGPVVDGVDPPDEILMQQGEFLNYDMLGVNQGEGLKFEVGVVDPE 398

399 DGVSASAFDTVSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNGEMRKTLLALFTDH 458
Db 399 DGVSAGTDFDYSVSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNPETRRKTLVALFTDH 458

459 QWVAPAVATAKLHADYQSPVYFTFYHHCQAGRPEDWADAAGHDELPLYVFGVPMVGATDL 518
Db 459 QWVPSVTVADLEARYGSPYFYAFVHHQCSLMKPKAWSDAAGHDEVPYVFGVPMVGPTDL 518

519 FPCNFSKNDVMSAVVMTYNTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSFKNSKEK 578
Db 519 FPCNFSKNDVMSAVVMTYNTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSFKNSKEK 578

579 QYHLHGLKPRVRNRYEANKVAFWLELVPHLNLHTELFTTTTLPP-----YATRWPP 631

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Db 579 LYHLGKRVDRHRAKVAFWKHLVPHLNLH--DMFHYTSTTTTKVPPDTHSHSHTR 637
Qy 632 RPPAGAGTRRRPPPPATUPPEPEPEPGPRAYDRPPGDS-----RDYSTELSVTA 681
Db 638 RPNKGTWSTKRP-----AISPAYSENAPGSWN--GDQDAGFLLVENPRDYSTELSVTA 690
Qy 682 VGASLLPLNLFAALYAKRDRQELRCRLSPPGGSGVFGGGLLPAGRELPEEE 741
Db 691 VGASLLPLNLFAALYAKRDRQELRCRLSPPGGSGVFGGGLLPAGRELPEEE 739
Qy 742 LVSLQLKRGVGV-----GADPAALRACPDYTLALRAPPDVLPLAPGALLPLSGLG 796
Db 740 LAAALQ-----GPHHSCAGRPDTHLALPDYTLALRAPPDVLPLAPGALLPLSGLG 795
Qy 797 PPPPPPPSLHFGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 835
Db 796 ----VGLQTLHPYNTF-----AAGFNSTGLFHSHTTRV 825

RESULT 5
Q62765 PRELIMINARY; PRT; 843 AA.
AC Q62765;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neuroigin I.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95254653; PubMed=7736595;
RA Ichtchenko K., Hata Y., Nguyen T., Ullrich B., Missler M., Moomaw C.,
RA Suchof J.C.;
RT "Neuroigin I: a splice site-specific ligand for beta-neurexins.";
RL Cell 81:435-443(1995).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; U22952; AAA85720.1; -.
DR HSSP; P37967; IQE3.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000450; Neuroigin.
DR InterPro; IPR000379; Sex_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydroilase.
SQ SEQUENCE 843 AA; 94294 MW; 90A18540245B789D CRC64;

Query Match
Best Local Similarity 61.1%; Score 2771; DB 11; Length 843;
Matches 546; Conservative 100; Mismatches 133; Indels 114; Gaps 21;

Qy 1 MW-----LLALCLVLGAGAQGGGGGAPGGGLGSLG-----EERF 41
Db 7 MFNPNYVRAMACV-----HRGSGAP-----ITLCLGLCLCTFHLVSKLDDVD 52
Qy 42 PVNTAYGRVGRVRELNEILGPVQFLGVYATPPLGARRFQPPAPASWPGVRNAT 101
Db 53 PLVTTFNGKIRGKRELNEILGPVQFLGVYATPPLGARRFQPPAPASWPGVRNATQ 112
Qy 102 LPPACQON-LHAGALPAIMLPWNTONLEAATYVQNSQEDCLYLNLYPTEDGLTKRD 160
Db 113 FAPVCPQNIIDGRLPEWLPVNTNLDVSVYQDSQEDCLYLNLYPTEDGLTKRD 169
Qy 161 EATINPDDT-----DIRDP-GKKFVMLFLHGGSTWEGTGNMFGSVLAAYGNVIVATLN 213
Db 170 KECARPGKKICRKGDIRSGGPKPWWYIHGGSWEGTGNLYGSLVSLVGNVIVITVN 229
Qy 214 YRLGVGLFSTGQAAGKNGYGLDQLQALRWLSENIAHFQGDPERITFGSGAGSCVNL 273

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Db 230 YRLGVGLFSTGQAAGKNGYGLDQLQALRWLSENIAHFQGDPERITFGSGAGSCVNL 289
Qy 274 LIISHSE-----GLFQKAIAGSTAISSWSVNYQPLKYTRLLAAKVCGRDSDAE 324
Db 290 LTLSHYSEGNRNSKGLFQRAIAQSGTALSWSAVSQPAKYARILATKVCNCVSDTVE 349
Qy 325 AVECLRRKPSRELVDQVOPARYHIAFGVPVDDVPPDPEILMOQGBFLNMDLIGNVQ 384
Db 350 LVECLQKKPKYELVDQVOPARYHIAFGVPVDDVPPDPEILMOQGBFLNMDLIGNVQ 409
Qy 385 GEGGLKVEDSAGSSEDGVSASAFDTVSNFVNLGYVPEGKOVLRITIKFMYTDMADRONG 444
Db 410 GEGGLKVENIVSDGVSASDFDFAVSFVNLGYVPEGKOVLRITIKFMYTDMADRONG 469
Qy 445 EMRRKTLALLFTDQWVAPAVATADLHNSFGSFTFYAFYHHCQTDQVPAWADAAGDEV 504
Db 470 ETRKTLALLFTDQWVAPAVATADLHNSFGSFTFYAFYHHCQTDQVPAWADAAGDEV 529
Qy 505 PYVFGVPMVGCATDLFCNFSKNDVMSAVVMTYTNFAKTGDPNCPQVQDTKFIHTKENR 564
Db 530 PYVFGVPMVGCATDLFCNFSKNDVMSAVVMTYTNFAKTGDPNCPQVQDTKFIHTKENR 589
Qy 565 FEEVNSKFSKQYLHLGLKPRVDRNDYRANKVAFWLELPHLNLH--TELFTTTTTL 622
Db 590 FEEVNTRYSKQDLYHLGLKPRVDRNDYRANKVAFWLELPHLNLHNDISQYTSITTKV 649
Qy 623 PPVATRWPPPPAGAPGTRPPPPAT-----LPPEPEPGPRAYDRPGSDRYSDEL 676
Db 650 P--STDITLAP-----TRNSTPVTSAFTAKQDDPKQSPS-----FSDQRDYSDEL 696
Qy 677 SVTVAVGASLLPLNLFAALYAKRDRQELRCRLSPPGGSGVFGGGLLPAGREL 736
Db 697 SVTVAVGASLLPLNLFAALYAKRDRQELRCRLSPPGGSGVFGGGLLPAGREL 745
Qy 737 PPBEELVSLQKGGGVGAD-----PAE-ALRACPDYTLALRAPPDVLPLAPGAL 788
Db 746 -PBEELVSLQKGGGVGAD-----PAE-ALRACPDYTLALRAPPDVLPLAPGAL 801
Qy 789 TLPSGLGPPPPPPPPPSLHFGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 835
Db 802 TMIPNTI-----FGIQPLHTFNTF-----TGQNNTLPHPHPHSHSTTRV 843

RESULT 6
Q62765 PRELIMINARY; PRT; 828 AA.
AC Q62765;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neuroigin 3 isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231756; PubMed=10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Ginns E.I.;
RT "The structure and expression of the human neuroigin-3 gene.";
RL Gene 246:303-310(2000).
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF217413; IMA71232.1; -.
DR HSSP; P21836; IMA7.
DR Genew; HGNC:14289; NLGN3.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000460; Neuroigin.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydroilase.

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Db 461 TDHQWFAVAATADLHNGFGSTFYFAFHCQDQVPAWADAAGDEVPYVGLPMLGP 520
QY 516 TDLFCNFKNDVMSLVAVVMTYTNFAKTGDPNPQVPQDTKFIHTKPNRFEVWWSKENS 575
Db 521 TELFFCNFKNDVMSLVAVVMTYTNFAKTGDPNPQVPQDTKFIHTKPNRFEVWWSKENS 580
QY 576 KEKQVHLHGLKPRVDRNVRANKVAFWELVPHLNLH--TELFSTTTTTLRPPVATRWPPRP 633
Db 581 KDOLVHLHGLKPRVKEHVRANKVNLWLELVPHLNLHNDISQVSTTTTKVPSDITFRPFR 640
QY 634 PAGAFGTRPPPPATLPEPEPEPEGPRAYDRFPGDSDRDSYSTELSVTVAVGASLLFNILA 693
Db 641 KNSVEVTSFAFTAKODDFKQFSP-----FSDQDSDYSTELSVTVAVGASLLFNILA 693
QY 694 FAALYKKDRQELRCRLSPGSGSGVPGGGLPAPAGRELPPPEELVSLQKRGGV 753
Db 694 FAALYKKDRHVDHRRCSQRTTNDLTHA-----QEEIIMSLQMKH--T 738
QY 754 GAD-----PAB-ALRPACPDYTLALRAPDDVLLAPCALTLPSGLGPPPPPPPS 805
Db 739 DUDHECEBIHVEVLRVTRACPDYTLAWRRSPDDVPLMTNTITMPTNTI 793
QY 806 LHPFGFPFPPTATSHNNLPHP-----HSTRV 835
Db 794 LHTFNTF-----TGGQNTLPHPHPHSHSTRV 823

RESULT 8
ID Q9NZ97 PRELIMINARY; PRT; 828 AA.
AC Q9NZ97;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-WAR-2002 (TREMELrel. 20, Last annotation update)
DE Neuroigin 3 isoform HNL3.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231756; PubMed=10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Ginns E.I.;
RT "The structure and expression of the human neuroigin-3 gene.";
RL Gene 246:303-310(2000)
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL; AF217411; AAF71230.1; -.
DR HSSP; P37967; IQE3.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000460; Neuroigin.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROIGIN.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolyase.
SQ SEQUENCE 828 AA; 91554 MW; A896C059326780AA CRC64;

Query Match 61.3%; Score 2763; DB 4; Length 828;
Best Local Similarity 62.5%; Pred. No. 1.3e-195;
Matches 536; Conservative 101; Mismatches 143; Indels 78; Gaps 16;

QY 1 MWLLALCVLAGAQGGGGGPGGLGLSLGEERFPVNTAYGVRVREANN 60
Db 26 LWFSLAL--RSTQ-----APA-----PTVTHFGKIRGARVPLPS 60
QY 61 EILGPVQFLGVYATPLGARRFQPEAPASWPGVNRATLTPACQNLHGALPMLP 120
Db 61 EILGPVQFLGVYAAFTIGKRFPLPPEPPPSWSGIRNATHFFPVCFQNIHTAVPEWMLP 120
QY 121 VNFNTNLEAAVYVQNSQEDCLYLNLYVPTDGLTKKRDEATLN---PDDTDIRPGKK 177
Db 121 VNFNTNLDIVAYIQEPNEDCLYLNLYVPTDGLTKKRDEATLN---PDDTDIRPGKK 180

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QY 178 PVMFLHGSWEGTGMFDSVLAAYGNVIVATLNYRLGVLSLSTGDOAAKNGYGLD 237
Db 181 PVMVHGSWEGTGMFDSVLAAYGNVIVATLNYRLGVLSLSTGDOAAKNGYGLD 240
QY 238 QIQALRWSENIAHFGDPERITITFGSGAGASCYNLLILSHHSEGLFKQIAQSGTAISS 297
Db 241 QIQALRWSENIAHFGDPERITITFGSGAGASCYNLLILSHHSEGLFKQIAQSGTAISS 300
QY 298 WSNVTOPLKYLTLAAKVGCDREDSAEAVECLRKSPRELVDQVQARYHIAFGPVVDG 357
Db 301 WAVNYQPKYITSLADKVGCVNLDVTVDWDCRQKSAKELVEQDIQARHYVAFGPVIDG 360
QY 358 DVVPDPEILMOQGFPLNYDMLIGNVQSEGKLFVEDSAESDGVSGSAFAFTVSNFVNL 417
Db 361 DVIPDPEILMEQGFPLNYDMLIGNVQSEGKLFVEDSAESDGVSGSAFAFTVSNFVNL 420
QY 418 YGVPEGKDVLRITIKFMTYDADRNGEMRKTLLALFTDHWVAPAVATAKLHAYQSP 477
Db 421 YGVPEGKDVLRITIKFMTYDADRNGEMRKTLLALFTDHWVAPAVATAKLHAYQSP 480
QY 478 VPIPTTHCQAGRPPEWADAAGDELPIYFVGVPMVGATDLFPCNFKNDVMSLVAVVMTY 537
Db 481 TYFYAFYHHCQSLMKPWSDAAGDEVEYFVGVPMVGATDLFPCNFKNDVMSLVAVVMTY 540
QY 538 WTNPAKTGDPNPQVPQDTKFIHTKPNRFEVWWSKENSKEQYHLHGLKPRVDRNVRANK 597
Db 541 WTNPAKTGDPNPQVPQDTKFIHTKPNRFEVWWSKENSKEQYHLHGLKPRVDRNVRANK 600
QY 598 VAPWLELVPHLNLHTELF-----TTTTLPP-----YATEWPPRPAGAGTTRPPPPATLP 650
Db 601 VAPWLELVPHLNLHTELF-----TTTTLPP-----YATEWPPRPAGAGTTRPPPPATLP 659
QY 651 PE-----PEPEGPRAYDRFPGDSDRDSYSTELSVTVAVGASLLFNILAFAALYKRRD 703
Db 660 NENAQGSWNGDQDAGPLVE-----NPRDYSYSTELSVTVAVGASLLFNILAFAALYKRRD 715
QY 704 RQELRCRLSPGSGSGVPGGGLPAPAGRELPPPEELVSLQKRGGV-----GADPA 758
Db 716 RQELRCRLSPGSGSGVPGGGLPAPAGRELPPPEELVSLQKRGGV-----GADPA 761
QY 759 EALRPACPDYTLALRAPDDVLLAPCALTLPSGLGPPPPPPPPPPPPPPPPPPPPPT 818
Db 762 DTLRLTALPDYTLALRAPDDVLLAPCALTLPSGLGPPPPPPPPPPPPPPPPPPPPPT 810
QY 819 ACSHNT-LPHEHSTRV 835
Db 811 AGFNSTGLPHSHSTRV 828

RESULT 9
Q9NZ95 PRELIMINARY; PRT; 848 AA.
AC Q9NZ95;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE Neuroigin 3 isoform.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231756; PubMed=10767552;
RA Philibert R.A., Winfield S.L., Sandhu H.K., Martin B.M., Ginns E.I.;
RT "The structure and expression of the human neuroigin-3 gene.";
RL Gene 246:303-310(2000)
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL; AF217413; AAF71233.1; -.
DR HSSP; P21836; IMAA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000460; Neuroigin.

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DR InterPro: IPR000379; Ser_estr_1.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR01090; NEUROLIGIN.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 848 AA; 93895 MW; B3EE2FAB7E427C82 CRC64;

Query Match
 Best Local Similarity 61.0%; Score 2750; DB 4; Length 848;
 Matches 537; Conservative 101; Mismatches 142; Indels 98; Gaps 17;

QY 1 MWLLALCLVLGLAGAQRGCGGPGGAPGGGLGSLGSEERPPVNTAYGRVGRVRELN 60
 DB 26 LWFLSLAL--RSTQ-----APA-----PTVTHFGKLGARVPLPS 60

QY 61 ELIGVWQFLGVPTATPLGARRQPPEAPASWPGVNRNATLPPACQNLHGALPAIMLP 120
 DB 61 ELIGVWQFLGVPTATPLGARRQPPEAPASWPGVNRNATLPPACQNLHGALPAIMLP 120

QY 121 VWFDTNLEAAATYVQNOSEDCLYLNLYVPTD-----GELTKKRD 160
 DB 121 VWFDTNLEAAATYVQNOSEDCLYLNLYVPTD-----GELTKKRD 160

QY 161 EATLN---PPDTRDPGKPVMLFLHGSGYMEGTGMFDGSLVLAAYGNVIVATLNYRLG 217
 DB 161 EATLN---PPDTRDPGKPVMLFLHGSGYMEGTGMFDGSLVLAAYGNVIVATLNYRLG 217

QY 218 VLGLSTGDOAKNGYLLDQIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLTSL 277
 DB 218 VLGLSTGDOAKNGYLLDQIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLTSL 277

QY 241 VLGLSTGDOAKNGYLLDQIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLTSL 300
 DB 241 VLGLSTGDOAKNGYLLDQIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLTSL 300

QY 278 HSEGLFQKAIQAQSGTAISSWSVNYQPLKTRLLAAKVGCDREDSAEVCLRRKPSREL 337
 DB 278 HSEGLFQKAIQAQSGTAISSWSVNYQPLKTRLLAAKVGCDREDSAEVCLRRKPSREL 337

QY 301 HSEGLFORAIQSGSALSWSVNYQPKYTSLLADKVGCVNLTVDVMDCLQKSAKEL 360
 DB 301 HSEGLFORAIQSGSALSWSVNYQPKYTSLLADKVGCVNLTVDVMDCLQKSAKEL 360

QY 338 VDQVQPARVHIAFGPVVDGVPDDPEILMQOGEFLNYDMLGVNQGEGLKFVEDSAES 397
 DB 338 VDQVQPARVHIAFGPVVDGVPDDPEILMQOGEFLNYDMLGVNQGEGLKFVEDSAES 397

QY 361 VEQDIQPARVHIAFGPVVDGVPDDPEILMQOGEFLNYDMLGVNQGEGLKFVEDSAES 420
 DB 361 VEQDIQPARVHIAFGPVVDGVPDDPEILMQOGEFLNYDMLGVNQGEGLKFVEDSAES 420

QY 398 EDGVSASAFDFTVSNFVNLGYVPEGKDLVRETIKFMYTDWADRDNGEMRKTLLALFTD 457
 DB 398 EDGVSASAFDFTVSNFVNLGYVPEGKDLVRETIKFMYTDWADRDNGEMRKTLLALFTD 457

QY 421 EDGVSAGTDFDYSVSNFVNLGYVPEGKDLVRETIKFMYTDWADRDNGEMRKTLLALFTD 480
 DB 421 EDGVSAGTDFDYSVSNFVNLGYVPEGKDLVRETIKFMYTDWADRDNGEMRKTLLALFTD 480

QY 458 HOWAPAVATAKLHADYQSPVYFTFHHQOAGSRPEWADAAGDELPPYVFGVMVGATD 517
 DB 458 HOWAPAVATAKLHADYQSPVYFTFHHQOAGSRPEWADAAGDELPPYVFGVMVGATD 517

QY 481 HOWVEPSVVTADLHARYGSPYFYAFYHHCQSLMKPAWSDAAGHDEVPYVFGVMVGPTD 540
 DB 481 HOWVEPSVVTADLHARYGSPYFYAFYHHCQSLMKPAWSDAAGHDEVPYVFGVMVGPTD 540

QY 518 LFPNFSKNDVMSAVVMTYNTNFATKDPNQVPQDTKEIHTKPNRFEVWVSKNSKE 577
 DB 518 LFPNFSKNDVMSAVVMTYNTNFATKDPNQVPQDTKEIHTKPNRFEVWVSKNSKE 577

QY 541 LFPNFSKNDVMSAVVMTYNTNFATKDPNQVPQDTKEIHTKPNRFEVWVSKNSKE 600
 DB 541 LFPNFSKNDVMSAVVMTYNTNFATKDPNQVPQDTKEIHTKPNRFEVWVSKNSKE 600

QY 578 KOYLHGLKPRVDRNVRANKVAFWLELVLPHLNLHTLFTLPP-----YATRW 630
 DB 578 KOYLHGLKPRVDRNVRANKVAFWLELVLPHLNLHTLFTLPP-----YATRW 630

QY 601 QLYLHGLKPRVDRNVRANKVAFWLELVLPHLNLHTLFTLPP-----YATRW 659
 DB 601 QLYLHGLKPRVDRNVRANKVAFWLELVLPHLNLHTLFTLPP-----YATRW 659

QY 631 PRPPAGAGTFRPPPTATLPE-----PEPPGPRVDRPFGDSDSTELSVTVAVG 683
 DB 631 PRPPAGAGTFRPPPTATLPE-----PEPPGPRVDRPFGDSDSTELSVTVAVG 683

QY 660 RRNGKWTWTKRAIIPAYSNENAGSWNGDQDAGELLVE-----NPRDYSTELSVTVAVG 715
 DB 660 RRNGKWTWTKRAIIPAYSNENAGSWNGDQDAGELLVE-----NPRDYSTELSVTVAVG 715

QY 684 ASLLFNLILAFALYKRRQRRLCRRLSPGCGSGVPGGQPLLPAAAGRELPPEELV 743
 DB 684 ASLLFNLILAFALYKRRQRRLCRRLSPGCGSGVPGGQPLLPAAAGRELPPEELV 743

QY 716 ASLLFNLILAFALYKRRQRRLCRRLSPGCGSGVPGGQPLLPAAAGRELPPEELV 764
 DB 716 ASLLFNLILAFALYKRRQRRLCRRLSPGCGSGVPGGQPLLPAAAGRELPPEELV 764

QY 744 SLOLKRGGV-----GADPAALRPACPDYTLALRRAPDDVPLIAPAGALTLLPGLGPP 798
 DB 744 SLOLKRGGV-----GADPAALRPACPDYTLALRRAPDDVPLIAPAGALTLLPGLGPP 798

QY 765 ALQL-----GPTHCEAGPHDTLRLTALPDYTLALRRAPDDVPLIAPAGALTLLPGLGPP 818
 DB 765 ALQL-----GPTHCEAGPHDTLRLTALPDYTLALRRAPDDVPLIAPAGALTLLPGLGPP 818

QY 799 PPPPPPSLHPFGPPPPPPPTATSHNT-LPHPHSHSTRV 835
 DB 799 PPPPPPSLHPFGPPPPPPPTATSHNT-LPHPHSHSTRV 835

QY 819 --VGLQTLHPYNTF-----AAGFNSTGLPHSHSTRV 848
 DB 819 --VGLQTLHPYNTF-----AAGFNSTGLPHSHSTRV 848

RESULT 10

Q62889
 ID Q62889 PRELIMINARY; PRT; 848 AA.
 AC Q62889;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Neurologin 3.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN [1]_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Forebrain;
 RX MEDLINE=96162010; PubMed=8576240;
 RA Ichtchenko K., Nguyen T., Sudhof T.C.;
 RT "Structures, alternative splicing, and neurexin binding of multiple
 RT neurologins."; J. Biol. Chem. 271:2676-2692(1996).
 RL J. Biol. Chem. 271:2676-2692(1996).
 CC 1- SIMILARITY; BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 DR EMBL; U41663; AAA97871.1; -.
 DR HSSP; P21836; 1MAA.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000460; Neurologin.
 DR InterPro; IPR000379; Ser_estr_1.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR01090; NEUROLIGIN.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 848 AA; 93888 MW; 7520653B3253E750 CRC64;

Query Match
 Best Local Similarity 60.9%; Score 2746; DB 11; Length 848;
 Matches 538; Conservative 101; Mismatches 138; Indels 104; Gaps 18;

QY 1 MWLLALCLVLGLAGAQRGCGGPGGAPGGGLGSLGSEERPPVNTAYGRVGRVRELN 60
 DB 26 LWFLSLVL--RSTQ-----APA-----PTVTHFGKLGARVPLPS 60

QY 61 ELIGVWQFLGVPTATPLGARRQPPEAPASWPGVNRNATLPPACQNLHGALPAIMLP 120
 DB 61 ELIGVWQFLGVPTATPLGARRQPPEAPASWPGVNRNATLPPACQNLHGALPAIMLP 120

QY 121 VWFDTNLEAAATYVQNOSEDCLYLNLYVPTD-----GELTKKRD 160
 DB 121 VWFDTNLEAAATYVQNOSEDCLYLNLYVPTD-----GELTKKRD 160

QY 161 EATLN---PPDTRDPGKPVMLFLHGSGYMEGTGMFDGSLVLAAYGNVIVATLNYRLG 217
 DB 161 EATLN---PPDTRDPGKPVMLFLHGSGYMEGTGMFDGSLVLAAYGNVIVATLNYRLG 217

QY 181 EDLADNDGDEDEDIRDSGAKFWVYIHGSGYMEGTGMFDGSLVLAAYGNVIVATLNYRVG 240
 DB 181 EDLADNDGDEDEDIRDSGAKFWVYIHGSGYMEGTGMFDGSLVLAAYGNVIVATLNYRVG 240

QY 218 VLGLSTGDOAKNGYLLDQIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLTSL 277
 DB 218 VLGLSTGDOAKNGYLLDQIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLTSL 277

QY 241 VLGLSTGDOAKNGYLLDQIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLTSL 300
 DB 241 VLGLSTGDOAKNGYLLDQIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLTSL 300

QY 278 HSEGLFQKAIQAQSGTAISSWSVNYQPLKTRLLAAKVGCDREDSAEVCLRRKPSREL 337
 DB 278 HSEGLFQKAIQAQSGTAISSWSVNYQPLKTRLLAAKVGCDREDSAEVCLRRKPSREL 337

QY 301 HSEGLFORAIQSGSALSWSVNYQPKYTSLLADKVGCVNLTVDVMDCLQKSAKEL 360
 DB 301 HSEGLFORAIQSGSALSWSVNYQPKYTSLLADKVGCVNLTVDVMDCLQKSAKEL 360

QY 338 VDQVQPARVHIAFGPVVDGVPDDPEILMQOGEFLNYDMLGVNQGEGLKFVEDSAES 397
 DB 338 VDQVQPARVHIAFGPVVDGVPDDPEILMQOGEFLNYDMLGVNQGEGLKFVEDSAES 397

QY 361 VEQDIQPARVHIAFGPVVDGVPDDPEILMQOGEFLNYDMLGVNQGEGLKFVEDSAES 420
 DB 361 VEQDIQPARVHIAFGPVVDGVPDDPEILMQOGEFLNYDMLGVNQGEGLKFVEDSAES 420

QY 398 EDGVSASAFDFTVSNFVNLGYVPEGKDLVRETIKFMYTDWADRDNGEMRKTLLALFTD 457
 DB 398 EDGVSASAFDFTVSNFVNLGYVPEGKDLVRETIKFMYTDWADRDNGEMRKTLLALFTD 457

QY 421 EDGVSAGTDFDYSVSNFVNLGYVPEGKDLVRETIKFMYTDWADRDNGEMRKTLLALFTD 480
 DB 421 EDGVSAGTDFDYSVSNFVNLGYVPEGKDLVRETIKFMYTDWADRDNGEMRKTLLALFTD 480

QY 458 HOWAPAVATAKLHADYQSPVYFTFHHQOAGSRPEWADAAGDELPPYVFGVMVGATD 517
 DB 458 HOWAPAVATAKLHADYQSPVYFTFHHQOAGSRPEWADAAGDELPPYVFGVMVGATD 517

QY 481 HOWVEPSVVTADLHARYGSPYFYAFYHHCQSLMKPAWSDAAGHDEVPYVFGVMVGPTD 540
 DB 481 HOWVEPSVVTADLHARYGSPYFYAFYHHCQSLMKPAWSDAAGHDEVPYVFGVMVGPTD 540

QY 518 LFPNFSKNDVMSAVVMTYNTNFATKDPNQVPQDTKEIHTKPNRFEVWVSKNSKE 577
 DB 518 LFPNFSKNDVMSAVVMTYNTNFATKDPNQVPQDTKEIHTKPNRFEVWVSKNSKE 577

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Db 541 LFCNFKNDVMSAVVNTWTFNFAKTGDDNKVPQDTKFIHTKANRFEVANSKYNPRD 600
Qy 578 KOYLHIGLKPRVDRNRYANKVAFWLELVPHLHNLHTELF---TTTTRLP---YATRW 630
Db 601 QLYLHIGLKPRVDRNRYANKVAFWLELVPHLHNLH---DMFYHTT---TKVPPDTHSSHT 659
Qy 631 PRPAGAPGTRPPPPATLPEPEPEGPAYDRFPGDS-----RDYSTELSVTV 680
Db 660 RRPNGKTWSTKRP-----AISPAYSNNAPGSWN---GDQAGPLLVENPRDYSTELSVTV 712
Qy 681 AVGASLLFLNLAFALYLYKRRRQELRCRLSPGGSGSGVPGGGLPLPAAGRELPPPE 740
Db 713 AVGASLLFLNLAFALYLYKRRRQELRCRLSPGGSGSGVPGGGLPLPAAGRELPPPE 761
Qy 741 ELVSLQIKRGGV-----GADPAELRPACPPDYTLALRAPDVLAPGALTLLPSGL 795
Db 762 ELAALQL---GPTHCEAGAPPHDTLRLTALPDYTLTLRSPDDIPLMTPTNTIPIENSL 818
Qy 796 GPPPPPPPSLHPFGPPPPPPPTATSHNNT-LPHPHSTTRV 835
Db 819 -----VGLQLHPYNTF-----AAGFNSIGLPSHSTTRV 848

RESULT 11
Q8NOW4
ID Q8NOW4 PRELIMINARY; PRT; 816 AA.
AC Q8NOW4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neurologin X.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Janain S., Quach H., Fellous M., Bourgeron T.;
RT "Evolution and expression of the human neurologin family, including
RT two primate specific members on the X and Y chromosomes.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: BC034018; AAH34018.1;
DR EMBL: AF376803; AAM4612.1;
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000460; Neurologin.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00135; Coesterase_1.
DR PRINTS: PR01090; NEUROLIGIN.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE. 816 AA; 91915 MW; EA1320D690F76BBD CRC64;

Query Match 60.2%; Score 2713.5; DB 4; Length 816;
Best Local Similarity 63.6%; Pred. No. 6e-192;
Matches 520; Conservative 96; Mismatches 139; Indels 63; Gaps 13;

Qy 38 EERFFVNTAYGVRGVRRLNNEILGPVVQFLGVYATPPGARRFQPEAPASWPGVR 97
Db 42 QAQYPVVNTYKIRGLRTPLEILGPVEQVLGVYASPPPTGERFQPEPPSWTGR 101
Qy 98 NATTLPPACPNL-HGALPAILMPPVMTDNLEAAATYVQNSHEDCLNLYVPTEDGLPT 156
Db 102 NTTQFAACVCPHLDESLHDMLPINFNTANLDTLMTYVQDQEDCLNLYVPTED---- 157
Qy 157 KKDEATLNPDPDTRDP-GKKPVMLFLHGSGSTMEGTGNMFGSVLAAYGNVIVATLNYR 215
Db 158 -----DIHQNSKKFVWYIRGGSTMEGTGNMIDGSLIAYGNVIVITINX 204

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Qy 216 LGVLGFLSTGQAAKNGYLLDQIQALRWLSENIAHFGDPERITIFSGAGASCWILLI 275
Db 205 LGILGFLSTGQAAKNGYLLDQIQALRWLSENIAHFGDPERITIFSGAGASCWILLI 264
Qy 276 LSHSSEGLFQKAIQAQSGTAISSWVNYQPLKYITLLAAKVGCCDREDSAAVECLRRKPSR 335
Db 265 LSHSSEGLFQKAIQAQSGTAISSWVNYQPLKYITLLAAKVGCCDREDSAAVECLRRKPSR 324
Qy 336 ELVDQDQAPARYHIAFGVVDGVDVVDPPPEILMOQGEFLNYDMLIGVNOQSGGLKFVEDSA 395
Db 325 ELIQTIIPAYHIAFGVVDGVDVVDPPPEILMOQGEFLNYDMLIGVNOQSGGLKFVEDSA 384
Qy 396 ESEGVASASAFDTVSNFVNLGYPEGKQVLRITIKFMTYDMDADRNGENRRTKILALF 455
Db 385 DNEGVTENDDFDSVSNFVNLGYPEGKQVLRITIKFMTYDMDADRNGENRRTKILALF 444
Qy 456 TDHQWVAFVATAKLHADYQSPVYFYFHHCOAGRPENADAAGDELPPVFGVPMVGA 515
Db 445 TDHQWVAFVATADLHAQYGSFTFYFHHCOAGRPENADAAGDELPPVFGVPMVGA 504
Qy 516 TDLPCNFSKNDVMSAVVMTYTNFAKTGDPNPQDPTKFIHTKPNRFEVVVWSKPS 575
Db 505 TELFSCNFSKNDVMSAVVMTYTNFAKTGDPNPQDPTKFIHTKPNRFEVVVWSKPS 564
Qy 576 KEKOYLHIGLKPRVDRNRYANKVAFWLELVPHLHNLHTELF---TTTTRLP---PY 625
Db 565 KDQYLHIGLKPRVDRNRYANKVAFWLELVPHLHNLHTELF---TTTTRLP---PY 623
Qy 626 ATRWPPPPAGAG-EGTRPPPPATLPEPEPEP---GPRAYDRPFGSDRSTELSVTV 681
Db 624 GTR---RSPAKIWP---TKRPAITPANNPKSKDPKHTGPTDVTTLTKRSTELSVTV 680
Qy 682 VGASLLFLNLAFALYLYKRRRQELRCRLSPGGSGSGVPGGGLPLPAAGRELPPPEE 741
Db 681 VGASLLFLNLAFALYLYKRRRQELRCRLSPGGSGSGVPGGGLPLPAAGRELPPPEE 728
Qy 742 LVSLQLKX---GGVGADFAELRPACPPDYTLALRAPDVLAPGALTLLPSGLP 797
Db 729 IMSLQMKLEHDEHCESLQAHDTLRLTCPPDYTLTLRSPDDIPLMTPTNTIPIENSL 788
Qy 798 PPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV 835
Db 789 MQP-----LHTFNTF-----SGQNSTNLPHGSHSTTRV 816

RESULT 12
Q9ULG0
ID Q9ULG0 PRELIMINARY; PRT; 817 AA.
AC Q9ULG0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein KIAA1260 (Fragment).
GN KIAA1260.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345 (1999).
CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AB033086; BAA86574.1;
DR HSSP; P21836; IMAA.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000460; Neurologin.

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DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 DE Neurologin Y.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Sutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jamin S., Quach H., Fellous M., Bourgeron T.;
 RT "Evolution and expression of the human neurologin family, including
 RT two primate specific members on the X and Y chromosomes.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLTERASE/LIPASE FAMILY.
 DR EMBL; AF376804; AAM46113.1; -
 DR InterPro; IPR002018; CarbesteraseB.
 DR InterPro; IPR000460; Neurologin.
 DR InterPro; IPR003379; Ser estrs _site.
 DR Pfam; PF00135; Coesterase6; 1.
 DR PRINTS; PRO1090; NEUROLOGIN.
 DR PROSITE; PS00941; CARBOXYLTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 816 AA; 92020 MW; PB68910773B1BBP6 CRC64;
 Query Match 59.4%; Score 2678.5; DB 4; Length 816;
 Best Local Similarity 62.7%; Pred. No. 2.4e-189;
 Matches 513; Conservative 101; Mismatches 141; Indels 63; Gaps 13;
 QY 38 EERFPVNTAYGRVGRVRRLENNELGVPVQVGLGVPYATPPLGARRFPQPEAPASWQVGR 97
 DB 42 QAQYPVNTYNGKIQGLRTPLESEILGPVQYGLGVPYASPTGERRFPQPESSMTGIR 101
 QY 98 NATLPPACQNL-HGALPAIMLPVWFTDNLAAATVYQNSDCLYLNLYPTEDGPLT 156
 DB 102 NATQSAVCPQHLDERFLHDMLEPIWFTSLDTMTYVQDQNEDECLYNTYVPMED 157
 QY 157 KKRDEATLNPDDTIRDP-GKKPVMLFLHGGSYMEGTGNMFGDSGLAAYGNVIVATLNYR 215
 DB 158 -----DIHEQNSKKPVWYIHGGSYMEGTGNMIDGSLAAYGNVIVATLNYR 204
 QY 216 LGVIGFLSTGQAAKNGYGLLDQIALRWLSJENIAHFGDPERITIFGSGAGASCVNLLI 275
 DB 205 LGIIGFLSTGQAAKNGYGLLDQIALRWIENENYVAFGSDPKRVTIFGSGAGASCVSLLT 264
 QY 276 LSHHSEGLFQKAIQSGTALSSWVNYQPKYTRLLAAKVGCDREDSAEAVECLRRKPSR 335
 DB 265 LSHYSEGLFQKAITQSGTALSSWAVNYQPKYTRILADKVCNMDDTDMVECLRNKRYK 324
 QY 336 ELVDQDQVQARYHIAFGPVDGVDVDPDPEILMQQGEFLNYDMLGVNQEGELKFVEDSA 395
 DB 325 ELIQQTITPATYHIAFGPVIDGVDVDPDQILMEQGEFLNYDMLGVNQEGELKFVDGIV 384
 QY 396 ESEGVASAFDFVSNFVNLGYPEGKDVLRSETIKWYTDKADNDCGEMREKTLALF 455
 DB 385 DNEGVTPNDFSVSNFVNLGYPEGKDTLRSETIKWYTDWADNKENPRTKTLVALF 444
 QY 456 TDHGWAPAVATAKLHADYQSPVYFTFYHHCQAGRPWADAAHGDDELPIYFGVPMVGA 515
 DB 445 TDHGWAPAVATAADLHAQYGSPTFYFAYHHCQSEKMPKSWADSAHGDEVYVFGIWMIGP 504
 QY 516 TDLFPNFSKNDVMSAVWMTYNTNFAKTGDPNQVPQDTKFTHTKPNRFEVYVWVKFNS 575
 DB 505 TELFSCNFSKNDVMSAVWMTYNTNFAKTGDPNQVPQDTKFTHTKPNRFEVYVWVKFNS 564
 QY 576 KEQYLIHGLKPRVRDNRANKVAFWLELVPHLNLHTELF-----TTTTLPL 625
 DB 565 KDQYLIHGLKPRVRDNRANKVAFWLELVPHLNLH-----EIFQYVSTTTKVPDMTSPFY 623
 QY 626 ATRWPPRPAGA-PGTRRRPPPPATLPPEPEPEP---GPRAYDRFGDSRDYSTELSVTVA 681
 DB 624 QTR---RSPAKIMPTTKRPAITPANNPKSKDPKHTGPEDTTTLTIBTKRDYSTELSVTIA 680
 DT 01-OCT-2002 (TREMELrel. 22, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 DE Neurologin Y.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Sutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jamin S., Quach H., Fellous M., Bourgeron T.;
 RT "Evolution and expression of the human neurologin family, including
 RT two primate specific members on the X and Y chromosomes.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLTERASE/LIPASE FAMILY.
 DR EMBL; AF376804; AAM46113.1; -
 DR InterPro; IPR002018; CarbesteraseB.
 DR InterPro; IPR000460; Neurologin.
 DR InterPro; IPR003379; Ser estrs _site.
 DR Pfam; PF00135; Coesterase6; 1.
 DR PRINTS; PRO1090; NEUROLOGIN.
 DR PROSITE; PS00941; CARBOXYLTERASE_B_2; 1.
 KW Hydrolase.
 SQ SEQUENCE 817 AA; D991ACGBAC378763 CRC64;
 Query Match 60.2%; Score 2713.5; DB 4; Length 817;
 Best Local Similarity 63.6%; Pred. No. 6.1e-192;
 Matches 520; Conservative 96; Mismatches 139; Indels 63; Gaps 13;
 QY 38 EERFPVNTAYGRVGRVRRLENNELGVPVQVGLGVPYATPPLGARRFPQPEAPASWQVGR 97
 DB 43 QAQYPVNTYNGKIRGLRTPLENEILGPVQYGLGVPYASPTGERRFPQPESSMTGIR 102
 QY 98 NATLPPACQNL-HGALPAIMLPVWFTDNLAAATVYQNSDCLYLNLYPTEDGPLT 156
 DB 103 NTTQFAAVCPQHLDERSLHDMLEPIWFTANLDTMTYVQDQNEDECLYNTYVPMED 158
 QY 157 KKRDEATLNPDDTIRDP-GKKPVMLFLHGGSYMEGTGNMFGDSGLAAYGNVIVATLNYR 215
 DB 159 -----DIHQNSKKPVWYIHGGSYMEGTGNMIDGSLAAYGNVIVATLNYR 205
 QY 216 LGVIGFLSTGQAAKNGYGLLDQIALRWLSJENIAHFGDPERITIFGSGAGASCVNLLI 275
 DB 206 LGIIGFLSTGQAAKNGYGLLDQIALRWIENENYVAFGSDPKRVTIFGSGAGASCVSLLT 265
 QY 276 LSHHSEGLFQKAIQSGTALSSWVNYQPKYTRLLAAKVGCDREDSAEAVECLRRKPSR 335
 DB 266 LSHYSEGLFQKAITQSGTALSSWAVNYQPKYTRILADKVCNMDDTDMVECLRNKRYK 325
 QY 336 ELVDQDQVQARYHIAFGPVDGVDVDPDPEILMQQGEFLNYDMLGVNQEGELKFVEDSA 395
 DB 326 ELIQQTITPATYHIAFGPVIDGVDVDPDQILMEQGEFLNYDMLGVNQEGELKFVDGIV 385
 QY 396 ESEGVASAFDFVSNFVNLGYPEGKDVLRSETIKWYTDKADNDCGEMREKTLALF 455
 DB 386 DNEGVTPNDFSVSNFVNLGYPEGKDTLRSETIKWYTDWADNKENPRTKTLVALF 445
 QY 456 TDHGWAPAVATAKLHADYQSPVYFTFYHHCQAGRPWADAAHGDDELPIYFGVPMVGA 515
 DB 446 TDHGWAPAVATAADLHAQYGSPTFYFAYHHCQSEKMPKSWADSAHGDEVYVFGIWMIGP 505
 QY 516 TDLFPNFSKNDVMSAVWMTYNTNFAKTGDPNQVPQDTKFTHTKPNRFEVYVWVKFNS 575
 DB 506 TELFSCNFSKNDVMSAVWMTYNTNFAKTGDPNQVPQDTKFTHTKPNRFEVYVWVKFNS 565
 QY 576 KEQYLIHGLKPRVRDNRANKVAFWLELVPHLNLHTELF-----TTTTLPL 625
 DB 566 KDQYLIHGLKPRVRDNRANKVAFWLELVPHLNLH-----EIFQYVSTTTKVPDMTSPFY 624
 QY 626 ATRWPPRPAGA-PGTRRRPPPPATLPPEPEPEP---GPRAYDRFGDSRDYSTELSVTVA 681
 DB 625 QTR---RSPAKIMPTTKRPAITPANNPKSKDPKHTGPEDTTTLTIBTKRDYSTELSVTIA 681
 QY 682 VGSLLFLNIPALAYYKDRQELRRLRSPGSGSGVGGGPPGLLPAAAGRELPEEE 741
 DB 682 VGSLLFLNIPALAYYKDRRTHRRPSPQRTNTNDIAH-----IQNEE 729
 QY 742 LVSLQLKR---GGGVGADPAALPACPPDVTALREAPDDVLLPAGLTLTLPSCGLP 797
 DB 730 IMSLQKQLEHDECSLOAHTLRLTCTPDTTLTKRSPDIDPLMTNTITMPTNLGT 789
 QY 798 PPPPPPSLHPGPPPPPPPTATSNHTLPHPHSTTRV 835
 DB 790 MQP-----LHTNFT-----SGQNSNLPHGHSSTRV 817
 RESULT 13
 Q8NF23
 ID Q8NF23
 AC Q8NF23; PRELIMINARY; PRT; 816 AA.

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QY 682 VGASLLFLNIIAALYKRRRQELRCRLSPGGSGGVPGGGLLPAGRELPPPEE 741
Db 681 VGASLLFLNIIAALYKRRRQELRCRLSPGGSGGVPGGGLLPAGRELPPPEE 728
QY 742 LVSLQLKE- ---GGGAGVADPAELRACPPDYITLARRAPDDVLLAFGALTLLPSGLGP 797
Db 729 IMSLQMKLEHDEHCESIQANDTLRLACPPDYITLARRSPDDIPPMPTNITWIPNLMG 788
QY 798 PPPPPPSLHPGPPPPPPPTATSHNNVTLPHPHSTTRV 835
Db 789 MQP-----LHTFKTF-----SGGQNSTNLPHGHSTTRV 816

RESULT 14
Q9P248 PRELIMINARY; PRT; 682 AA.
ID Q9P248
AC Q9P248;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE Hypothetical protein KIAA1480 (Fragment).
GN KIAA1480
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human
RT genes.XVII.The complete sequences of 100 new cDNA clones from brain
RT which code for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AB040913; BAA96004.1; -.
DR HSP; P21836; 1MAA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
KW Hypothetical protein; Hydrolase.
FT NON_TER
SQ SEQUENCE 682 AA; 75592 MW; 9B6E6DBF44F5DC31 CRC64;

Query Match 52.0%; Score 2344; DB 4; Length 682;
Best Local Similarity 65.7%; Pred. No. 1e-164;
Matches 452; Conservative 82; Mismatches 104; Indels 50; Gaps 12;

QY 168 DTDTRDGGKPKVMLFLHGGSYMGTGMFDGSLVLAAYGNVIVATLNYRLGVFLSTGQ 227
Db 25 DEDIRDSGAKPVMVYIHGGSYMGTGMFDGSLVLAAYGNVIVATLNYRLGVFLSTGQ 84
QY 228 AAKNGYLLDQIQALRWLSNIAHFGDPRITIFSGAGASCNLLIILSHSEGLFQKA 287
Db 85 AAKNGYLLDQIQALRWLSNIAHFGDPRITIFSGAGASCNLLIILSHSEGLFQKA 144
QY 288 IAQSGTAISSWSVNYQPLKYLRLAAVCGDREDSAEAECLRRKPSRELVDQVQARY 347
Db 145 IIQSGSALSSWVNYQPVKYSLLADVGVNLDVDMVDCIAKSAKEIVQDIQARY 204
QY 348 HIARGPVVDGVDDPEILMQOGEFLNYDMLGVNQGEGLKVEBSASESDGVSASF 407
Db 205 HVAFGPVVDGVDDPEILMQOGEFLNYDMLGVNQGEGLKVEBSASESDGVSASF 264
QY 408 FTVSNFVDNLYGYPEGKXDLRETIKFMVTDWDRDNGEMRKTLLALFTDHWVAPAV 467
Db 265 YSVSNFVDNLYGYPEGKXDLRETIKFMVTDWDRDNGEMRKTLLALFTDHWVAPAV 324
QY 468 AKLHADYQSPVYFTFYHHCQAEGRPEWADAAGDELPHYVFGVPMVGATDLFPNFSK 527
Db 325 ADLHARYGSPTYFYFYHHCQSLMKPAWSADAAGDEVYVFGVPMVGATDLFPNFSK 384

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RESULT 15

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QY2F8 PRELIMINARY; PRT; 648 AA.
ID QY2F8
AC QY2F8;
DT 01-NOV-1999 (TremBLrel. 12, Created)
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)
DE Hypothetical protein KIAA0951.
GN KIAA0951.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99246063; PubMed=10231032;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AB023168; BAA76795.1; -.
DR HSP; P21836; 1MAA.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000460; Neurologin.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR01090; NEUROLIGIN.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 648 AA; 72885 MW; 1A2E6727A709BFBC CRC64;

Query Match 50.7%; Score 2287; DB 4; Length 648;
Best Local Similarity 64.8%; Pred. No. 1.5e-160;
Matches 437; Conservative 80; Mismatches 113; Indels 44; Gaps 10;

QY 180 MLFLHGGSYMGTGMFDGSLVLAAYGNVIVATLNYRLGVFLSTGQAAKNGYLLDQI 239
Db 1 MVYIHGGSYMGTGMFDGSLVLAAYGNVIVATLNYRLGVFLSTGQAAKNGYLLDQI 60
QY 240 QALRWLSNIAHFGDPRITIFSGAGASCNLLIILSHSEGLFQKAIASQSTAISSWS 299
Db 61 QALRWLSNIAHFGDPRITIFSGAGASCNLLIILSHSEGLFQKAIASQSTAISSWS 120
QY 300 VNYQPLKYLRLAAVCGDREDSAEAECLRRKPSRELVDQVQARYHIAFGVVDGV 359

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Db      ||||| ||||| ||||| : : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
121 VNYQAKYTRILADKVGCMMLDTTDMVECLKNKNYKELIQOITPATYHIAFGVIDGDV 180
QY      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
360 VPDDPEILMOQGEFLNYDMLGVNQEGLEKVEDSASEDGVSASAPDFTVSNFVDNLYG 419
Db      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
181 IPDDPQILMEQGEFLNYDMLGVNQEGLEKVEDSASEDGVSASAPDFTVSNFVDNLYG 240
QY      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
420 YPEGKDVLRRETIKMYTDMARDNGEMERKTLALFTDHOQWAPAVATAKLHADYQSPVY 479
Db      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
241 YPEGKDVLRRETIKMYTDMARDNGEMERKTLALFTDHOQWAPAVATAKLHADYQSPVY 300
QY      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
480 FYTFYHHCQAGRPWADAAGDELPHYVGVPMVGATDLFPNFSKNDVMSAVVMTYWT 539
Db      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
301 FYAFYHHCQAGRPWADAAGDELPHYVGVPMVGATDLFPNFSKNDVMSAVVMTYWT 360
QY      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
540 NPAKTGDPNQVPQDTKFIHTKPNRFEVWVSKNSKEKQYLHIGLKRVRDNYRANKVA 599
Db      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
361 NPAKTGDPNQVPQDTKFIHTKPNRFEVWVSKNSKEKQYLHIGLKRVRDNYRANKVA 420
QY      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
600 FWLELVPHLHNLHTLFP---TTTTLP-----PYATRWPPRPAGA-PGTRPPPPAT 648
Db      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
421 FWLELVPHLHNLHTLFP---TTTTLP-----PYATRWPPRPAGA-PGTRPPPPAT 476
QY      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
649 LPPEPEPEP---GPRAYDRFPDGRDYSTELSVTVAVGASLLFLNLAFAALYKRRDRQ 705
Db      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
477 NNPXHSKDPFKTGPDITVLIETKDYSTELSVTVAVGASLLFLNLAFAALYKRRDRQ 536
QY      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
706 ELRCRLSPGPGSGSGVFGGGLLPAGRELPPBEELVSLQKR-----GGVVGADPAEAL 761
Db      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
537 HETHRHSFQRNTTNDITH-----IQNEEIMSLQMKQLEHCECESLQAHDTL 584
QY      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
762 RPACPPDYTLALRAPDDVPLLAGALTLPLSGLGPPPPPPPSLHPGPPPPPPPPPPPP 821
Db      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
585 RLTCPPDYTLALRAPDDVPLLAGALTLPLSGLGPPPPPPPPPSLHPGPPPPPPPPPP 634
QY      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
822 HNNTLPHPHSTTRV 835
Db      : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
635 NSTNLPHGHSITRV 648

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Search completed: February 13, 2004, 13:13:38
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 13, 2004, 13:11:12 ; Search time 22 Seconds
(without alignments)
1605.889 Million cell updates/sec

Title: US-09-934-323-2
Perfect score: 4508
Sequence: 1 MWLLALCLVLAGAQRGGGG.....PPTATSHNLTLPHPHSTTRV 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/6C COMB.pep:*
6: /cgn2_6/prodata/1/iaa/6D COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4415.5	97.9	836	4	US-09-491-356C-21
2	2771.6	61.5	843	4	US-09-491-356C-20
3	2746.6	60.9	848	4	US-09-491-356C-22
4	2741.6	60.8	823	4	US-09-491-356C-23
5	1996.4	44.3	553	4	US-09-491-356C-24
6	872.1	19.3	723	6	5200183-4
7	855.1	19.0	602	3	US-08-446-100-1
8	855.1	19.0	602	3	US-08-446-100-3
9	855.1	19.0	602	3	US-08-446-100-4
10	855.1	19.0	602	3	US-08-446-100-6
11	855.1	19.0	602	3	US-08-446-100-24
12	855.1	19.0	602	3	US-09-334-489-3
13	855.1	19.0	602	3	US-09-334-489-4
14	855.1	19.0	602	6	5215903-11
15	854.1	18.9	602	3	US-08-446-100-2
16	854.1	18.9	602	3	US-08-446-100-7
17	853.1	18.9	602	3	US-08-446-100-13
18	852.1	18.9	602	3	US-08-446-100-8
19	852.1	18.9	602	3	US-08-446-100-17
20	852.1	18.9	602	3	US-08-446-100-18
21	851.1	18.9	602	3	US-08-446-100-5
22	849.1	18.8	602	3	US-08-446-100-10
23	849.1	18.8	602	3	US-08-446-100-14
24	848.1	18.8	602	3	US-08-446-100-15
25	848.1	18.8	602	3	US-08-446-100-16
26	846.1	18.8	602	3	US-08-446-100-9
27	844.1	18.7	602	3	US-08-446-100-12

28	843.5	18.7	602	3	US-08-446-100-11	Sequence 11, Appl
29	836.5	18.6	617	2	US-08-370-156-6	Sequence 6, Appl
30	836.5	18.6	617	3	US-08-814-095-6	Sequence 4, Appl
31	831.1	18.4	600	3	US-08-370-156-4	Sequence 4, Appl
32	831.1	18.4	600	3	US-08-814-095-4	Sequence 4, Appl
33	831.1	18.4	600	3	US-08-975-084-1	Sequence 7, Appl
34	829.5	18.4	722	1	US-08-445-050-7	Sequence 1, Appl
35	829.5	18.4	722	2	US-08-204-691-7	Sequence 7, Appl
36	828.5	18.4	722	1	US-08-347-718B-1	Sequence 3, Appl
37	828.5	18.4	722	1	US-08-445-050-3	Sequence 1, Appl
38	828.5	18.4	722	2	US-08-482-262-1	Sequence 3, Appl
39	828.5	18.4	722	2	US-08-204-691-3	Sequence 1, Appl
40	828.5	18.4	722	4	US-09-355-295B-4	Sequence 4, Appl
41	828.5	18.4	722	6	5200183-3	Patent No. 5200183
42	828.5	18.4	742	1	US-08-347-718B-2	Sequence 2, Appl
43	828.5	18.4	742	2	US-08-482-262-2	Sequence 2, Appl
44	828.5	18.4	742	6	5200183-2	Patent No. 5200183
45	828.5	18.4	745	1	US-08-445-050-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-491-356C-21

Sequence 21, Application US/D9491356C

Patent No. 8566061

GENERAL INFORMATION:

APPLICANT: Philibert, Robert A.

APPLICANT: Ginns, Edward I.

APPLICANT: Delisi, Lynn

TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13

FILE REFERENCE: 9465-GUST1

CURRENT APPLICATION NUMBER: US/09/491,356C

CURRENT FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: PCT/US99/09365

PRIOR FILING DATE: 1999-04-29

PRIOR APPLICATION NUMBER: 60/083,465

PRIOR FILING DATE: 1998-04-29

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 836

TYPE: PRT

ORGANISM: Rattus norvegicus

US-09-491-356C-21

Query Match 97.9%; Score 4415.5; DB 4; Length 836;

Best Local Similarity 98.3%; Pred. No. 0;

Mismatches 822; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

Qy	1	MWLLALCLVLAGAQRGGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVRELNN	60
Db	1	MWLLALCLVLAGAQRGGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVRELNN	60
Qy	61	EILGPVVQFLGVPYATPPLGARFPQPEAPASPGVGRNATLPPACFQNLHGALPAIMLP	120
Db	61	EILGPVVQFLGVPYATPPLGARFPQPEAPASPGVGRNATLPPACFQNLHGALPAIMLP	120
Qy	121	VWFTDNLEAATYVQNSDECLYINLYVPTDGLTKRDEATINPDTDIRPGKKPVM	180
Db	121	VWFTDNLEAATYVQNSDECLYINLYVPTDGLTKRDEATINPDTDIRPGKKPVM	180
Qy	181	LFTHGGSYMEGTGNMFDGSLVLAAYGNIVATLNYRLGVGLFSTGDOAAKNGYGLDQIQ	240
Db	181	LFTHGGSYMEGTGNMFDGSLVLAAYGNIVATLNYRLGVGLFSTGDOAAKNGYGLDQIQ	240
Qy	241	ALRWLSNIAHFHGGDPERITIFGSGAGASCNNLLIILSHHSEGLFQKAIAGSGTAISSWSV	300
Db	241	ALRWLSNIAHFHGGDPERITIFGSGAGASCNNLLIILSHHSEGLFQKAIAGSGTAISSWSV	300
Qy	301	NYQPLKYLTRLLAAKVGCDRDSABAVECLRRKPSRELVDQDQVQPARVHIAFGPVWDGVV	360

Db 301 NYQPLKYTRLLAAKVGCDREDS TEAVECLRRKSRRLVDQVQARYHIAFGVVDGVV 360
QY 361 PDDPEILMOQGEFLNVDMLIGNVQSGELKXVEDSAESDGVASAPDFTVSNFVNLXYG 420
Db 361 PDDPEILMOQGEFLNVDMLIGNVQSGELKXVEDSAESDGVASAPDFTVSNFVNLXYG 420
QY 421 PEGKDVIRETIKMYTWDADRDNGEMRRKTLTLLALFTDQWVAPAVATAKLHADYQSPVYF 480
Db 421 PEGKDVIRETIKMYTWDADRDNGEMRRKTLTLLALFTDQWVAPAVATAKLHADYQSPVYF 480
QY 481 YTFYHHCQAEGRPEWADAAGDELPLYVFGVMYGATDLFCNFSKNDVMSAVVMTYTN 540
Db 481 YTFYHHCQAEGRPEWADAAGDELPLYVFGVMYGATDLFCNFSKNDVMSAVVMTYTN 540
QY 541 FAKTGDPNQVPQDTKFIHTKPNRPEVWVSKFNSKEKQYLIHGLKPRVDRNRYRANKVAF 600
Db 541 FAKTGDPNQVPQDTKFIHTKPNRPEVWVSKFNSKEKQYLIHGLKPRVDRNRYRANKVAF 600
QY 601 WLELVPHLNLHTELETTTTTRLPYATRWPPPPA-GAPGTRRRPPPPATLPPEPEPECP 659
Db 601 WLELVPHLNLHTELETTTTTRLPYATRWPPPPA-GAPGTRRRPPPPATLPPEPEPECP 659
QY 660 RAYDRFPGSDRYSTELSVTVAVGASLLFNILAFALYKRRQELRCRLSPGSG 719
Db 661 RAYDRFPGSDRYSTELSVTVAVGASLLFNILAFALYKRRQELRCRLSPGSG 720
QY 720 SGVPGGGLPAPAGRELPEELVSLQKRGSGVADPAELRACPPDYTLALRRAPDD 779
Db 721 SGVPGGGLPAPAGRELPEELVSLQKRGSGVADPAELRACPPDYTLALRRAPDD 780
QY 780 VPLLAGALTLPGLGPPPPPPPSLHPFPFPPPPPTATSHNNTLPHPHSTTRV 835
Db 781 VPLLAGALTLPGLGPPPPPPPSLHPFPFPPPPPTATSHNNTLPHPHSTTRV 836

RESULT 2

US-09-491-356C-20
; Sequence 20, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-491-356C-20

Query Match 61.5%; Score 2771; DB 4; Length 843;
Best Local Similarity 61.1%; Pred. No. 1.4e-202;
Matches 546; Conservative 100; Mismatches 133; Indels 114; Gaps 21;
QY 1 MW-----LLALCLVLGAGAQGGGGGAGFGPLGLGSLG-----EERF 41
Db 7 MNPVYVRAMACV-----HRGSGAP-----LTLCLLGLLQTFHVLSQLDSDVD 52
QY 42 PVVNTAYGVRGVRRLNNEILGVVQFLGVYATPPLGARRFQPEAPASHPGVRNATT 101
Db 53 PLVTTNFGKIRGKKELNNEILGVVQFLGVYATPPLGARRFQPEAPASHPGVRNATT 112
QY 102 LPPACFQNLHGLALPAILMVPVNTNLEAAATVQNSDEDCLYLNLYVPTDGLTKKRD 160

Db 113 PAPVCPQNIIDGRLEFVWLPWFNTNNDLVSSVQDSBEDCLYINIVPTD---VKRIS 169
QY 161 EATLNPPDT-----DIRDP-GKKPVMFLFHGGSYMEGTGNMFDGSLAAYGNVIVATLN 213
Db 170 KECARKPKKXICRKGDIRDSGGPKPVWVYIHGGSYMEGTGNLYDGSVLASVGNVIVITVN 229
QY 214 YRLQVIGFLSTGDOAAKNGNYGLDIOALRWLSEN-AHFGGDDPERITIFSGGAGASCNL 273
Db 230 YRLQVIGFLSTGDOAAKNGNYGLDIOALRWLSEN-AHFGGDDPERITIFSGGAGASCNL 289
QY 274 LILSHHSE-----GLFKAIAGSGTAISSWSVNYQPLKYLTRILAAKVGCDREDSAE 324
Db 290 LTLSHVSEGNRWSNSTKGLFQRAIAQSGTALSNAVSPQAKYARILATVGCNVSTVE 349
QY 325 AVECLRKPRRELVDQVQPARYHIAFGPVVDGVDVDDPEILMOQGEFLYDMLIGNVQ 384
Db 350 LVECLQKPKYKELVDQVQPARYHIAFGPVVDGVDVDDPEILMOQGEFLYDMLIGNVQ 409
QY 385 GEGKLFVEDSAESDGVASAFDFTVSNFVDNLYGYPEGKDVIRETIKMYTWDADRDNG 444
Db 410 GEGKLFVENIVDSDGVSASDFDFAVSNFVDNLYGYPEGKDVIRETIKMYTWDADRDNG 459
QY 445 EMRRKTLTLLALFTDQWVAPAVATAKLHADYQSPVYTFYHHCQAEGRPEWADAAGDEL 504
Db 470 ETRRKTLLALFTDQWVAPAVATAKLHADYQSPVYTFYHHCQAEGRPEWADAAGDEL 529
QY 505 PYVFGVMYGATDLFCNFSKNDVMSAVVMTYTNFAKTGDPNQVPQDTKFIHTKPNR 564
Db 530 PYVFGVMYGATDLFCNFSKNDVMSAVVMTYTNFAKTGDPNQVPQDTKFIHTKPNR 589
QY 565 FEEVWVSKFNSKEKQYLIHGLKPRVDRNRYRANKVAFWLELVPHLNLH---TELTFTTTR 622
Db 590 FEEVWVSKFNSKEKQYLIHGLKPRVDRNRYRANKVAFWLELVPHLNLHNDISQVTSITTKV 649
QY 623 PYVATRWPPPPAGACGCTRRPPPPAT-----LPPPEPEPEGRPRAYDRFPDGRDYSTEL 676
Db 650 P--STDITLTP-----TRKNSTFVTSAPPTAKQDDPKQPS-----FSDVDQDYSTEL 696
QY 677 SVTVAVGASLLFNILAFALYKRRQELRCRLSPGSGSGVPGGGLPAPAGREL 736
Db 697 SVTVAVGASLLFNILAFALYKRRQELRCRLSPGSGSGVPGGGLPAPAGREL 745
QY 737 PPEELVSLQKRGSGVAD-----PAP-ALRPACPPDYTLALRRAPDDVPLLAGAL 788
Db 746 -PEEEMSLQMKH---TDLDEHCESTHPHEVVLRTACPDYTLAMRRSPDDVPLMPTNTI 801
QY 789 TLPSGLGPPPPPPPSLHPFPFPPPPPTATSHNNTLPHP-----HSTTRV 835
Db 802 TMIPNTI-----PGIPLATFNTF-----TGGQNNTLPHPHPHSHSTTRV 843

RESULT 3

US-09-491-356C-22
; Sequence 22, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 22
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Rattus norvegicus

US-09-491-356C-22

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Query Match      60.9%; Score 2746; DB 4; Length 848;
Best Local Similarity 61.1%; Pred. No. 1.2e-200;
Matches 538; Conservative 101; Mismatches 138; Indels 104; Gaps 18;

QY 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGSEERFPVNTAYGRVGRVRELN 60
DB 26 LWFSLVL--RASQ-----APA-----PTVNTHFGKLGARVPLPS 60

QY 61 EILGPVQFLGVYATPPLGARRPQPEAPASWPGVRNATLTPACPNLHGAIPALMLP 120
DB 61 EILGPVQFLGVYATPPLGARRPQPEAPASWPGVRNATLTPACPNLHGAIPALMLP 120

QY 121 VWFNTDLAAATVYQNSECLYLNLYPTED-----PTVNTHFGKLGARVPLPS 160
DB 121 VWFNTDLAAATVYQNSECLYLNLYPTED-----PTVNTHFGKLGARVPLPS 160

QY 161 EATLN---PPDTRDRPKKPVMLFLGSGSYMEGTGNNFDSVLAAGNVIVATLNYRLG 217
DB 161 EATLN---PPDTRDRPKKPVMLFLGSGSYMEGTGNNFDSVLAAGNVIVATLNYRLG 217

QY 181 EDLADNGDEDEDIRDSGAKPVVYIHGGSYMEGTGNNFDSVLAAGNVIVATLNYRLG 240
DB 181 EDLADNGDEDEDIRDSGAKPVVYIHGGSYMEGTGNNFDSVLAAGNVIVATLNYRLG 240

QY 218 VLGFSLTGDQAAGNYGLLDQIQALRWLSNIAHFGGDPERITIFGSGAGSCVNLILS 277
DB 241 VLGFSLTGDQAAGNYGLLDQIQALRWLSNIAHFGGDPERITIFGSGAGSCVNLILS 300

QY 278 HHSEGLFQKAIQAQSGTAISNSVNYQFLKYTRLLAAKVGCDREDSABAEVCLRRKPSREL 337
DB 301 HHSEGLFQKAIQAQSGTAISNSVNYQFLKYTRLLAAKVGCDREDSABAEVCLRRKPSREL 337

QY 338 VDQVQPARVIAFPVVDGVPVDDPEILMQQGEFLNYDMLGVNQGEGLKFEVDSAS 397
DB 361 VEQDIQARVHVAFGPIDGVIPDDPEILMQQGEFLNYDMLGVNQGEGLKFEVDSAS 420

QY 398 EDGVSASAFPTVSNFVNDIYGPPEGKDLRETIKMYTWDARDNGEMRRKTLALFTD 457
DB 421 EDGVSASAFPTVSNFVNDIYGPPEGKDLRETIKMYTWDARDNGEMRRKTLALFTD 480

QY 458 HOWAPAVATAKLHADYQSPVYFTFVHHCOAGRPWADAAGHDELPHYVGVPMVGTAD 517
DB 481 HOWAPAVATAKLHADYQSPVYFTFVHHCOAGRPWADAAGHDELPHYVGVPMVGTAD 540

QY 518 LFCNFSKNDVMSAVVMTYNTNFAKTGDPNQVPQDTKFIHTKPNRFEVVMKFSNKE 577
DB 541 LFCNFSKNDVMSAVVMTYNTNFAKTGDPNQVPQDTKFIHTKPNRFEVVMKFSNKE 600

QY 578 KQYLHGLKPRVDRDYANKVATWELVPHLNHTELF---TTTTLPP-----YATRNP 630
DB 601 KQYLHGLKPRVDRDYANKVATWELVPHLNHTELF---TTTTLPP-----YATRNP 659

QY 631 PRPPAGAGTRPPPPATLPEPEPEPEPRAYDRFPDGS-----RDYSTELSVTV 680
DB 660 PRPPAGAGTRPPPPATLPEPEPEPEPRAYDRFPDGS-----RDYSTELSVTV 712

QY 681 AVASLLFLNLAFAALYKRDROELCRRLSPGSGSGVPGGGLPLPAAGRELPPPEE 740
DB 713 AVASLLFLNLAFAALYKRDROELCRRLSPGSGSGVPGGGLPLPAAGRELPPPEE 761

QY 741 ELVSLQKRGGV-----GADPAELRACPPDYTLALRAPDDVILLAPGALTLLPSGL 795
DB 762 ELVSLQKRGGV-----GADPAELRACPPDYTLALRAPDDVILLAPGALTLLPSGL 818

QY 796 GPPPPPPPPHPPGPPPPPPPTATSHNNT-LPHPHSHSTRV 835
DB 819 GPPPPPPPPHPPGPPPPPPPTATSHNNT-LPHPHSHSTRV 848

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RESULT 4

US-09-491-356C-23
; Sequence 23, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.

```

; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.GUSII
; CURRENT APPLICATION NUMBER: US/09/491.356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 23
; LENGTH: 823
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-491-356C-23

```

```

Query Match      60.8%; Score 2741; DB 4; Length 823;
Best Local Similarity 62.1%; Pred. No. 2.7e-200;
Matches 530; Conservative 102; Mismatches 143; Indels 78; Gaps 16;

QY 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGSEERFPVNTAYGRVGRVRELN 60
DB 26 LWFSLVL--RASQ-----APA-----PTVNTHFGKLGARVPLPS 60

QY 61 EILGPVQFLGVYATPPLGARRPQPEAPASWPGVRNATLTPACPNLHGAIPALMLP 120
DB 61 EILGPVQFLGVYATPPLGARRPQPEAPASWPGVRNATLTPACPNLHGAIPALMLP 120

QY 121 VWFNTDLAAATVYQNSECLYLNLYPTEDPLTKRDEATLN---PPDTRDRPKK 177
DB 121 VWFNTDLAAATVYQNSECLYLNLYPTEDPLTKRDEATLN---PPDTRDRPKK 180

QY 178 PWMLFHGGSYMEGTGNNFDSVLAAGNVIVATLNYRLGVGLFSLTGDQAAGNYGLLD 237
DB 181 PWMLFHGGSYMEGTGNNFDSVLAAGNVIVATLNYRLGVGLFSLTGDQAAGNYGLLD 240

QY 238 QIQALEWLSNIAHFGGDPERITIFGSGAGSCVNLILSHSEGLFQKAIQAQSGTAISS 297
DB 241 QIQALEWLSNIAHFGGDPERITIFGSGAGSCVNLILSHSEGLFQKAIQAQSGTAISS 300

QY 298 WSNVYQPLKYTRLLAAKVGCDREDSABAEVCLRRKPSRELVDQVQPARVIAFPVVDG 357
DB 301 WSNVYQPLKYTRLLAAKVGCDREDSABAEVCLRRKPSRELVDQVQPARVIAFPVVDG 360

QY 358 DVPPDDPEILMQQGEFLNYDMLGVNQGEGLKFEVDSASAFDFTVSNFVNDL 417
DB 361 DVPPDDPEILMQQGEFLNYDMLGVNQGEGLKFEVDSASAFDFTVSNFVNDL 420

QY 418 YGYPEGKDLRETIKMYTWDARDNGEMRRKTLALFTDHOWVAPAVATAKLHADYQSP 477
DB 421 YGYPEGKDLRETIKMYTWDARDNGEMRRKTLALFTDHOWVAPAVATAKLHADYQSP 480

QY 478 VYFTFVHHCOAGRPWADAAGHDELPHYVGVPMVGTADLPCNFSKNDVMSAVVMTY 537
DB 481 VYFTFVHHCOAGRPWADAAGHDELPHYVGVPMVGTADLPCNFSKNDVMSAVVMTY 540

QY 538 WTNFAKTGDPNQVPQDTKFIHTKPNRFEVVMKFSNKEKQYLHGLKPRVDRDYANK 597
DB 541 WTNFAKTGDPNQVPQDTKFIHTKPNRFEVVMKFSNKEKQYLHGLKPRVDRDYANK 600

QY 598 VAFMLELVPHLNHTELF---TTTTLPP-----YATRNPTRPPAGAGTRPPPPATLP 650
DB 601 VAFMLELVPHLNHTELF---TTTTLPP-----YATRNPTRPPAGAGTRPPPPATLP 659

QY 651 PE-----PEPEPEPRAYDRFPDGSRDYSTELSVTVAVGASLLFLNLAFAALYKRD 703
DB 660 NENAQSGMNGQDAGPLLE---NPRDYSTELSVTVAVGASLLFLNLAFAALYKRD 715

QY 704 ROELCRRLSPGSGSGVPGGGLPLPAAGRELPEPEELVSLQKRGGV-----GADPA 758
DB 716 ROELCRRLSPGSGSGVPGGGLPLPAAGRELPEPEELVSLQKRGGV-----GADPA 761

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QY 759 EALRPACPPDYTLARRADDVPLLAGALTLPLSGLGPPPPPPPSLHPFGFPFPPPT 818
Db 762 DTLRLTALPDYTLRLRRSPDDIPMTENTITIPNSL-----VGLQTLHPYNTF----- 810
QY 819 ATSHNNT-LPHPH 830
Db 811 AAGFNSGTGLPHSH 823

RESULT 5
US-09-491-356C-24
; Sequence 24, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491,356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-491-356C-24

Query Match 44.3%; Score 1996; DB 4; Length 553;
Best Local Similarity 67.1%; Pred. No. 8, 2e-144;
Matches 371; Conservative 58; Mismatches 76; Indels 48; Gaps 5;

QY 1 MWLLALCLVLAGAQRGGGPGGAPGGPLGLGLGSLGERFPVNTAYGRVGRVRELN 60
Db 26 LWFLSLAL--RSTQ-----APA-----PTVNTHEGLRGARVPLPS 60
QY 61 EILGPVQFLGVPYATPPIGARRFPPEAPAPSWPGVNRATTLPPACPNLHGAIPALMLP 120
Db 61 EILGPVQFLGVPYAAPPGERFLPPEPPPPSWSGIRNATHFPVPCPNIIHTAVDEVMLP 120
QY 121 VNFDTNLEAAATVQVQSDCLYLYVPTD-----GPIITKRD 160
Db 121 VNFDTNLDIVATYIQEPNEDCLYLYVPTDVKRISKECAKPNKKICRGGGAKKQG 180
QY 161 EATLN---PPDTDIRDPGKKPVMLFHGGSYMEGTGNMFDGSLAAYGNVIVATLNYRLG 217
Db 181 EDLADNDGDEDEIRDSGAKPVWVYTHGGSYMEGTGNMIDGSLASYGNVIVITLNYRAG 240
QY 218 VLGLSTGDAQAKNGYLLDQIALRWLSENIAHFGGDPERITIFGSGAGASCYNLLIS 277
Db 241 VLGLSTGDAQAKNGYLLDQIALRWLSENIAHFGGDPERITIFGSGAGASCYNLLIS 300
QY 278 HSEGLFQKAIQAQSGTAISSWSVNYQPLKYTLRLAAYGCDDREDSAEAVECLRRKPSREL 337
Db 301 HSEGLFQRAIIQSGALSWSAVNYQPVKYSLLADKVCNCVLDVDMVDCLRQKSAKEL 360
QY 338 VQDVQPARHYHAFGRVVDGVDPDDPEILMQQGEFLNYDMLIGNQGEGLKFVEDSAES 397
Db 361 VQDQIQPARHYHAFGEVVDGVDPDDPEILMQQGEFLNYDMLIGNQGEGLKFVEGVYDF 420
QY 398 EDCVSASAFDFTVSNFVNDLYGYPEGKQVLRRTIKFMTYDWRONGEMRKTLLALPTD 457
Db 421 EDGVSCTDFDYSVSNFVNDLYGYPEGKQVLRRTIKFMTYDWRNDPRTKTLVALETD 480
QY 458 HQWAPAVATAKLHADYQSPVYTFYHHCAQEGPEWADAAGDELVPFGVPMVGATD 517
Db 481 HQWEPVSVVATLHARYGSPYTFYAFYHHCAQEGPEWADAAGDELVPFGVPMVGATD 540
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QY 518 LFPCNFSKNDVML 530
Db 541 LFPCNFSKNDVML 553
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RESULT 6
5200183-4
; Patent No. 5200183
; APPLICANT: TANG, JORDAN J.N.; WANG, CHI-SUN
; TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,426
; FILING DATE: 12-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 504,635
; FILING DATE: 04-APR-1990
; APPLICATION NUMBER: 122,410
; FILING DATE: 19-NOV-1987
; SEQ ID NO:4
; LENGTH: 723
5200183-4
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Query Match 19.3%; Score 872; DB 6; Length 723;
Best Local Similarity 30.9%; Pred. No. 4, 6e-58;
Matches 255; Conservative 103; Mismatches 280; Indels 186; Gaps 32;

QY 46 TAYGRVGRVRELNNEILG--FVVQFLGVFPYATPPIGARRFPPEAPAPSWPGVNRATTL 103
Db 8 TEGGFVEGVNKKLS--LLGDSVDIFKGPFFAT---ATKLENFQRHPQWQGTAKATDFK 62
QY 104 PACQNLHGAIPALMLPVNFTDNLEAAATVQVQSDCLYLYVPTDCLPLTKRD 160
Db 63 KRCLQ-----ATTQDSTYQEDCLYLNWVP--QGRKQVHRD 98
QY 161 EATLNPPDITDIRDPGKKPVMLFHGGSYMEGTGN-----MFDGSLAAYGNVIVATL 212
Db 99 -----LPVWVWYGGAFMGSGQGANFLKNLYLDGEIATRGVIVWTF 142
QY 213 NYRLGVGLSTGDAQAKNGYLLDQIALRWLSENIAHFGGDPERITIFGSGAGASCYN 272
Db 143 NYRVGVLGLSTGDANLPGNFGLDQDMAWKRNIAAFGGDPDNITIFGSGAGAIYS 202
QY 273 LLTSLHSEGLFQKAIQAQSGTAISSWSVNYQPLKYTLRLAAYGCDDREDSAEAVECLRRK 332
Db 203 LQTLSPFNKGLIRRAISQSGVALSPWAIQENPLFWAKTIKKVGCPTEDTAKWAGCLKIT 262
QY 333 PSREL-----VDQDVQPARHYHAFGRVVDGVDPDDPEILMQQGEFLNYDMLIGNQ 385
Db 263 DPRALTALVRLPLKSOEYPIVHYLAFIPVVDGDFIPDDPINLYDNAADIDY--LAGINDM 320
QY 386 EGLKFVEDSAESDEGVSASAFDFTVSNFVNDLYGYPEGKQVLRRTIKF--MYTD--WADRON 443
Db 321 DGHLFATVDMVAIDKAKQ--DVTEEDFYRLVSGHTVAKGLGKGTQATFYIHESWAQDPS 377
QY 444 GEMRKTLLALFTDHWQVAP---AVATAKLHADYQSPVYTFYHHCAQEGPEWADAHAH 500
Db 378 QENMKKTVAFAETDILFLIPTEMALAQHRAHAK-SAKTYSYLFSSHPSRMPYIPKWMGADH 436
QY 501 GDELPVVEGVPVVGATDLFPCNFSKNDVMLSAVWMTYNTNFAKTGDP---NQPVQDTKF 557
Db 437 ADDLQVFGKPF--AT---PLGYRAQDRTVSKAMTAYNTNFAKSGDPNMGNSFVPTH--- 488
QY 558 IHTKPNRFEVWNSKFSKEQYLIHGLK---PRVRDNYRANKVAFW---LELVPHLHNL 611
Db 489 -----WYPYTMENGVNDINKKITSMEHLREKLFKFWAVTFEMLP----- 531
QY 612 HTLFTTTTLLPYPATRWPRPPAGATRRPPPPATLPPPEPEPGPAYDRFFGCDSD 671
Db 532 -----TVWGEATHYPPEDDEA-----APVPTDSDSQGGP-----VPPTDSD 569
QY 672 YSTELSVTVAVGASLLFLNLAFALYYKRRRQRLCRRLSPPGSGSGSVPGGGLLPA 731
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Db 570 QTPVPPTDNSQAGPV-----PPTGD-SGAP---PVPT 599
QY 732 AGRELPEELSVLQKGGVGADPAELRACPPDYTLALRAPDDVPLAPGALTLL 791
Db 600 GDSGAPP-----VPPTGDSGAPPV-----PPTGDSG---APPVPTGDSGAPPVP 641
QY 792 PSG-LGPPPPPP-----PPSLHPFGPPPPPPPTATSHNNVTLPHP 829
Db 642 PTGDAGPPVPPTGDSGAPPVPPTGDSGAPPVPTGDSGAPPVP 665

RESULT 7
US-08-446-100-1
; Sequence 1, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-1

Query Match 19.0%; Score 855; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

QY 2 LLALCLVGLAGAQGGGGPGGAPGGGLGSLGEERFPVVNTAYGRVGRVRELNNE 61
Db 15 WFLLCML-----IKSHTEDDIIATKXKVRG-----WMLT 47
QY 62 IL-SPVVQFVGVYATPPLGARFQPEAPASWPGVYRNATLTPACFQNLHGLPAIMP 120
Db 48 VFGTVAFLGIPVAPPLGRFLKPKQSLTKNSDIWNATKYANSCQNDQSFPGFHS 107
QY 121 VWTDNLEAATYVQNSEDCLYNLVYPTDGLTKRDEATLNPDDTDIRDGPKPYW 180

Db 108 EWMNPNTDL-----SEDCLYNLVWVIPAP-----KPKNATVL 138
QY 181 LFLHGGSYMEGTGM--FDGSVLAAYGNVIATNLVRLVGLVGLS--TQDQAAGNYGLD 237
Db 139 IWIYGGGQTSLSLHYDYGKFLARVERVIVVWNYRVGALGFALPQNPAPNGMLFD 198
QY 238 QIOALRWLSENIAHFPGDPERITIFGSGAGASCYNLLILSHSHSGLFKAIQAQSGTAISS 297
Db 199 QOLALQWYOKNIAAFGGNPKSVTLFGSAGAASVSLHLLSPGSHSLFTRAILQSGSFNAP 258
QY 298 WSVN--YQPLKYTRLAAKVCDDREDSAEAVECLRRKESRELVDQDVPARY-----HIAF 351
Db 259 WAVTSLYEARNRTLAKLTGCSRENETEIKLRNKDPOBILNEAFVVPVYGTPLSVNF 318
QY 352 GPVVDGDVVPDDPEILMQQGEFLNYDMLIGVNOGEGKLFVEDSAE--SEDCVSASAEFT 409
Db 319 GPTVDGDLTMDPDLLELQFKTKQILGVNKGDEGTAFLVYGAPGFSKNNSI---IT 374
QY 410 VSNFVDNL-YGYPEGKDVLRITIKFMTDADRNGEWRKTYLLALFTDHOWVAPAVATA 468
Db 375 RKEFQEGKLIFFPGVSEFGKESILFHYTDWDDQRPENYREALGDVVDYVNFICPALEFT 434
QY 469 KLHAYQSPVYFYTFYHCOAEGRPENWADAAGDELFPVFGVPMVGATDLPPCNFSKNDV 528
Db 435 KKFSEWGNNAFFYFEHRSSKLWPENWGMVHGVEIEFVGLPLERRD-----NYTKAE 489
QY 529 MLSAVMYTNTNFAKTGDPNPQVPQDTKFHTKPNRFEVVVWSKFNSEKQYHLHGLK-P 587
Db 490 ILSRIVKRWANFAKYNPNETQNNST-----WPVFKSTEQKYLTLNTEST 536
QY 588 RVRDNYRANKVAFWLELVP 606
Db 537 RIMTKLRAQCRFWTSFPF 555

RESULT 8
US-08-446-100-3
; Sequence 3, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single


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; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-24

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Query Match      19.0%; Score 855; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

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QY 2 WLLALCLVLAGAQRGGGPGGAPGGLGSLGSERPVNTAYGRVGRVRELNNE 61
DB 15 WFLLLCML-----IGKSHTEDDIIATKNGKVRG-----WNLT 47

QY 62 IL-GPVVQFLGVPYATPPLGARFPQPEAPASWPGVNRNATLPPACQNLHGALPAIMLP 120
DB 48 VFGTIVTAFLGIPYAQPPLGRLRFKPKQSLTKWSDIWNATKYANSCCQNDQSPFGFHS 107

QY 121 VMFTDNLLEAAATYVQNSQSDCLYLNLYVPTDGLTKRDEATLNPDPDTRDPPGKPYM 180
DB 108 EMNPNITDL-----SEDCLYLNWIPAP-----KPKNATVL 138

QY 181 LFLHGGSYMEGTGNN--FDGSVLAAYGNVIVATLNYRLGLVGLFSL-TGDOAAKGNVGLLD 237
DB 139 IWIYGGGFGTSSLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNWGLFD 198

QY 238 QIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISS 297
DB 199 QQLALQWQKNIAAFGNGPKSVTLFGESAGAASVSLHLSFGSHSLFTRAILQSGSFNAP 258

QY 298 WSVN--YQPLKYTRLAAKVGCDREDSAAVECLRRKPSRELVDQVQPARV---HIAF 351
DB 259 WATVSLYEARNRTLNLAUKLTGCSRENETEIIKLRNKDQOEILLNEAFVVPYGTPLSVNF 318

QY 352 GPVVDGVDVDDPEILMQOGEFLNYDMLIGVNGOEGKLKVEDSAE--SDGVSASAFDFT 409
DB 319 GPTVDGDFLTDMPDILLELQGFKKTQILGVNKGDEGTAFLVYGAPGFSKONNSI---IT 374

QY 410 VSNFVDNL-YGYPEGKDVLRETIKFMYTWDADRDNGEMRKTLALLFTDHWAPAVATA 468
DB 375 RKEFQGLKIFFGVSEFGKESILFYHTDWDQDRPENTREALGDVVGVDYNFICALEFT 434

QY 469 KLHADYQSPVYFTFYHHCOAQRPEWADAAGDELPPYVFGVPMVGATDLFPNFSKNDV 528
DB 435 KKFSEWGNNAFFYYFEHRSKLPWPENWGMVHGVEYEFVGLPLEERD-----NYTKAE 489

QY 529 MLSAVMTWTWNTAKTGDNPQVPQDTKFIHTKPNRFEVVMWKSFKNSKEKQYHLGLK-P 587
DB 490 ILSRSIVKRWANFAKYGPNETQNNSTS-----WPFVKSTEQKYLTLNTEST 536

QY 588 RVRDNYRANKVAFWLELVP 606
DB 537 RIMTKLRAQOCRWTSFPP 555

```

RESULT 12

```

US-09-334-489-3
; Sequence 3, Application US/09334489
; Patent No. 6291175

```

GENERAL INFORMATION:

```

; APPLICANT: Pierre Sevigny
; APPLICANT: Keith Schappert
; APPLICANT: Heiko Wiesbusch
; TITLE OF INVENTION: METHODS FOR TREATING A NEUROLOGICAL
; FILE REFERENCE: 08523/013002
; CURRENT APPLICATION NUMBER: US/09/334,489
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: 60/089,406
; PRIOR FILING DATE: 1998-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 602

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-334-489-3

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```

Query Match      19.0%; Score 855; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

```

```

QY 2 WLLALCLVLAGAQRGGGPGGAPGGLGSLGSERPVNTAYGRVGRVRELNNE 61
DB 15 WFLLLCML-----IGKSHTEDDIIATKNGKVRG-----WNLT 47

QY 62 IL-GPVVQFLGVPYATPPLGARFPQPEAPASWPGVNRNATLPPACQNLHGALPAIMLP 120
DB 48 VFGTIVTAFLGIPYAQPPLGRLRFKPKQSLTKWSDIWNATKYANSCCQNDQSPFGFHS 107

QY 121 VMFTDNLLEAAATYVQNSQSDCLYLNLYVPTDGLTKRDEATLNPDPDTRDPPGKPYM 180
DB 108 EMNPNITDL-----SEDCLYLNWIPAP-----KPKNATVL 138

QY 181 LFLHGGSYMEGTGNN--FDGSVLAAYGNVIVATLNYRLGLVGLFSL-TGDOAAKGNVGLLD 237
DB 139 IWIYGGGFGTSSLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNWGLFD 198

QY 238 QIQALRWLSENIAHFQGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISS 297
DB 199 QQLALQWQKNIAAFGNGPKSVTLFGESAGAASVSLHLSFGSHSLFTRAILQSGSFNAP 258

QY 298 WSVN--YQPLKYTRLAAKVGCDREDSAAVECLRRKPSRELVDQVQPARV---HIAF 351
DB 259 WATVSLYEARNRTLNLAUKLTGCSRENETEIIKLRNKDQOEILLNEAFVVPYGTPLSVNF 318

QY 352 GPVVDGVDVDDPEILMQOGEFLNYDMLIGVNGOEGKLKVEDSAE--SDGVSASAFDFT 409
DB 319 GPTVDGDFLTDMPDILLELQGFKKTQILGVNKGDEGTAFLVYGAPGFSKONNSI---IT 374

QY 410 VSNFVDNL-YGYPEGKDVLRETIKFMYTWDADRDNGEMRKTLALLFTDHWAPAVATA 468
DB 375 RKEFQGLKIFFGVSEFGKESILFYHTDWDQDRPENTREALGDVVGVDYNFICALEFT 434

QY 469 KLHADYQSPVYFTFYHHCOAQRPEWADAAGDELPPYVFGVPMVGATDLFPNFSKNDV 528
DB 435 KKFSEWGNNAFFYYFEHRSKLPWPENWGMVHGVEYEFVGLPLEERD-----NYTKAE 489

QY 529 MLSAVMTWTWNTAKTGDNPQVPQDTKFIHTKPNRFEVVMWKSFKNSKEKQYHLGLK-P 587
DB 490 ILSRSIVKRWANFAKYGPNETQNNSTS-----WPFVKSTEQKYLTLNTEST 536

QY 588 RVRDNYRANKVAFWLELVP 606
DB 537 RIMTKLRAQOCRWTSFPP 555

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RESULT 13

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US-09-334-489-4
; Sequence 4, Application US/09334489
; Patent No. 6291175

```

GENERAL INFORMATION:

```

; APPLICANT: Pierre Sevigny
; APPLICANT: Keith Schappert
; APPLICANT: Heiko Wiesbusch
; TITLE OF INVENTION: METHODS FOR TREATING A NEUROLOGICAL
; FILE REFERENCE: 08523/013002
; CURRENT APPLICATION NUMBER: US/09/334,489
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: 60/089,406
; PRIOR FILING DATE: 1998-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 602
; TYPE: PRT

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ORGANISM: Homo sapiens
US-09-334-489-4

Query Match 19.0%; Score 855; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

QY 2 WLALCLVGLAGACGGGPGGAPGGLGSLGEEFPVNTAYGRVGRVRELNNE 61
DB 15 WFLLLCML-----IGKSHTEDDIIATKNGKVRG-----NNLT 47
QY 62 IL-GPVVQFLGVPYATPPLGARRFOPPEAPAPGWGVRNATTLPPACQNLHGALPAIMLP 120
DB 48 VFGGTVTAFLGIPYAQPPLGRFKKPSQSLTKWSDIWNATKYANSCQNDIQSPFGFHGS 107
QY 121 VFTDNLEAAATYVQNSDCLYLNLYVPTDGLTKKRDEATLNPPTDIRDPGKPKVM 180
DB 108 EMWNPNTDL-----SEDCLYLNWIPAP-----KPKNATVL 138
QY 181 LFLHGSYMEGTGNM--PDGSLVLAAYGNVIVATLNYRLGVLGFLS--TGDQAAGNYGLLD 237
DB 139 IWIYGGGFGTQSSHLVYDGFARVERVIVSMYRVGALGFLALPENGPEAPGNMGLFD 198
QY 238 QIQLRWLSENIAHFGDPERITIFSGAGASCYNLLILSHSEGLFQKAIQSGTAISS 297
DB 199 QQLALQWQKNIAAFAGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAP 258
QY 298 WSVN--YQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVOPARY-----HIAF 351
DB 259 WATVSLYEARNRTLNKLTKGCSRENETEIKLANKDQOEILLNEAFVVPYGTPLSVNF 318
QY 352 GPVVDGVDVDDPEILMOQGEFLYDMLIGNVQEGELKFVEDSAE--SEDGVASAFDFT 409
DB 319 GPTVDGDLTMDPILLELQGFKTQILVGVNKGDEGTAFLVYGAPGSKNNNSI---IT 374
QY 410 VSNFVDNL--YGYPEGKDVLRITKFMYTDWADRDNGEMRRKTLALFTDHWVAPAVATA 468
DB 375 RKEFOEGLKIPFGVSEFGKSIILFHYTDWDDQRPENYREALGDVVDYNYFCPALEFT 434
QY 469 KLHAYQSPVYFTFYHHCQAEGRPEWADAAGDELPPYVGVPMVGATDLFPNPKNDV 528
DB 435 KKFSEWGNNAFFYFHRSSKLPWPMWGVHGEIEFVGLPLERRD-----NYTKAE 489
QY 529 MLSAVMTYNTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSKNSKEQVLIHLGLK-P 587
DB 490 ILRSIVRWNANFAKYNPNETQNNST-----WPFKSTEQKYLTLNTEST 536
QY 588 RVRDNYRANKVAFWLELVP 606
DB 537 RINTKLRAQOCRFWTSFPF 555

RESULT 14
5215909-11
; Patent No. 5215909
; APPLICANT: SOREO, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:11;
; LENGTH: 602
5215909-11

Query Match 19.0%; Score 855; DB 6; Length 602;
Best Local Similarity 32.5%; Pred. No. 7.1e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

QY 2 WLALCLVGLAGACGGGPGGAPGGLGSLGEEFPVNTAYGRVGRVRELNNE 61
DB 15 WFLLLCML-----IGKSHTEDDIIATKNGKVRG-----NNLT 47
QY 62 IL-GPVVQFLGVPYATPPLGARRFOPPEAPAPGWGVRNATTLPPACQNLHGALPAIMLP 120
DB 48 VFGGTVTAFLGIPYAQPPLGRFKKPSQSLTKWSDIWNATKYANSCQNDIQSPFGFHGS 107
QY 121 VFTDNLEAAATYVQNSDCLYLNLYVPTDGLTKKRDEATLNPPTDIRDPGKPKVM 180
DB 108 EMWNPNTDL-----SEDCLYLNWIPAP-----KPKNATVL 138
QY 181 LFLHGSYMEGTGNM--PDGSLVLAAYGNVIVATLNYRLGVLGFLS--TGDQAAGNYGLLD 237
DB 139 IWIYGGGFGTQSSHLVYDGFARVERVIVSMYRVGALGFLALPENGPEAPGNMGLFD 198
QY 238 QIQLRWLSENIAHFGDPERITIFSGAGASCYNLLILSHSEGLFQKAIQSGTAISS 297
DB 199 QQLALQWQKNIAAFAGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAP 258
QY 298 WSVN--YQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVOPARY-----HIAF 351
DB 259 WATVSLYEARNRTLNKLTKGCSRENETEIKLANKDQOEILLNEAFVVPYGTPLSVNF 318
QY 352 GPVVDGVDVDDPEILMOQGEFLYDMLIGNVQEGELKFVEDSAE--SEDGVASAFDFT 409
DB 319 GPTVDGDLTMDPILLELQGFKTQILVGVNKGDEGTAFLVYGAPGSKNNNSI---IT 374
QY 410 VSNFVDNL--YGYPEGKDVLRITKFMYTDWADRDNGEMRRKTLALFTDHWVAPAVATA 468
DB 375 RKEFOEGLKIPFGVSEFGKSIILFHYTDWDDQRPENYREALGDVVDYNYFCPALEFT 434
QY 469 KLHAYQSPVYFTFYHHCQAEGRPEWADAAGDELPPYVGVPMVGATDLFPNPKNDV 528
DB 435 KKFSEWGNNAFFYFHRSSKLPWPMWGVHGEIEFVGLPLERRD-----NYTKAE 489
QY 529 MLSAVMTYNTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSKNSKEQVLIHLGLK-P 587
DB 490 ILRSIVRWNANFAKYNPNETQNNST-----WPFKSTEQKYLTLNTEST 536
QY 588 RVRDNYRANKVAFWLELVP 606
DB 537 RINTKLRAQOCRFWTSFPF 555

RESULT 15
US-08-446-100-2
; Sequence 2, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-2

Query Match      18.9%; Score 854; DB 3; Length 602;
Best Local Similarity 32.5%; Pred. No. 8.4e-57;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

QY      2 WLLALCLVGLAGORGGPGGAGPGGGLGSLGEERPPVNTAYGRVGVRELNNE 61
Db      15 WFLLCML-----IGKSHTEDDIIATKNGKVRG---MNL 47

QY      62 IL-GPVVQFLGVPYATPPLGARFPQPEAPASWPGVNRNATLPPACQNLHGLPALMLP 120
Db      48 VFGGTVTAFLGIPYAPQPLGLRPFKPSLTWSDIWNATKYANSCCNIDQSFPGFHGS 107

QY      121 WFTDNLEAAATVYQVQSEDCLYINLYVPTDQPLTKRDEATLNPPTDIRDPGKKPYM 180
Db      108 EMNPNL-----SEDCLYLNWIPAP-----KPKNATVL 138

QY      181 LFLHGGSYMEGTGMW--FDGSLAAVGNVIVATLNVGLVGLS-TGDAQAKGNVGLLD 237
Db      139 IWYGGHFGTSLHVDGKFLARVERVIVSNYRVGALGFLALPGNPEAPGNMGLFD 198

QY      238 QIQALRWLSNIAHFQGDPERITIFGSGAGACVNLIIISHHSEGLFQKAIQSGTAISS 297
Db      199 QQLALQWQVQNIAAFQGNPKSVILFGESAGASVSLHLLSPGSHSLFTRAILQSGFNAP 258

QY      298 WSVN--YQPLKYTRLLAAKVGCDREDSAEVCELRKPSRELVDQVQPARY-----HIAP 351
Db      259 WAVTSLEYARNRTLNLAQLTGCSENETETIKLRNKPQEIILLNEAFVVPYGTPLSVNF 318

QY      352 GPVVGDVDPDDPEILMQQGEFLNYDMLGVNQGEGLEKVEDSAE--SEDGVSASAFDFT 409
Db      319 GPTVGDGFLTMDPDLLELGQFKQTQILGVNVKDEGTAFIVGAPGFSKNNSI-----IT 374

QY      410 VSNFVNL-YGYPEGKDVLRRTIKFMYTDWADRDNGEMERKTLALFTDHWVAPAVATA 468
Db      375 RKEFQGLKIFPGVSEFGKESILFHYTDWDDQRPENREALGDVVGDFNYFCPALFT 434

QY      469 KLHADVQSPVYFVYVHHCAGRPEDWADAAGDELPPYGVPMVGATDLFCNFSKNDV 528
Db      435 KFSSEGNNAFFYFHRSSKLPWPMWGMVHGHEIEFVFGPLERRD-----NYTKAE 489

QY      529 MLSAVVMYTNFAKTGDPNQVPQDTKFIHTKPNRFEVWMSKFNSEKQVLIHLK-P 587
Db      490 ILRSIVKRWANFAKYNFNETQNNTS-----WPFVKSTEQKYLTLNTEST 536

QY      588 RVRDNYRANKVAFWLELVP 606
Db      537 RIMTKLRAQOCREWTSTFFP 555
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Search completed: February 13, 2004, 13:14:50
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 13, 2004, 13:06:01 ; Search time 47 Seconds
(without alignments)
2819.930 Million cell updates/sec

Title: US-09-934-323-2
Perfect score: 4508
Sequence: 1 MWLLALCLVGLAGRGGGG.....PPATSHNHTLPHPHSTTRV 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4508	100.0	835	AAE25020	Human drug metabol
2	4508	100.0	835	ABB97215	Novel human protei
3	4508	100.0	835	ABB07675	Human carboxyleste
4	4422	98.1	837	AAE62400	Human MESP4 polype
5	4075.5	50.4	801	23 ABB07524	Human drug metabol
6	2770	61.4	828	23 ABB43803	3 isoform protein.
7	2731	60.6	816	20 AAY41740	Human PRO701 prote
8	2731	60.6	816	21 AAB44296	Human PRO701 (UN03
9	2731	60.6	816	21 AAB33427	Human PRO701 prote

10	2731	60.6	816	24	ABU61126	Human PRO701 polyp
11	2713.5	60.2	817	24	ABB82852	CES2 related polyp
12	2678.5	59.4	816	23	AA448908	Human neurotrophin
13	2361	52.4	1434	22	ABG10270	Novel human diagno
14	1747	38.8	726	22	ABG10264	Novel human diagno
15	1745.5	38.7	509	22	AAW93205	Human polypeptide,
16	1685	37.4	308	21	AA440734	Human ORFX ORF438
17	1681	37.3	509	22	AA44127	Human protein sequ
18	1681	37.3	509	24	ABB82853	CES2 related polyp
19	1381	30.6	396	22	AAU87273	Novel central nerv
20	1359	30.1	271	22	ABG10266	Novel human diagno
21	993	22.0	229	21	AA444913	Human secreted pro
22	954	21.2	335	22	AAW93345	Human polypeptide,
23	906	20.1	229	21	AA444914	Human secreted pro
24	863	19.1	165	22	ABG10269	Novel human diagno
25	859	19.1	574	23	AAO18905	Rat butyrylcholine
26	858.5	19.0	614	24	ABP59222	Human drug metabol
27	855	19.0	602	14	AA374442	Full-length human
28	855	19.0	602	21	AA444573	Human wild type Bu
29	855	19.0	602	21	AA444574	Human Butyrylcholi
30	855	19.0	602	21	AA444575	Human wild-type bu
31	855	19.0	602	21	AA444576	Human butyryl chol
32	855	19.0	602	21	AA444577	Human butyryl chol
33	855	19.0	602	21	AA444578	Human butyryl chol
34	855	19.0	602	21	AA444579	Human butyryl chol
35	854	18.9	602	21	AA444580	Human butyryl chol
36	854	18.9	602	21	AA444581	Human butyryl chol
37	853	18.9	602	21	AA444582	Human butyryl chol
38	853	18.9	602	23	AAO18897	Human butyrylcholi
39	852	18.9	602	21	AA444583	Human butyryl chol
40	852	18.9	602	21	AA444584	Human butyryl chol
41	852	18.9	602	21	AA444585	Human butyryl chol
42	851	18.9	602	21	AA444586	Human butyryl chol
43	849	18.8	602	21	AA444587	Human butyryl chol
44	849	18.8	602	21	AA444588	Human butyryl chol
45	848	18.8	602	21	AA444589	Human butyryl chol

ALIGNMENTS

RESULT 1
AAE25020 standard; Protein; 835 AA.
ID AAE25020 standard; Protein; 835 AA.
AC AC
XX AC
XX AC
DT 30-OCT-2002 (first entry)
DE Human drug metabolising enzyme (DME-5).
DE Human; drug metabolising enzyme; autoimmune; inflammatory disorder;
KW acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;
KW proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;
KW asthma; neurological disorder; Alzheimer's disease; Huntington's disease;
KW dementia; Parkinson's disease; developmental disorder; anaemia; adenoma;
KW drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract;
KW renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer;
KW anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;
KW goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant;
KW anticonvulsant; nootropic; enzyme; DME-5.
XX Homo sapiens.
XX OS
XX Key
XX Location/Qualifiers
XX 1..14
XX /label= Signal_peptide
XX 15..835
XX /note= "Mature human DME-5"
XX 1..16
XX /label= Signal_peptide
XX 17..835
XX /note= "Mature human DME-5"

FT	Domain	192..215
FT	/note= "Transmembrane domain"	
FT	671..699	
FT	Domain	
FT	/note= "Transmembrane domain"	
XX	NO200246426-A2	
XX	PN	
XX	PD	13-JUN-2002.
XX	PP	04-DEC-2001; 2001WO-US47429.
XX	PR	08-DEC-2000; 2000US-254308P.
XX	PR	15-DEC-2000; 2000US-256189P.
XX	PR	21-DEC-2000; 2000US-259713P.
XX	PR	19-JAN-2001; 2001US-262706P.
XX	PR	02-FEB-2001; 2001US-266020P.
XX	PA	(INCYTE GENOMICS INC.
XX	PI	Sanjaywala MM, Yao MG, Au-young J, Baughn MR,
XX	PI	Lee EA, Ding L, Hafalia AJA, Tang YT, Yue H,
XX	PI	Lu DAM, Lal PG, Warren BA, Yang J, Wallia NK,
XX	PI	Gandhi AR, Lu Y, Ison CH;
XX	PS	WPI; 2002-519668/55.
DR	DR	N-PSDB; AAD40569.
XX	PT	Novel human drug metabolizing polypeptide, useful in diagnosis,
XX	PT	prevention or treatment of autoimmune/inflammatory, cell proliferative,
XX	PT	neurological, developmental, endocrine, metabolic and gastrointestinal disorders -
XX	PS	Claim 60; Page 147-149; 169pp; English.
XX	CC	The invention relates to an isolated human drug metabolising enzyme (DME)
XX	CC	and its nucleotide. DME is useful for diagnosing, treating or preventing
XX	CC	disorders associated with aberrant expression of DME, where the disorders
XX	CC	are selected from autoimmune/inflammatory disorder such as acquired
XX	CC	immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,
XX	CC	uveitis; a cell proliferative disorder such as arteriosclerosis,
XX	CC	cirrhosis, hepatitis, and cancer; a neurological disorder such as
XX	CC	Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;
XX	CC	a developmental disorder such as renal tubular acidosis, epilepsy,
XX	CC	anaemia; an endocrine disorder such as adenoma, thrombosis and
XX	CC	infections; an eye disorder such as conjunctivitis, glaucoma, cataract;
XX	CC	metabolic disorder such as cystic fibrosis, diabetes and goitre; a
XX	CC	gastrointestinal disorder such as anorexia, peptic ulcer; and liver
XX	CC	disorders. DME is useful in a number of drug screening techniques and to
XX	CC	analyse the proteome of a tissue or cell type. The invention is useful
XX	CC	for creating knock-in humanised animals or transgenic animals to model
XX	CC	human diseases, in somatic or germline gene therapy, to generate a
XX	CC	transcript image of a tissue or cell type, for detecting differences in
XX	CC	the chromosomal location due to translocation, inversion, etc. among
XX	CC	normal, carrier or affected individuals, and as hybridisation probes for
XX	CC	mapping naturally occurring genomic sequences. The present sequence is
XX	CC	human DME-5.
XX	Sequence	835 AA;
XX	SQ	
XX	Query Match	100.0%; Score 4508; DB 23; Length 835;
XX	Best Local Similarity	100.0%; Pred. No. 4.3e-316;
XX	Matches 835; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MWLALCLVLGLAGAQRGGGPGGAGCGGPGGLGLGSIGERFPVVTAYGRVGARELN	60
Ddb	1 MWLALCLVLGLAGAQRGGGPGGAGCGGPGGLGLGSIGERFPVVTAYGRVGARELN	60
OY	61 EILGPVVQFLGVYPATPLGARFOPPEAPASWPGVNATTLLPPACQNHLGALLPALMLP	120
Ddb	61 EILGPVVQFLGVYPATPLGNRFOPEEAPASWPGVNATTLLPPACQNHLGALLPALMLP	120
OY	121 VWFDNLSEAAATYYQNSECLYLNIYVPTEDGPLTKGDEATLPDPDTDIRDQKPKVM	180

Qy	661	AYDRFPGDSRDYSTEISVTVAVGASLLFLNILAFAALYYKDRRQELRCRLSPFGSGS	720
Db	661	AYDRFPGDSRDYSTEISVTVAVGASLLFLNILAFAALYYKDRRQELRCRLSPFGSGS	720
Qy	721	GVPGGGPLLPAAGRELPPPEELVSLQKRGGGVGADPAELRACPPDYTLARRAPDDV	780
Db	721	GVPGGGPLLPAAGRELPPPEELVSLQKRGGGVGADPAELRACPPDYTLARRAPDDV	780
Qy	781	PLIAPGALTLPSGLGPPPPPPPSLHPFGPPPPPTATSHNNTLPHPHSTTRV	835
Db	781	PLIAPGALTLPSGLGPPPPPPPSLHPFGPPPPPTATSHNNTLPHPHSTTRV	835
RESULT 3			
ABB07675			
ID	ABB07675 standard; Protein; 835 AA.		
XX	AC	ABB07675;	
XX	AC	ABB07675;	
DT	10-JUN-2002 (first entry)		
XX			
DE	Human carboxylesterase family member, 33410 polypeptide.		
XX			
KW	Carboxylesterase; 33410; cytostatic; cardiant; dermatological; human;		
KW	antidiabetic; antirheumatic; antiarthritic; antiarrhythmic; vasotropic;		
KW	vulnerable; neuroprotective; antiinflammatory; antilicer; antiasthmatic;		
KW	antiallergic; antiviral; hepatotropic; nephrotropic; anti-HIV; enzyme;		
KW	antiparkinsonian; tuberculostatic; hypotensive; antithrombotic;		
KW	nootropic; antisense therapy; angiogenesis; gene therapy.		
XX			
OS	Homo sapiens.		
XX			
XX	WC0204216616-A2.		
XX			
PD	28-FEB-2002.		
XX			
XX	21-AUG-2001; 2001WO-US26091.		
PF			
XX			
XX	21-AUG-2000; 2000US-226774P.		
PR			
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Curtis RAJ;		
XX			
XX	WPI; 2002-257916/30.		
DR			
DR	N-PSDB; ABA95199, ABA95200.		
XX			
PT	New carboxylesterase nucleic acid 33410, useful for the treatment and		
PT	diagnosis of immune, cardiovascular, reproductive and cancerous		
PT	disorders -		
XX			
PS	Claim 1; Page 110; 123pp; English.		
XX			
XX	The invention provides a novel carboxylesterase family member, designated		
CC	33410. Compounds that binds to or modulate the activity or expression of		
CC	33410, are useful for treating or preventing a disorder such as cellular		
CC	proliferative or differentiative, neural, cardiovascular, prostatic, skin		
CC	brain and skeletal muscular disorders, protein-protein interaction		
CC	disorders, signal transduction disorders, immune (e.g. diabetes and		
CC	rheumatoid arthritis), reproductive, cardiovascular (e.g. hypertension,		
CC	atherosclerosis, coronary artery disease, arrhythmia, ischaemic heart		
CC	disease and angina pectoris), vascular disorders (e.g. varicose veins,		
CC	Wegener's granulomatosis and wound healing) or cancerous disorders,		
CC	multiple sclerosis, Crohn's disease, ulcers, asthma, allergy, infection,		
CC	kidney disease (glomerulonephritis), idiopathic thrombocytopenic purpura,		
CC	hepatitis, tuberculosis, human immunodeficiency virus, Alzheimer's and		
CC	Parkinson's. The 33410 polynucleotide and polypeptide are useful for		
CC	diagnosis of a predisposition to a disorder, for evaluating the efficacy		
CC	of a therapeutic or prophylactic disorder, for chromosome mapping, as		
CC	immunogens, for drug screening, for the detection of mutations in the		
CC	gene and for tissue typing. The present sequence represents the human		
CC	carboxylesterase family member, 33410.		
XX			

SQ		Sequence	835 AA;
Query Match		100.0%;	Score 4508; DB 23; Length 835;
Best Local Similarity		100.0%;	Pred. No. 4.3e-316;
Matches		835; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MWLLALCLVLAGAQRGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVREINN	60
Db	1	MWLLALCLVLAGAQRGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVREINN	60
QY	61	ELTGVVQFLGVVYATPLGARFPQPEAPASWFGVNRNATLPPACQNLHGLPALMLP	120
Db	61	ELTGVVQFLGVVYATPLGARFPQPEAPASWFGVNRNATLPPACQNLHGLPALMLP	120
QY	121	VWFTDNLEAAATYVQNQSEDCLYNLVYPTEDGTLTKRDEATLNPEDTIRDPGKPFVM	180
Db	121	VWFTDNLEAAATYVQNQSEDCLYNLVYPTEDGTLTKRDEATLNPEDTIRDPGKPFVM	180
QY	181	LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATLNLVGLFSLTGDQAAKNGYLLDQIQ	240
Db	181	LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATLNLVGLFSLTGDQAAKNGYLLDQIQ	240
QY	241	ALRWLSENIAHFGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISSWSV	300
Db	241	ALRWLSENIAHFGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISSWSV	300
QY	301	NYQPLKYTRLLAAKVGCDREDSABAECLRRKPSRELVDQDVQPARVHIAFGPVVDGVV	360
Db	301	NYQPLKYTRLLAAKVGCDREDSABAECLRRKPSRELVDQDVQPARVHIAFGPVVDGVV	360
QY	361	PDDPEILMQQGEFLNYDMLIGNQGEGLKFVEDSAESDGVSAFDTVSFVNDNLGY	420
Db	361	PDDPEILMQQGEFLNYDMLIGNQGEGLKFVEDSAESDGVSAFDTVSFVNDNLGY	420
QY	421	PEGKDVLRRTIKFMYTDWADRDNGEMRKTLALFTDQWVAPAVATAKLHADYQSPVYF	480
Db	421	PEGKDVLRRTIKFMYTDWADRDNGEMRKTLALFTDQWVAPAVATAKLHADYQSPVYF	480
QY	481	YTFYHHCQAEGRPEWADAAGDELPHYVGVPMVGATDLFFCNFSKNDVWLSAVVMYWTN	540
Db	481	YTFYHHCQAEGRPEWADAAGDELPHYVGVPMVGATDLFFCNFSKNDVWLSAVVMYWTN	540
QY	541	FAKTDGDNQPVQDTKIHTKPNRPFEEVWVSKNSKEQYLHGLKPRVRDNRANKVAF	600
Db	541	FAKTDGDNQPVQDTKIHTKPNRPFEEVWVSKNSKEQYLHGLKPRVRDNRANKVAF	600
QY	601	WLELVPHLNLHTELTFTTTLPPYATRWPPRPAGAPGTRRPPPPATLPPEPEPGR	660
Db	601	WLELVPHLNLHTELTFTTTLPPYATRWPPRPAGAPGTRRPPPPATLPPEPEPGR	660
QY	661	AYDRFGDSRDYSELSTVAVGASLLFLNLAFAALYYKDRRQELRCRLSPGGSGS	720
Db	661	AYDRFGDSRDYSELSTVAVGASLLFLNLAFAALYYKDRRQELRCRLSPGGSGS	720
QY	721	GVPGGGPLLPAAGRELPEELVSLQKRGGGVADPAEALRACPPDYTLALRRAPDDV	780
Db	721	GVPGGGPLLPAAGRELPEELVSLQKRGGGVADPAEALRACPPDYTLALRRAPDDV	780
QY	781	PLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPPPPTATSHNLTLPHPHSTTRV	835
Db	781	PLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPPPPTATSHNLTLPHPHSTTRV	835
RESULT 4			
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XX	ID	AAB62400	standard; Protein; 837 AA.
XX	AC	AAB62400;	
XX	AC	AAB62400;	
DT	29-JUN-2001	(first entry)	
XX	DE	Human MBSP4 polypeptide (clone 21417374.0.9).	

KW MBSPX; cancer; preclampsia; immune system; neurological; cytostatic;
KW synecological; antiinflammatory; neuroprotective; inotropic; relaxant;
KW cardiant; dermatological; gene therapy; human; MBSP4.
OS Homo sapiens.
XX
EN WO200127277-A2.
XX
PD 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-0528480.
XX
PR 13-OCT-1999; 99US-0159231.
PR 12-JAN-2000; 2000US-0175670.
PR 12-OCT-2000; 2000US-0159231.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Lichenstein H, Boldog FL;
XX
XX WPI; 2001-282030/29.
DR N-PSDB; AAF82996.
XX
PT Novel human polynucleotide sequences and the membrane bound or secreted
XX polypeptides encoded by these sequences, designated MBSPX -
XX
PS Claim 1; Page 26-29; 157pp; English.
XX
XX The invention relates to novel polypeptides, termed MBSPX and
XX polynucleotides encoding the MBSPX polypeptides. The MBSPX polypeptide,
XX nucleic acid and an MBSPX antibody are useful for treating or preventing
XX a pathology associated with the protein especially in humans. The MBSPX
XX nucleic acid can be used to express MBSPX protein (e.g. via a recombinant
XX expression vector in a host cell in gene therapy applications), an to
XX detect MBSPX mRNA in a biological sample or a genetic lesion in a MBSPX
XX gene. Disorders associated with insufficient or excessive production of
XX MBSPX protein include cancer, preclampsia, immune system disorders and
XX inflammation, neurological disorders, cardiovascular disorders; and skin
XX and muscle abnormalities. The anti-MBSPX antibodies can be used to detect
XX and isolate MBSPX proteins and modulate MBSPX activity. The present
XX sequence represents the amino acid sequence of MBSP4, a human neurologin
XX 2 homologue.

SQ Sequence 837 AA;

Query Match 98.1%; Score 4422; DB 22; Length 837;

Best Local Similarity 98.6%; Pred. No. 6.9e-310; Mismatches 10; Indels 2; Gaps 2;
Matches 825; Conservative 0;

QY	1	MWLLALCLVLAGAQRGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVREINN	60
Db	1	MWLLALCLVLAGAQRGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRVREINN	60
QY	61	ELTGVVQFLGVVYATPLGARFPQPEAPASWFGVNRNATLPPACQNLHGLPALMLP	120
Db	61	ELTGVVQFLGVVYATPLGARFPQPEAPASWFGVNRNATLPPACQNLHGLPALMLP	120
QY	121	VWFTDNLEAAATYVQNQSEDCLYNLVYPTEDGTLTKRDEATLNPEDTIRDPGKPFVM	180
Db	121	VWFTDNLEAAATYVQNQSEDCLYNLVYPTEDGTLTKRDEATLNPEDTIRDPGKPFVM	180
QY	181	LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATLNLVGLFSLTGDQAAKNGYLLDQIQ	240
Db	181	LFLHGGSYMEGTGNMFDGSLVLAAYGNVIVATLNLVGLFSLTGDQAAKNGYLLDQIQ	240
QY	241	ALRWLSENIAHFGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISSWSV	300
Db	241	ALRWLSENIAHFGDPERITIFGSGAGASCYNLLILSHHSEGLFQKAIAGSGTAISSWSV	300
QY	301	NYQPLKYTRLLAAKVGCDREDSABAECLRRKPSRELVDQDVQPARVHIAFGPVVDGVV	360
Db	301	NYQPLKYTRLLAAKVGCDREDSABAECLRRKPSRELVDQDVQPARVHIAFGPVVDGVV	360

QY 361 PDDPEILMOQGEFLNDYMLIGNQEGKLFVEDSASESDGVSASAFDFTVSNFVNDLYGY 420
 Db 361 PDDPEILMOQGEFLNDYMLIGNQEGKLFVEDSASESDGVSASAFDFTVSNFVNDLYGY 420
 QY 421 PEGKDLVRETIKFMVYTDWADRDNGEMRRKTLTLLAFTDQHWAPAVATAKLHADYQSPVYF 480
 Db 421 PEGKDLVRETIKFMVYTDWADRDNGEMRRKTLTLLAFTDQHWAPAVATAKLHADYQSPVYF 480
 QY 481 YTFYHHCQAEGRPEWADAAGDELPIYFGVPMVGATDLFPCNFKNDVMLSAVVMTYWTN 540
 Db 481 YTFYHHCQAEGRPEWADAAGDELPIYFGVPMVGATDLFPCNFKNDVMLSAVVMTYWTN 540
 QY 541 FAKTGDNPQPDQTKFTHTKPNRPEEVVWKSFKSEKQYLIHGLKPRVRDNYRANKVAF 600
 Db 541 FAKTGDNPQPDQTKFTHTKPNRPEEVVWKSFKSEKQYLIHGLKPRVRDNYRANKVAF 600
 QY 601 WLELVPHLHNLHTELTFTTTTLPPVATWPPRP-AGAPGTRRPPPPATLPPPEPEPFGP 659
 Db 601 WLELVPHLHNLHTELTFTTTTLPPVATWPPRP-AGAPGTRRPPPPATLPPPEPEPFGP 660
 QY 660 RAYDRFPDSDRSDYSELVTVAVGASLFLNILAFAALYKRRRQELRCERLSPPGSG 719
 Db 661 RAYDRFPDSDRSDYSELVTVAVGASLFLNILAFAALYKRRRQELRCERLSPPGSG 720
 QY 720 SGVPGGGLLPAAGRELPEELVSLQKRGGGVADPAEALRACPPDYTLALRRAPDD 779
 Db 721 SGVPGGGLLPAAGRELPEELVSLQKRGGGVADPAEALRACPPDYTLALRRAPDD 780
 QY 780 VLLAPGALTLLPSGLPDPDPDPDP-LLHPPGPPPPPPPTATSHNNTLPHPHSTTRV 835
 Db 781 VLLAPGALTLLPSGLPDPDPDPDP-LLHPPGPPPPPPPTATSHNNTLPHPHSTTRV 837

RESULT 5

ABB07524 standard; Protein; 801 AA.

AC ABB07524;
 XX ABB07524;

DT 23-APR-2002 (first entry)

DE Human drug metabolizing enzyme (DME) (ID: 7473875CD1).

XX Drug metabolizing enzyme; DME; antiallergic; antianemic; antiasthmatic;
 KW osteopathic; antirheumatic; antiarthritic; dermatological; nephrotropic;
 KW antiinflammatory; vulnery; antibacterial; virucide; antiparasitic;
 KW protozoacide; fungicide; antihelminthic; cytostatic; ophthalmologic;
 KW antiarteriosclerotic; hepatotropic; antidiabetic; anorectic; human;
 KW thrombolytic; metabolic; anticoagulant; antithyroid; gynecological;
 KW antianginal; antitumor; antidiarrhoeic; laxative; enzyme.

OS Homo sapiens.

XX WO200204612-A2.

PN 17-JAN-2002.

PD 05-JUL-2001; 2001WO-US21324.

XX 07-JUL-2000; 2000US-216804P.

PR 14-JUL-2000; 2000US-218948P.

PR 21-JUL-2000; 2000US-220037P.

PR 28-JUL-2000; 2000US-221837P.

XX (INCY-) INCYTE GENOMICS INC.

FA Baughn MR, Bruns CM, Das D, Ding L, Elliott VS, Gandhi AR;
 PI Hafalia AJA, Kearney L, Khan PA, Lal P, Lee EA, Lu DAM, Lu Y;
 PI Nguyen DB, Patterson C, Ramkumar J, Ring HZ, Sanjanwala MS; Lu Y;
 PI Tang YJ, Thangavelu K, Thornton M, Tribouley CM, Wallia NK, Xu Y;
 PI Yang Y, Yao MG, Yue H;
 XX WPI; 2002-164641/21.

DR N-PSDB; ABA94727.

XX Novel drug metabolizing enzymes and polynucleotides encoding the
 PT enzymes, useful for treating, diagnosing or preventing
 PT autoimmune/inflammatory, cell proliferative, developmental and
 PT endocrine disorders -
 XX

PS Claim 1; Page 148-149; 167pp; English.

XX The invention provides human drug metabolizing enzyme (DME) polypeptides
 CC and polynucleotides. DMEs can be expressed by standard recombinant
 CC methodology. The DME polypeptides, polynucleotides, modulators and
 CC antibodies are useful from diagnosing, treating and preventing autoimmune
 CC /inflammatory (e.g. allergies, anemia, osteoporosis, rheumatoid
 CC arthritis, atopic dermatitis, glomerulonephritis and irritable bowel
 CC syndrome, trauma, and bacterial, viral, parasitic, protozoal, fungal or
 CC helminthic infections), cell proliferative (e.g. cancer, atherosclerosis,
 CC and hepatitis), developmental (e.g. cerebral palsy and cataract),
 CC endocrine (e.g. thrombosis, goiter, hyperplasia, amenorrhea and,
 CC gynecomastia), eye (e.g. iritis and glaucoma, metabolic (e.g. Addison's
 CC disease, diabetes and obesity), and gastrointestinal disorders (e.g.
 CC anorexia, nausea, abdominal angina, ulcerative colitis, diarrhoea and
 CC constipation). The DME polypeptides are useful in drug screening
 CC techniques, and to analyse the proteome of a tissue or cell type. The DME
 CC polynucleotides are useful for creating knock-in humanized animals or
 CC transgenic animals to model human diseases, and in somatic or germ-line
 CC gene therapy. The present sequence represents a human DME polypeptide
 CC sequence.

XX Sequence 801 AA;

SQ Query Match 90.4%; Score 4075.5; DB 23; Length 801;
 Best Local Similarity 95.1%; Pred No. 6.1e-285;
 Matches 770; Conservative 3; Mismatches 18; Indels 19; Gaps 3;

QY 1 MMLLALCLVLGAGQGGGPGGAPGGGLGSLGSEERFFVNTVYGRVGVRELN 60

Db 1 MMLLALCLVLGAGQGGGPGGAPGGGLGSLGSEERFFVNTVYGRVGVRELN 60

QY 61 EILGPVQFLGVYATPPLGAREFQPPAPASWPGVRNATLPPACPNLHGAIPALMP 120

Db 61 EILGPVQFLGVYATPPLGAREFQPPAPASWPGVRNATLPPACPNLHGAIPALMP 120

QY 121 WFTDNLEAAATVYQSEDCLYLNLVYPTEDGPTLTKRDEATLNPPTDTRDPPCKPVM 180

Db 121 WFTDNLEAAATVYQSEDCLYLNLVYPTEDGPTLTKRDEATLNPPTDTRDPPCKPVM 180

QY 181 LFLHGGSYMEGTGNMFDGSLVLAAYGNVTVATNLVGLVGLSTGDAQAKNYGLLDIQ 240

Db 181 LFLHGGSYMEGTGNMFDGSLVLAAYGNVTVATNLVGLVGLSTGDAQAKNYGLLDIQ 240

QY 241 ALRWLSENIAHFQGDPERITIFGSGAGASCYNLLILSHHSEGLFQKALQSGTAISSWSV 300

Db 241 ALRWLSENIAHFQGDPERITIFGSGAGASCYNLLILSHHSEGLFQKALQSGTAISSWSV 300

QY 301 NYQPLKYTRLLAAKVGCDREDSAEVCELRKPSRELVDQVQPARVHIAFGPVVDGVW 360

Db 301 NYQPLKYTRLLAAKVGCDREDSAEVCELRKPSRELVDQVQPARVHIAFGPVVDGVW 360

QY 361 PDDPEILMOQGEFLNDYMLIGNQEGKLFVEDSASESDGVSASAFDFTVSNFVNDLYGY 420

Db 361 PDDPEILMOQGEFLNDYMLIGNQEGKLFVEDSASESDGVSASAFDFTVSNFVNDLYGY 420

QY 421 PEGKDLVRETIKFMVYTDWADRDNGEMRRKTLTLLAFTDQHWAPAVATAKLHADYQSPVYF 480

Db 421 PEGKDLVRETIKFMVYTDWADRDNGEMRRKTLTLLAFTDQHWAPAVATAKLHADYQSPVYF 480

QY 481 YTFYHHCQAEGRPEWADAAGDELPIYFGVPMVGATDLFPCNFKNDVMLSAVVMTYWTN 540

Db 481 YTFYHHCQAEGRPEWADAAGDELPIYFGVPMVGATDLFPCNFKNDVMLSAVVMTYWTN 540

QY 541 FAKTGDNPQPDQTKFTHTKPNRPEEVVWKSFKSEKQYLIHGLKPRVRDNYRANKVAF 600

Db 541 FAKTGDNPQVPQDTKFIHTKPNRFEVWVSKFNSEKQYLHGLKPRVDNRANKVAF 600
Qy 601 WLELVPHLNLHNLHTELFTTTTLPPVATRWPPRPAGAPCTRPPTATLPPPEPEPGPR 660
Db 601 WLELVPHLNLHNLHTELFTTTTLPPVATRWPPRPAGAPCTRPPTATLPPPEPEPGPR 660
Qy 661 AYDRFPDGRDYSTELSVTVAVGASLLFLNLAFAALYYKDRRQELRCRLSPGGSGS 720
Db 661 AYDRFPDGRDYSTELSVTVAVGASLLFLNLAFAALYYKDRRQELRCRLSPGGSGS 720
Qy 721 GVPGGPPLPAAGRELPEELVSLQKGGGVCADPAEALRPACPDYTLALRRAPDDV 780
Db 721 GVPGGPPLPAAGRELPEELVSLQKGGGVCADPAEALRPACPDYTLALRRAPDDV 780
Qy 781 PLLAPGALTLLPSGLGPPPPPPPSLHPFG 810
Db 776 -----LSSLGPDQRP-----HPWG 791

RESULT 6

ABP43803
ID ABP43803 standard; Protein; 828 AA.
XX AC ABP43803;
XX DT 26-FEB-2003 (first entry)
XX DE 3 isoform protein.

KW Neuroprotective; immunomodulator; cancer; chromosome Xq13.1;
KW cytosolic; anti-inflammatory; gene therapy; nutritional supplement;
KW wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
KW vulnary.

XX Homo sapiens.
XX WO200231111-A2.
XX FN 18-APR-2002.
XX PD 11-OCT-2001; 2001WO-US27760.
XX PR 12-OCT-2000; 2000US-0687527.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX PI Xue AJ, Yang Y, Wehrman T, Drmatrac RT;
XX WPI; 2002-426278/45.
XX N-PSDB; ABQ61047.

New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or inflammation
Claim 20; SEQ ID # 706; 357pp + sequence listing; English.
The invention relates to 446 newly isolated polynucleotide sequences.
The activity of polynucleotides of the invention may be described as, vulnary, neuroprotective, immunomodulator, cytosolic and anti-inflammatory. Compositions comprising nucleic acids of the invention are useful for treating a mammalian subject, or as nutritional sources or supplements. These are useful in gene therapy, particularly for treating amyotrophic lateral sclerosis, autoimmune disorders, cancer or inflammation. The nucleic acids and polypeptides are also useful in diagnostic and research methods. The sequences given in records ABP43544-ABP43989 represent polypeptides encoded by polynucleotides of the invention.

NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 828 AA;
Query Match 61.4%; Score 2770; DB 23; Length 828;
Best Local Similarity 62.6%; Pred. No. 7.7e-191;
Matches 537; Conservative 101; Mismatches 142; Indels 78; Gaps 16;
Qy 1 MWLLALCVLAGAQRGGGPGGAPGPGGLGSLGEERFFVNTAYGRVGRVRELN 60
Db 26 LWFSLAL--RASTQ-----APA-----PTVTHFGKLGARVPLPS 60
Qy 61 ELGVPVQFLGVYATPPLGARRQPPAPASWQVRNATTLTPACPNLHGALPAIMLP 120
Db 61 ELGVPVQFLGVYATPPLGARRQPPAPASWQVRNATTLTPACPNLHGALPAIMLP 120
Qy 121 VMTDNLEAAATYYQNSQEDCLYMLYVPTEDGILTKKRDEATLN---PPDTDRDPCKK 177
Db 121 VMTANLDIVATYIQEPNEDCLYMLYVPTEDGSGAKKQGEDADNDCDEDEDIRDSAK 180
Qy 178 PVMLFLHGGSYMEGTGNMFDGSLAAYGNVIVATINLRYLGVFLSTGDAQAKNGYGLLD 237
Db 181 PVMTYHGGSYMEGTGNMFDGSLAAYGNVIVATINLRYLGVFLSTGDAQAKNGYGLLD 240
Qy 238 QIQLRWLSENIAHFGDPERITIFGSGAGASCYNLLIILSHHSEGLFOKAIAQSGTAISS 297
Db 241 QIQLRWVSENIAPFGDPRITIVFGSGIGASCYLLTLSSHSEGLFQRAIIQSSALSS 300
Qy 298 WSNVYQPKYTRLLAAKVGCDREDSAEVCELRKPSRELVDQVQPARVHIAFGPVVDG 357
Db 301 WAVNYQPKYTSLLADKVCNVLDTDMVDCRLQKSAKELVEQIQPARVHIAFGPVVDG 360
Qy 358 DWVPDDPEILMOQGEFLNYDMLIGNOGEGLKFVEDSAESDGSASAFDPTVSNFVDNL 417
Db 361 DVIPDDPEILMEQGEFLNYDMLIGNOGEGLKFVEGVDDGSGDFFDVSFNVDNL 420
Qy 418 YGYPEGKDVLRBTIKFMYTDWADRDNGEMRRKTLALLFTDQWVAPAVATAKLHAYQSP 477
Db 421 YGYPEGKDVLRBTIKFMYTDWADRDNPETRRKTLVALLFTDQWVAPAVATAKLHAYQSP 480
Qy 478 VYFTFYHHCQAEGRPEWADAAGDELPHYVGVPMVGATDLFCNFSKNDVMSAVVMTY 537
Db 481 TYFYAFYHHCOSLMKPAWSDAAGDEVYVGVPMVGPTDLFCNFSKNDVMSAVVMTY 540
Qy 538 WTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNSEKQYLHGLKPRVDNRANK 597
Db 541 WTNFAKTGDPNQVPQDTKFIHTKPNRFEVWVSKFNSEKQYLHGLKPRVDNRANK 600
Qy 598 VAFWLELVPHLNLHNLHTELFTTTTLPPVATRWPPRPAGAPCTRPPTATLPPPEPE 650
Db 601 VAFWLELVPHLNLHNLHTELFTTTTLPPVATRWPPRPAGAPCTRPPTATLPPPEPE 659
Qy 651 PE-----PEPECPRAYDRFPQDSRDYSTELSVTVAVGASLLFLNLAFAALYYKDR 703
Db 660 NENAGQSWNGDQDAGPLIVE-----NPRDYSTELSVTVAVGASLLFLNLAFAALYYKDR 715
Qy 704 ROELRCRLSPGGSGSGVPGGGLPLPAAKRELPPPEELVSLQKGGV-----GADPA 758
Db 716 RRQRLPQSPQSGAGA-----PELCAA-----PSEELAAALQ-----GPTHECEAGPPH 761
Qy 759 BALRPACPPDYTLALRRAPDDVPLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPPT 818
Db 762 DTLELTALPYTLRLRSPDDIFLMTPTITMIPNSL-----VGLQTLHPYNTF----- 810
Qy 819 ATSHNNT-LPHPHSTTRV 835
Db 811 AAGFNS*GLPHSHSTTRV 828
RESULT 7
AAY41740
ID AAY41740 standard; Protein; 816 AA.

XX AC AAY41740;
 XX DT 07-DEC-1999 (first entry)
 XX DE Human PRO701 protein sequence.
 XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 XX KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 XX KW secreted protein; transmembrane protein.
 XX OS Homo sapiens.
 XX PN WO9946281-A2.
 XX PD 16-SEP-1999.
 XX PF 08-MAR-1999; 99WO-US05028.
 XX PR 10-MAR-1998; 98US-0077450.
 XX PR 11-MAR-1998; 98US-0077632.
 XX PR 11-MAR-1998; 98US-0077641.
 XX PR 11-MAR-1998; 98US-0077649.
 XX PR 12-MAR-1998; 98US-0077791.
 XX PR 13-MAR-1998; 98US-0078004.
 XX PR 17-MAR-1998; 98US-0040220.
 XX PR 20-MAR-1998; 98US-0078888.
 XX PR 20-MAR-1998; 98US-0078910.
 XX PR 20-MAR-1998; 98US-0078936.
 XX PR 20-MAR-1998; 98US-0078939.
 XX PR 25-MAR-1998; 98US-0079294.
 XX PR 26-MAR-1998; 98US-0079656.
 XX PR 27-MAR-1998; 98US-0079663.
 XX PR 27-MAR-1998; 98US-0078664.
 XX PR 27-MAR-1998; 98US-0079689.
 XX PR 27-MAR-1998; 98US-0079728.
 XX PR 27-MAR-1998; 98US-0079786.
 XX PR 30-MAR-1998; 98US-0079920.
 XX PR 30-MAR-1998; 98US-0079923.
 XX PR 31-MAR-1998; 98US-0080105.
 XX PR 31-MAR-1998; 98US-0080107.
 XX PR 31-MAR-1998; 98US-0080165.
 XX PR 31-MAR-1998; 98US-0080194.
 XX PR 01-APR-1998; 98US-0080327.
 XX PR 01-APR-1998; 98US-0080328.
 XX PR 01-APR-1998; 98US-0080333.
 XX PR 01-APR-1998; 98US-0080334.
 XX PR 08-APR-1998; 98US-0081049.
 XX PR 08-APR-1998; 98US-0081070.
 XX PR 08-APR-1998; 98US-0081071.
 XX PR 09-APR-1998; 98US-0081195.
 XX PR 09-APR-1998; 98US-0081203.
 XX PR 09-APR-1998; 98US-0081229.
 XX PR 15-APR-1998; 98US-0081817.
 XX PR 15-APR-1998; 98US-0081838.
 XX PR 15-APR-1998; 98US-0081952.
 XX PR 15-APR-1998; 98US-0081955.
 XX PR 21-APR-1998; 98US-0082568.
 XX PR 21-APR-1998; 98US-0082569.
 XX PR 22-APR-1998; 98US-0082700.
 XX PR 22-APR-1998; 98US-0082704.
 XX PR 22-APR-1998; 98US-0082804.
 XX PR 23-APR-1998; 98US-0082767.
 XX PR 23-APR-1998; 98US-0082796.
 XX PR 27-APR-1998; 98US-0083336.
 XX PR 28-APR-1998; 98US-0083322.
 XX PR 29-APR-1998; 98US-0083392.
 XX PR 29-APR-1998; 98US-0083435.
 XX PR 29-APR-1998; 98US-0083456.
 XX PR 29-APR-1998; 98US-0083499.
 XX PR 29-APR-1998; 98US-0083500.
 XX PR 29-APR-1998; 98US-0083545.
 XX PR 29-APR-1998; 98US-0083554.

PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0084366.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085338.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.

(GETH) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

WPI; 1999-551358/46.

N-PSDB; AA234209.

New secreted and transmembrane polypeptides and their polynucleotides,
 useful for treating blood coagulation disorders, cancers and cellular
 adhesion disorders -

Claim 12; Fig 151; 530pp; English.

The present invention describes secreted and transmembrane polypeptides
 and their polynucleotides. The nucleotide sequences are useful as
 sources of probes, primers, for chromosome mapping, and for generation
 of antisense sequences. They can also be used to create transgenic
 animals. The proteins can be used to treat a variety of diseases and
 disorders, depending on their function. Diseases that may be treated
 include blood coagulation disorders, cancers and cellular adhesion
 disorders. They may also be used to raise antibodies. AA233891 to
 AA234338, and AA241685 to AA241774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 invention.

XX SQ Sequence 816 AA;

Query Match 60.6%; Score 2731; DB 20; Length 816;

Best Local Similarity 64.2%; Pred. No. 4.9e-188;

Matches 527; Conservative 97; Mismatches 147; Indels 50; Gaps 15;

QY 38 EERFPVNTAYGRVGRVREINLEILGVVQFLGVYATPPLGARRFOPPPAPASWPOVR 97

Db 23 QAQYFVNTYNGKIRGLRPLLEILGEVQYLGVPYASPTGRRFOPPPSPSWTGR 82

QY 98 NATTLPPACPNLHGALPAIMLPWFFTDNLAAATVQNOSEDCGLNLYVPTEDGFLT 156

Db 83 NTTQFAAVCPQHLDERSLLHDMLEIFWFTANLDTMTYVQDQNECLYNIYVPTEDGANT 142

RESULT 13

Db 122 GDVVDPEILMQGEEFLNDMLGVNQGEGLKFEVDSASEDSGVSAFDTFVSNVDN 181
 QY 417 LYGYPEGKDVLRITIKFMYTDWADRDNGEMRRKTLALFTDHWAVAPATAKLHADYQS 476
 Db 182 LYGYPEGKD-----DWADRDNGEMRRKTLALFTDHWAVAPATAKLHADYQS 230
 QY 477 PVYFYTHHCQAEGRPEWADAAGHDELPLVYFGVPMVGATDLFPFCNKDVMLSAVVMT 536
 Db 231 PVYFYTHHCQAEGRPEWADAAGHDELPLVYFGVPM-----NDVMSAVVMT 277
 QY 537 YWTNFAKTGPNQVPQDTKFIHTKPNRFEVVMKFNSEKSKOYLHGLKPRVDNRYAN 596
 Db 278 YWTNFAKTGPNQVPQDTKFIHTKPNRFEVVMKFNSEKSKOYLHGLKPRVDNRYAN 337
 QY 597 KVAFWELVPHLNLHTELTFTTTRLPDYATRWPPRPPAGAPOTRPPPPATLPPPEPE 656
 Db 338 KVAFWELVPHLNLHTELTFTTTRLPDYATRWPPRPPAGAPOTRPPPPATLPPPEPE 397
 QY 657 PGPRAYDRFGDSRDYSTELSVTVAVGASLLFLNLAFALYKRRORRQELRCRLSPG 716
 Db 398 PSPRAYDRFGDSRDYSTELSVTVAVGASLLFLNLAFALYKRRORRQELRCRLSPG 457
 QY 717 GSGGVGPG-----GGPFLPAAGRELPPPEELVS--LQKRGGVGADPAE-----ALRPAC 765
 Db 458 GSGGVGPGRIYDARDMRRRLRELTREVEALSVCYPLASGSSSTABETSXNWNVRSITGR 517
 QY 766 PPDYTLALRRAP---DDVPLALPAGALTLLPSGL 795
 Db 518 CNQY-----QSPHDAEDILLLLGLVLVNI 546

RESULT 14

ABG10264
 ID ABG10264 standard; Protein; 726 AA.
 AC ABG10264;
 XX 13-FEB-2002 (first entry)
 XX Novel human diagnostic protein #10255.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 XX WO2001.75067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 XX 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX N-PSDB; AAS74451.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 40623; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (II) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 726 AA;

Query Match 38.8%; Score 1747; DB 22; Length 726;
 Best Local Similarity 57.4%; Pred. No. 3.5e-117;
 Matches 377; Conservative 27; Mismatches 105; Indels 148; Gaps 13;
 QY 171 IRDPGKKPVMLFLHGGSYMEGTGMNFDGSLAAYGNVIVATLNYRLGVGLSTGDOAAK 230
 Db 1 IRDPGKKPVMLFLHGGSYMEGTGMNFDGSLAAYGNVIVATLNYRLGVGLSTGDOAAK 60
 QY 231 GNYGLLDQIQALRWLSNIAHFHGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQA 290
 Db 61 GNYGLLDQIQALRWLSNIAHFHGGDPERITIFG-----QFGLSYHI 93
 QY 291 SGTAISSWVNYQLKYTRLIAAKVGCDDREDSABAVECLRRKPSRELVDQVQPA-RYHI 349
 Db 94 -----RYS-----QFGLSYHI 104
 QY 350 AFGPVWDGDDVVDPEILMQGEEFLNDMLGVNQGEGLKFEVDSASEDSGVSAFDT 409
 Db 105 AFGPVWDGDDVVDPEILMQGEEFLNDMLGVNQGEGLKFEVDSASEDSG-----ADFT 160
 QY 410 VSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNGEMRRKTLALFTDHWAVAPATAK 469
 Db 161 VSNFVDNLYGYPEGKDVLRITIKFMYTDWADRDNGEMRRKTLALFTDHWAVAPATAK 220
 QY 470 LHADYQSPVYFYTHHCQAEGRPEWADAAGHDELPLVYFGVPMVGATDLFPFCNKDVM 529
 Db 221 LHADYQSPVYFYTHHCQAEGRPEWADAAGHDELPLVYFGVPMVGATDLFPFCNKDVM 280
 QY 530 LSAYVMTYTNFAKTGPNQVPQDTKFIHTKPNRFEVVMKFNSEKSKOYLHGLKPRV 589
 Db 281 LSAYVMTYTNFAKTGPNQVPQDTKFIHTKPNRFEVVMKFNSEKSKOYLHGLKPRV 340
 QY 590 RDNVANKVAFWELVPHLNLHTELTFTTTRLPDYATRWPPRPPAGAPOTRPPPPATL 649
 Db 341 WSRFRG-----VLYQVFHDTICEKAPKSLRKQTQPPKQSSPAVHLRCLTMDPFVM 393
 QY 650 PPEPEPEPRAYDRFGDSRDYSTELSVTVAVGASLLFLNLAFALYKRRORRQELRC 709
 Db 394 TVSPPP-----AHRHRRGSGPTRC 412
 QY 710 RR--LSPFGSGSGVGGGGLLPAAAGRELPPPEELVSLQKRGGVGADPAEALRPACPP 767
 Db 413 AHCFVAPADPTDDEKPHQYPAICSYHWDVP--EDWEGFQHTQGTWV---PWSQAPESPP 467
 QY 768 DYTLLARRAPDDVPLALPAGALTLLPSGLGPPPPPPPPPPPPPPPPPPPPPPPPPPPP 824
 Db 468 Q-TIRQPTVEERPL-----KTCINSELG-----LRAYVFPNP-PFPPSPASHQN 512

RESULT 15
 AAM93205
 ID AAM93205 standard; Protein; 509 AA.

```

XX AC AAM93205;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide, SEQ ID NO: 2597.
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX OS Homo sapiens.
XX PN EP1130094-A2.
XX PD 05-SEP-2001.
XX PF 07-JUL-2000; 2000EP-0114089.
XX PR 08-JUL-1999; 99JP-0194486.
XX PR 11-JAN-2000; 2000JP-0118774.
XX PR 02-MAY-2000; 2000JP-0183765.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX DR WPI: 2001-524255/58.
XX DR N-PSDB; AAK94113.
XX FT
XX FT use in genetic manipulation -
XX PS Claim 8; SEQ ID NO 2597; 1380pp + sequence listing; English.
XX CC The invention relates to primers for synthesizing full length cDNA
XX CC clones. 830 cDNA molecules encoding a human protein have been
XX CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
XX CC molecules have been determined. Primers for synthesizing the full length
XX CC cDNA are useful for clarifying the function of the protein encoded by
XX CC the cDNA. The full length clones were obtained by construction of full
XX CC length enriched cDNA libraries that were synthesised by the oligo-capping
XX CC method. The primers enable the production of the full length cDNA easily
XX CC without any special methods. The present sequence is a polypeptide
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in CD-ROM format directly from EPO.
XX SQ Sequence 509 AA;

```

```

Query Match 38.7%; Score 1745.5; DB 22; Length 509;
Best Local Similarity 62.2%; Pred. No. 2.8e-117;
Matches 337; Conservative 62; Mismatches 94; Indels 49; Gaps 9;

QY 310 LLAAYGCDREDSAAVECLRRKPSRELVDQVQARYHAFGPVVDGVDVDDPEILMQ 369
DQ 1 MLATKVGCVNSDVELVECLQKPKYELVDQIQARYHAFGPVVDGVDVDDPEILME 60

QY 370 QGEFLNYDMLIGVNGQEGLEKVEDSASEDGYVSASAFDFTVGNFVNDLYGPEGKDVLR 429
DQ 61 QGEFLNYDMLIGVNGQEGLEKFEVNIYVSDGIGSASDFDFAVNFVNDLYGPEGKDVLR 120

QY 430 TIKFMYTDWADRDNGEMRKTLILALPTDQHWAPAVATAKLHADYQSPVYFTFYHCOA 489
DQ 121 TIKFMYTDWADRDNPETRRKTLILALPTDQHWAPAVATAKLHADYQSPVYFTFYHCOA 180

QY 490 EGRPEWADAAGDELPIYFVGMVGTDLFCNFKSKNDVMSAVVMTYNTNPAKTGDNQ 549
DQ 181 DQVPAWADAAGDEVYVIGIEMIGTELPFCNFKSKNDVMSAVVMTYNTNPAKTGDNQ 240

QY 550 PVPQDTKFIHTKPNRFEVVKFNKSKQYLIHLGKPRVDRNRYANKVAFWLELVPHLH 609
DQ 241 PVPQDTKFIHTKPNRFEVAVWTRYSQDQLYLHIGLKPRVKEHYRANKVNLWLELVPHLH 300

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Search completed: February 13, 2004, 13:12:09
Job time : 50 secs

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QY 610 NLH--TELFTTTTLLPPVATRWPPPPAGAGCTRRPPPPATLPPPEPEPEPGPRAYDRFEG 667
DQ 301 NLNDISQYTSITTTTKVPSTDTIFRPTKNSVPVTSAPFTAKQDDPKQFSP-----FSV 353
QY 668 DSDYSTELSVTVAVGASLLFLNILAFAALYYKRRQRELRCRLSPPGSGSGVPGGGP 727
DQ 354 DQDYSTELSVTVIAGASLLFLNILAALYYKDKRHDVHRRCSQRTTNDLTHA-- 411
QY 728 LLPAAAGRELPPPEELVSLQKGGVGAD-----PAE-ALRPACPDYTLALRAPDD 779
DQ 412 -----QEEINSLQMKH---TLDHECESIHPHEVLRVLTACPPDYTLAMERSDD 458
QY 780 VELLAPGALTLLPSGLGPPPPPPPSLHPFGPPPPPTATSHNNTLPHP-----HSTT 833
DQ 459 VELMTENTITMIPNTI-----PGIQPLHTFNTF-----TGGQNNTLPHPHPHSHSTT 507
QY 834 RV 835
DQ 508 RV 509

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OM protein - protein search, using sw model

Run on: February 13, 2004, 13:10:37 ; Search time 26 Seconds
(without alignments)
3088.494 Million cell updates/sec

Title: US-09-934-323-2
Perfect score: 4508
Sequence: 1 MWLLALCLVGLAGQRGGG.....PPTATSHNNTLPHPHSTTRV 835

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	858	19.0	581	2 C39768	cholinesterase (EC
2	855	19.0	602	1 ACHU	cholinesterase (EC
3	852	18.9	614	2 JH0314	acetylcholinestera
4	846.5	18.8	614	2 JH0811	acetylcholinestera
5	837	18.6	603	2 S70849	cholinesterase (EC
6	836.5	18.6	566	2 S19307	cholinesterase (EC
7	830	18.4	557	2 A47162	thiolesterase B (E
8	828.5	18.4	745	2 S13586	triacylglycerol li
9	827.5	18.4	614	2 A39256	acetylcholinestera
10	823.5	18.3	562	2 A55281	carboxylesterase (
11	819	18.2	561	2 JC2447	carboxylesterase (
12	817	18.1	567	1 A41010	carboxylesterase (
13	817	18.1	622	2 A34967	sterol esterase (E
14	813	18.0	536	1 ACRYE	acetylcholinestera
15	811.5	18.0	584	2 S48724	acetylcholinestera
16	802.5	17.8	583	2 S10712	acetylcholinestera
17	801	17.8	599	1 A38968	acetylcholinestera
18	797	17.7	559	1 JC5408	carboxylesterase (
19	793.5	17.6	561	2 S62788	carboxylesterase (
20	793	17.6	549	2 JX0054	carboxylesterase (
21	792	17.6	561	2 S71597	sterol esterase (E
22	792	17.6	599	2 A57701	gliotactin precurs
23	791	17.5	956	2 A56920	carboxylesterase (
24	788	17.5	565	2 S10367	carboxylesterase (
25	785.5	17.4	798	2 T13864	hypothetical prote
26	782.5	17.4	537	2 A33668	sterol esterase (E
27	776.5	17.2	540	2 A31584	carboxylesterase (
28	772.5	17.1	554	2 A39060	carboxylesterase (
29	766	17.0	561	2 S47655	carboxylesterase (

ALIGNMENTS

RESULT 1

C39768
cholinesterase (EC 3.1.1.8) - rabbit
N:Alternate names: butyrylcholinesterase
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 20-Jun-2000
C:Accession: S10255; C39768
R:Jubilo, O.; Chatonnet, A.
Nucleic Acids Res. 18, 3990, 1990
A:Title: Complete sequence of rabbit butyrylcholinesterase.
A:Reference number: S10255; MUID:90326526; PMID:2374720
A:Accession: S10255
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-581 <JBI>
A:Cross-references: EMBL:X52090; NID:G1476; PIDN:CAA36308.1; PID:G1370277
R:Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nogi
J. Biol. Chem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholinesterase.
A:Reference number: A39768; MUID:91201348; PMID:2016308
A:Accession: C39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 75-215 <ARP>
A:Cross-references: GB:M62779; NID:G164788; PIDN:AAA31169.1; PID:G164789
C:Genetics:
A:Introns: 485/2; 541/1
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:35-535/Domain: cholinesterase homology <CHE>

Query Match 19.0%; Score 858; DB 2; Length 581;
Best Local Similarity 32.9%; Pred. No. 2.5e-45;
Matches 200; Conservative 102; Mismatches 231; Indels 74; Gaps 14;

QY	43	VVNTAYGRVGRRELNNEILGPVQPLGYPATPPILGARRFQPPPEAPSPGVRNATTL	102
DB	12	IITTKNGRIGINLPVFG---GTVTFLGIPYAPQLRLRFKKPQSLTKWSDIWNATKY	68
QY	103	PPACPNLHGAALPAIMLPVWFTDNLEAAATVQNQSEDCILNLYVPTDGLTKRDEA	162
DB	69	ANSCCQNDQSFQFHGSEMNNTDL-----SEDCILNLYVPTDGLTKRDEA	109
QY	163	TLNPPDPTDIRDPGKPKVWMLFHGGSYMEGTGNM--PDGSLAAAYGNIVATNLVRLGVLG	220
DB	110	-----KPKNATVMIWYGGGFGTGTSSQLQVVDGKELTRVERVIVVSMYRVGALG	159
QY	221	FLS--TGQAAKNGVLLDQIALRWLSENTHFGGPPERITIFGSGAGASCVNLLISHH	279
DB	160	FLALPGNPEAPGNMGLFDQALQWQKNTAFGPNPKSVTLFGESAGASVSLHLSPR	219
QY	280	SEGLFQKAIQAQSGTAISSWSVN--YQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSREL	337

60K esterase (EC 3
carboxylesterase (
acetylcholinestera
carboxylesterase (
carboxylesterase (
acetylcholinestera
triacylglycerol li
acetylcholinestera
acetylcholinestera
para-nitrobenzyl e
acetylcholinestera
probable carboxyle
thryoglobulin - ra
carboxylesterase,
protein T28C12.4b

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Db 220 SHPLFTRALOGSSNAPWWSLHEARNRTLTAKFVGCSSTENETETIICLRNKAQEI 279
Qy 338 VDQVQPARY-----HIAFGPVVDGDDVPPDEILMQQGEFLNYDMILGVNQGEGLKAFVED 393
Db 280 LLNEVFVVPFDSLLSNVFGPTVDGDFLTDMPDITLQLGOLKTKQILGVNKGSGTAFVY 339
Qy 394 SAE--SEDGVSASAFDFTVSNFVNL-YGYPEGKDVLRITIKFMYTDWADRNGEWRKT 450
Db 340 GAPGSKDNTSI-----ITRKEFQGLKIFFPGVSEFGKESILFHYTDWDEQRPENYREA 395
Qy 451 LLALFTDHWAVAPATAKLHADYQSPVYFYTFVHHQCAEGRPWADAAGHDELPPVFGV 510
Db 396 LDDVGVGNFICPALETTKFESEGNNAFFYYEHRSSKLPFWEMGVGMHGYEIEFVGL 455
Qy 511 PMVGATDLFCNFSKNDVM.SAVVMTWTWPAKTGDPNQVPODTKPIHTKPNRFEVVM 570
Db 456 PLERSV-----NYTKAEILSRIMKRWANFAKYNPNGTQNNSTR-----W 497
Qy 571 SKFNSKEQYHLGLK-PRVRDNYRANKVAFW-----LELVPHLHNLHTELFTTTTL 622
Db 498 PVFKSTQKYLTLNTESPRYTKLRAQCQRFWILFPFKVLEMTGNIDBAEQWAGFHRW 557
Qy 623 PPVATRW 629
Db 558 NNYMAW 564

RESULT 2
ACHU
cholinesterase (EC 3.1.1.8) precursor [validated] - human
N/Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence revision 23-Feb-1996 #text_change 08-Dec-2000
C/Accession: A33769; A26613; A33887; A34668; A00772
R/Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.
Biochemistry 29, 124-131, 1990
A/Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single co
A/Reference number: A33769; MUID:90212557; PMID:2322535
A/Accession: A33769
A/Molecule type: DNA
A/Residues: 'MSVQSNLQAGAAASCSIPKYMIFTPCKLCHCCRESEIN', 1-602 <ARP>
A/Cross-references: GB:M32391; GB:J02879
R/Note: two ARG codons found upstream of Met-1 do not lie in a favorable context for tra
R/Prody, C.A.; Zevin-Sonkin, D.; Gnat, A.; Goldberg, O.; Soreg, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987
A/Title: Isolation and characterization of full-length cDNA clones coding for cholineste
A/Reference number: A26613; MUID:87231856; PMID:3035536
A/Accession: A26613
A/Molecule type: mRNA
A/Residues: 1-133, 'D', 135-602 <PRO>
R/McTiernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
A/Title: Brain cDNA clone for human cholinesterase.
A/Reference number: A33887; MUID:88016155; PMID:3477799
A/Accession: A33887
A/Molecule type: mRNA
A/Residues: 'MSVQSNLQAGAAASCSIPKYMIFTPCKLYHCCRESEIN', 1-602 <MCT>
R/Note: two ARG codons found upstream of Met-1 do not lie in a favorable context for tra
R/Nogueira, C.P.; McGuire, M.C.; Graesser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spek,
Am. J. Hum. Genet. 46, 934-942, 1990
A/Title: Identification of a frameshift mutation responsible for the silent phenotype of
A/Reference number: A34668; MUID:90252779; PMID:2339692
A/Accession: A34668
A/Molecule type: DNA
A/Residues: 143-145, 'VSNWNIIFTCL', <NOG>
R/Note: frameshift mutant in codon for residue 145 (Gly)
R/Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.
J. Biol. Chem. 262, 549-557, 1987
A/Title: Complete amino acid sequence of human serum cholinesterase.
A/Reference number: A00772; MUID:18710944; PMID:3542989
A/Accession: A00772
A/Molecule type: protein

```

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A/Residues: 29-602 <LOC>
A/Experimental source: plasma
C/Comment: Cholinesterase is present in most cells (except erythrocytes).
C/Genetics:
A/Gens: GDB:BCH; CHE1
A/Cross-references: GDB:120558; OMIM:177400
A/Map position: 3q26.1-3q26.2
A/Introns: 506/2; 562/1
C/Function:
A/Description: hydrolyzes acylcholines to choline and a carboxylic acid
A/Note: this cholinesterase is highly reactive with organophosphate esters
C/Superfamily: cholinesterase; cholinesterase homology
C/Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
F/1-28/Domain: signal sequence #status predicted <Sig>
F/29-602/Product: cholinesterase #status experimental <Mat>
F/56-556/Domain: cholinesterase homology <CHE>
F/45-85/134,269,284,369,483,509,514/Binding site: carbonyl site: (covalent) #status
F/226/Active site: Ser #status experimental

Query Match 19.0%; Score 855; DB 1; Length 602;
Best Local Similarity 32.5%; Pred. No. 4e-45;
Matches 201; Conservative 102; Mismatches 224; Indels 92; Gaps 15;

Qy 2 WLLALCLVLGAGAQKGGGGGPGGAPGGLGLSLGSERPVNTAYGRVGRRELNNE 61
Db 15 WFLLLML-----IGKSHTEDDIIATKNGKVRG-----WNL 47

Qy 62 IL-GPVVQFLGVPYATPPLGARRPQPPEAPASWFGVGNATLTPACQNTLHGALPAIMLP 120
Db 48 VFGTVAFLGIPYAPPLGRLRFPKQSLTKWSDIWNATKYANSCQNTDQSPGPHGS 107

Qy 121 VVETDNLAAATYQVQNSQEDCLVNLVPTEDGTLTKRDEATLNPDDTDIRPGKPKVM 180
Db 108 EMMNPNDL-----SEDCILVNWIPAP-----KPKNATVL 138

Qy 181 LFLHGGSYMEGTGMN--FDGSLVLAAYGNVIVATLNLVGLVGLS-TGDAQAKNGYLLD 237
Db 139 IWIYGGGFQRTSSLHVYDGFKLARVERVIVSMYRVGALFLALPGNPEAPGNMGLFD 198

Qy 238 QIQALRWLSENIAHFGDPERITIFGSGACASCNLLILSHHSEGLFQKAIAGSGTAISS 297
Db 199 QQLALQWQKNIAAFGNGPKSVTLFGESAGAAVSLLHLSPPGSHSLFTRAILQSGSFNAP 258

Qy 298 WSVN--YQPLKYRLLAAYGCDREDSAEVCLRRKPSRELVDQVQPARY-----HIAF 351
Db 259 WAVTSLYEARNLTNLAKLTGCSRENETHIICLRNKDQEIILNEAFVVPYCTPLSVNF 318

Qy 352 GPVVDGVDVDDPEILMQQGEFLNYDMILGVNQGEGLKAFVEDSAE--SEDGVSASAFDFT 409
Db 319 GPTVDGDFLTDMPDITLLELQGFKKTKQILGVNKGDEGTAFLVYGAPGFSKDNNSI----IT 374

Qy 410 VSNFVDNL-YGYPEGKDVLRITIKFMYTDWADRNGEMRRKTLALFTDHWAVAPATA 468
Db 375 RKEFQGLKIFFPGVSEFGKESILFHYTDWDDORPENTREALGDVVGYNFICPALEFT 434

Qy 469 KLHADYQSPVYFYTFVHHQCAEGRPWADAAGHDELPPVFGVPMVGATDLFCNFSKNDV 528
Db 435 KKFSEGNNAFFYYEHRSSKLPFWEMGVGMHGYEIEFVGLPLERRD-----NYTKASE 489

Qy 529 MLSAVVMTWTWPAKTGDPNQVPODTKPIHTKPNRFEVVMKSKQYHLGLK-P 587
Db 490 ILRSIVKRWANFAKYNPNGTQNNSTR-----WPFVKSTQKYLTLNTTEST 536

Qy 588 RVRDNYRANKVAFWLELVP 606
Db 537 RIMTKLRAQCQRFWTSFEP 555

RESULT 3
JH0314
acetylcholinesterase (EC 3.1.1.7) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1999

```

C;Accession: JH0314
 R;Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
 J. Neurochem. 5, 317-327, 1990
 A;Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternative splicing
 A;Reference number: JH0314; MUID:90380429; PMID:2400605
 A;Accession: JH0314
 A;Molecule type: mRNA
 A;Residues: 1-614 <RAC>
 A;Cross-references: EMBL:X56518; NID:949844; PTDN:CA399867.1; PID:g49845
 A;Experimental source: Brain
 C;Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic synapses
 C;Superfamily: cholinesterase; cholinesterase homology
 F;1-31/Domain: signal sequence #status predicted <SIG>
 F;32-614/Product: acetylcholinesterase #status predicted <SIG>
 F;63-569/Domain: cholinesterase homology <CHE>
 F;100-127/288-303,440-560/Disulfide bonds: #status predicted
 F;234/Active site: Ser #status predicted
 F;236,381,495/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 18.9%; Score 852; DB 2; Length 614;
 Best Local Similarity 33.3%; Pred. No. 6.3e-45;
 Matches 207; Conservative 96; Mismatches 235; Indels 83; Gaps 17;

QY	31	LGGLSGEERFP---VNTAYGRVGRVRELNNELGVPVQFLGVPYATPPLGARRFOPP	87
DB	25	LGCGARAEGRDPQLLVVRGGQLRGIRLKAPG---GPVSALGIFPAEPVPSRRFMP	81
QY	88	EAPASPGVGNATLPPACQNLHGALPAIMLPVWFTDNLEAAATVQNSDCLYLNLY	147
DB	82	EPKRPVSGILDATTFQNVQYVDTLYPFGEGTEMNPNREL-----SDCLYLNLY	133
QY	148	VPTEDGPLTKRDEATLNPDDTDIRDPKPKVMLFLHGGSYMEGTGNN--FDGSLVLAAYG	205
DB	134	TPYP-----RPSPTFLVIWYGGFYSGASLDVYDGRFLAQVE	173
QY	206	NVIVATLNYRLGVLGFLS-TGDOAAKNGYGLDQIALRWLSNIAHFGGDPERITFGS	264
DB	174	GAYLVSNMYRVGTFGLALPGSREAPGNVGLDQRLALQWQENIAAFGGDPMSVTLFGE	233
QY	265	GAGASCNLLILSHHSEGLFQKAIQSGTAISSWSV--NYQPLKYTRLAAKVGCD---	318
DB	234	SAGASVGMHILSLPSSSLFHRVAVLQSGTPNGPWATVSAGEARRRATLLARLVGCPPGA	293
QY	319	REDSAEAVECLRRKPSRELVDQD---VQPARHYAFGPVVDGVVDVDPPEILMQQGEFL	374
DB	294	GGNDTELLACLRTPAQDLVDHEHVLVQESIFRFSFVVDGDFLSDTFEALINTGDFQ	353
QY	375	NYDMLGVNQGEGLKFV-----EDSAESEDGVSASAFDFTVSNFVDNLYGYPEGKDVLE	429
DB	354	DLQVLGVVWVDEGSYFLVYGVPGFSKDNESLSRAQFLAGVR-----IGVQASDLAAE	407
QY	430	TIKFMVTDWADRDNGEMRRKTLALFTDQWVAPAVATAKLHADYQSPVYFYTFYHHCQA	489
DB	408	AVLVHTDMLHPEDTHLRDAMSAVVDHNVCPVAQLAGRLAAGARVAYIFERRAST	467
QY	490	EGRPWADAAGHDELPIYFGVPMVGATDLFPNFSKNDVMSAVVMTYTNFAKTGDPNQ	549
DB	468	LTWPLMVGPHGYEIEFIFGLPLDPS-----LNYTVEERIFAQRLMKYTNFARTGDPND	522
QY	550	PVQDQTKFIHTKPNREEVWVSKFNSEKQYLHIGLKP-RVRDNYRANKVAFWLELVPHL	608
DB	523	--PRDSK-----WPYTTAAQYVSLNKLPLEVRRLGLRAQTCAFWRFLP--	568
QY	609	HNHLTEFTTTTTLPPYATRW	629
DB	569	-----KLLSATDTLDEAERQW	584

RESULT 4
 JH0811
 acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Jun-1999

C;Accession: JH0811
 R;Legay, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulie, J.
 J. Neurochem. 60, 337-346, 1993
 A;Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of multiple cDNAs
 A;Reference number: JH0811; MUID:93107932; PMID:8417155
 A;Accession: JH0811
 A;Molecule type: mRNA
 A;Residues: 1-614 <LEG>
 A;Cross-references: GB:S50879; NID:g262092; PID:AA24586.1; PID:g262093
 A;Experimental source: striatum
 C;Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic synapses
 C;Superfamily: cholinesterase; cholinesterase homology
 F;1-31/Domain: signal sequence #status predicted <SIG>
 F;32-614/Product: acetylcholinesterase #status predicted <SIG>
 F;63-569/Domain: cholinesterase homology <CHE>
 F;100-127/288-303,440-560/Disulfide bonds: #status predicted
 F;234,365,478/Active site: Ser, Glu, His #status predicted
 F;296,381,495/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 18.8%; Score 846.5; DB 2; Length 614;
 Best Local Similarity 33.0%; Pred. No. 1.4e-44;
 Matches 205; Conservative 98; Mismatches 235; Indels 83; Gaps 17;

QY	31	LGGLSGEERFP---VNTAYGRVGRVRELNNELGVPVQFLGVPYATPPLGARRFOPP	87
DB	25	LGCGARAEGRDPQLLVVRGGQLRGIRLKAPG---GPVSALGIFPAEPVPSRRFMP	81
QY	88	EAPASPGVGNATLPPACQNLHGALPAIMLPVWFTDNLEAAATVQNSDCLYLNLY	147
DB	82	EPKRPVSGILDATTFQNVQYVDTLYPFGEGTEMNPNREL-----SDCLYLNLY	133
QY	148	VPTEDGPLTKRDEATLNPDDTDIRDPKPKVMLFLHGGSYMEGTGNN--FDGSLVLAAYG	205
DB	134	TPYP-----RPSPTFLVIWYGGFYSGASLDVYDGRFLAQVE	173
QY	206	NVIVATLNYRLGVLGFLS-TGDOAAKNGYGLDQIALRWLSNIAHFGGDPERITFGS	264
DB	174	GTVLVSNMYRVGTFGLALPGSREAPGNVGLDQRLALQWQENIAAFGGDPMSVTLFGE	233
QY	265	GAGASCNLLILSHHSEGLFQKAIQSGTAISSWSV--NYQPLKYTRLAAKVGCD---	318
DB	234	SAGASVGMHILSLPSSSLFHRVAVLQSGTPNGPWATVSAGEARRRATLLARLVGCPPGA	293
QY	319	REDSAEAVECLRRKPSRELVDQD---VQPARHYAFGPVVDGVVDVDPPEILMQQGEFL	374
DB	294	GGNDTELLACLRTPAQDLVDHEHVLVQESIFRFSFVVDGDFLSDTFEALINTGDFQ	353
QY	375	NYDMLGVNQGEGLKFV-----EDSAESEDGVSASAFDFTVSNFVDNLYGYPEGKDVLE	429
DB	354	DLQVLGVVWVDEGSYFLVYGVPGFSKDNESLSRAQFLAGVR-----IGVQASDLAAE	407
QY	430	TIKFMVTDWADRDNGEMRRKTLALFTDQWVAPAVATAKLHADYQSPVYFYTFYHHCQA	489
DB	408	AVLVHTDMLHPEDTHLRDAMSAVVDHNVCPVAQLAGRLAAGARVAYIFERRAST	467
QY	490	EGRPWADAAGHDELPIYFGVPMVGATDLFPNFSKNDVMSAVVMTYTNFAKTGDPNQ	549
DB	468	LTWPLMVGPHGYEIEFIFGLPLDPS-----LNYTVEERIFAQRLMKYTNFARTGDPND	522
QY	550	PVQDQTKFIHTKPNREEVWVSKFNSEKQYLHIGLKP-RVRDNYRANKVAFWLELVPHL	608
DB	523	--PRDSK-----WPYTTAAQYVSLNKLPLEVRRLGLRAQTCAFWRFLP--	568
QY	609	HNHLTEFTTTTTLPPYATRW	629
DB	569	-----KLLSATDTLDEAERQW	584

RESULT 5
 S70849
 cholinesterase (EC 3.1.1.8) - mouse
 N;Alternate names: butyrylcholine esterase

Db 490 EIFSRSTKWTWAFNFKYGHFN-----GTQGN-----STMPVPVFTSTEQKYLTLNTEK 536

Qy 587 PRVDNRYNRANKVAFWLELVPHLEHLHTEFLTPTTTRLLPPVATRW 629

Db 537 SKIYSKLRAPOCQFWRLFFPKVLEMTGDIDETQEWKAGFHRW 579

RESULT 6

S19307

carboxylesterase (EC 3.1.1.1) precursor - pig

N:Alternate names: proline-beta-naphthylamidase

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 04-Dec-1992 #sequence_revision 04-dec-1992 #text_change 18-Jun-1999

C:Accession: S19307; S23607

E:Matsumihama, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Takahashi; FEBS Lett. 293, 37-41, 1991

A:Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta- γ -glutamyl carboxylesterase

A:Reference number: S19307; MUID:92070571; PMID:1959668

A:Accession: S19307

A:Molecule type: mRNA

A:Residues: 1-566 <MAT>

A:Cross-references: EMBL:X63323; NID:g1930; PIDN:CAA44929.1; PID:g1931

A:Accession: S23607

A:Molecule type: protein

A:Residues: 19-40 <MAT2>

A:Note: 28-Lys and 33-Leu were also found

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-566/Product: carboxylesterase #status experimental <MAT>

F:51-552/Domain: cholinesterase homology <CHE>

F:80/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:222,467/Active site: Ser, His #status predicted

Query Match 18.8%; Score 836.5; DB 2; Length 566;

Best Local Similarity 32.7%; Pred. No. 5.1e-44;

Matches 206; Conservative 100; Mismatches 219; Indels 105; Gaps 18;

Qy 1 MWLLALCLVLGAGQGGGPGGAPGGGLGSLGERFPVWNTAYGVRGVRRELNN 60

Db 1 MWLLPLVLTSASS-----ATWAGQASP-----PVDTAQGRVLGKYVLEG 43

Qy 61 EILGPVQVLGVPYATPPGARRFQPEAPASWPGVNRATTLPPACPNLHGALPAI--M 118

Db 44 -LAQPAVAVLGVFPFAKPPGLSLRFAPPQPAEPWFSVKNTTSYPPMCCQD-----PVVEQM 97

Qy 119 LPWFETDNLAAATYYQNOSECLYLNLVPTEDGPLTKKRDEATLNPPDTDIRPGKKP 178

Db 98 TSDLFTNGKERLT-----EFSECLYINITYPAD---LTKR-----GRUP 135

Qy 179 VMLFLHGGSYMEGTGNMFDGSLAAYGNIVATLNYRLGVLTSTGDAQAKNGYGLLDQ 238

Db 136 VMVYIHGGGLVLGGA PMYDGVVLAAHENVVVAIVQLRGINGFFSTGDEHSRGNHGHLDD 195

Qy 239 IQALRWLSENIAHFQGDPRITIFQSGAGASCWNLLIISHHSEGLFQKAIQSGTAISW 298

Db 196 VAALHWQENIAFNGDGPQSVTIFESAGGESVVLVSLPAKLNFLHRAISSGVALTVA 255

Qy 299 SVNYPQLKYLTRLLAAKVGCDREDSAEAEVCLRRKPSRELVDQDVQ-----PARY 347

Db 256 LVKDKMAAKAQI AVLAGCKTTTSVAVFVHCLRQKSEDELLDLTKMKFLTLDPFHGDQRES 315

Qy 348 HIAFGVVDGVDVDDPEILMQQGKFLNYDMLIGVNNQGE-----GLKFEVDSASSE 398

Db 316 HPFLPTVVDGVLIPKMPKEIILAEKDFTVPTVGVINKQEFGLWLLPTMMGFPPLSEGLDQK 375

Qy 399 DGVASAFDFTVSNFDVNLGVPEKGQVLRETIKFMYTDMADRDNGEMERKTLALFTDH 458

Db 376 TATSLNWKSYPIANIPPEL---TPVATD-----KYL-----GGTDFVKKKFLDLMGDV 423

Qy 459 QWVAPAVATAKLHADYQSPVYFTTYHH---COAEGRPWEADAAGDELFPYVFGVPMVGAT 516

Db 424 VFGVPSVTVAROHRDAGAPTYWYFQYRFSFSSDKKPKTVIGDHQDIFSVFEGFLKKG- 482

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QY 517 DLFPNFKNDVMSAVVMTYWTNPAKTGDPN-QVPQDTKFIHTKPNRFEVVMKPN 575
Db -----DAPEEVSLSKTYMKFWANFARSGNPGEGCLPH-----WPMYD- 520
QY 576 KEKQYHLGILKPRVRDNYRANKVAFWLELV 605
Db ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: 521 QEEGYLIQVNTQAARLKGEEVAFWDL 550
QY 521 QEEGYLIQVNTQAARLKGEEVAFWDL 550
Db ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
RESULT 7
A47162
thioesterase B (EC 3.1.1.1) precursor - mallard
C:Species: Anas platyrhynchos (mallard)
C>Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 18-Jun-1999
C:Accession: A47162
R:Hwang, C.S.; Kolatukudy, P.E.
J. Biol. Chem. 268, 14278-14284, 1993
A:Title: Molecular cloning and sequencing of thioesterase B cDNA and stimulation of exp
A:Reference number: A47162; MUID:93300823; PMID:8314791
A:Accession: A47162
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-557 <BA>
A:Cross-references: GB:105493; NID:G213100; PIDN:AAA49223.1; PID:G213101
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: hydrolase
F:56-545/Domain: cholinesterase homology <CHE>
Query Match 18.4%; Score 830; DB 2; Length 557;
Best Local Similarity 34.5%; Pred. No. 1.3e-43;
Matches 203; Conservative 94; Mismatches 216; Indels 76; Gaps 18;
QY 42 PVNTAYGRVGRVRRRLNNEILGVVQFLGVYATPLGARRFQPPPEASPGVGNATT 101
Db 30 PEVNTYGVGRGVQKV-NAERSVNVFLGLPFAKPPVGLRESEFPQPPPEKMGVDAAS 88
QY 102 LPPACQNLHGALFALMPVWFTDNLEAAATVYQNC-SEDCLYNLVYPTEDGPTLTKKD 160
Db 89 YPWCLODK-----VLGQYSLDAITNRKEKVLQISEDCLYNLVYTPVS-----TEEQE 137
QY 161 EATLNPDPDITRDPGKPPVLMFLHGSGYMBGTGMFPGSVLAAYGNVIVATNLYRLVLG 220
Db 138 -----KLPPVFTTHGGGLVSGAASSYDGSALAADFNVVVVTTIYRIGIAG 182
QY 221 FLSTGDAQNGNYGLLDOIQALXWLSGENTAHFGGDPERTIFGSGAGACVNLILLSHS 280
Db 183 YFTGDXHARGNGYLLDQVAAQLQENIHFKDPGVTIIFGESAGGVSVSALVSLPLA 242
QY 281 EGIQKAIASGTAISSWSVNYOPLKYTRLLAAKVGCDREDSAAEVECLRRKPSRELVDQ 340
Db 243 KGLFHKAISSEGTAVRILFTE-QPEEQARIAAAGCEKSSAALVECLREKTEAEMEQI 301
QY 341 DVQPARVHIAFGPVVGDGVDDPEILMOQGEFLNYDMLIGVNOGE-----GLKFVED 393
Db 302 TLKVPWFISAS--LDGVFPFKSPRLLEKVINAVPYIIGVNNCEFGWILPRMKMFPEF 359
QY 394 SAESDGVCSASAFDTFVSFVNDLYGPEGKQVLRITIKFMYTDMAD-RDNGEMERKTL 452
Db 360 TEGLEXDVARQVLOSTLAL--SFKGAPS-----DIVLVNYEYIGVAENEAQVRDGL 410
QY 453 ALFTDQHWAPATATAKLHADYQSPVYFTFYH-CQAEQ-RPEWADAANGDELVPQGV 510
Db 411 DSIADELFPESAVEVARHHRDAGNPVYFQFRRPSSAAGVVPFVKADHADEIAFVFGK 470
QY 511 PMVGATDLFCPNSKNDVMSAVVMTYWTNPAKTGDPNQPVDTKFIHTKPNRFEVVM 570
Db 471 PFLAG-----NATEEEAKLSRTVMKYWTNFAENGPN-----GEGLVH-----W 509
QY 571 SKNSKEKQYHLGILKPRVRDNYRANKVAFWLELVPHL-----HNLTTEL 615
Db 510 PQYMDER-YLEDLTQCAAKLKERMEFWMLQTEQIMSDRRRKHTDL 557

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A;Residues: 24-40,135-170;278-286,'V',288-294,'L',296;305-340;534-543 <CHR>
 R;Wang, C.S.
 Biochem. Biophys. Res. Commun. 155, 950-955, 1988
 A;Title: Purification of carboxyl ester lipase from human pancreas and the amino acid se
 A;Reference number: A31520; MUID:88339990; PMID:3421974
 A;Accession: A31520
 A;Molecule type: protein
 A;Residues: 24-33 <WAN>
 R;Hui, D.Y.; Hayakawa, K.; Oizumi, J.
 Biochem. J. 291, 65-69, 1993
 A;Title: Lipomerase activity in normal and mutagenized pancreatic cholesterol esterase
 A;Reference number: S32318; MUID:93228634; PMID:8471055
 A;Accession: S32318
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 54,'X',56-75;77-79;359-377 <HUS>
 R;Roudani, S.; Miralles, F.; Margotat, A.; Escoribano, M.J.; Lombardo, D.
 Biochim. Biophys. Acta 1264, 141-150, 1995
 A;Title: Bile salt-dependent lipase transcripts in human fetal tissues.
 A;Reference number: S59907; MUID:96038831; PMID:7578248
 A;Accession: S59907
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 26-729 <ROU>
 R;Loomes, K.W.
 Eur. J. Biochem. 230, 607-613, 1995
 A;Title: Structural organisation of human bile-salt-activated lipase probed by limited p
 A;Reference number: S65641; MUID:95331299; PMID:7607235
 A;Accession: S65641
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 24-30;31-32;109-110;456-459;545-552 <LOO>
 C;Genetics:
 A;Gene: GDB:CEL
 A;Cross-references: GDB:127527; OMIM:114840
 A;Map position: 9q34.3-9q34.3
 C;Superfamily: cholinesterase, cholinesterase homology
 C;Keywords: carboxylic ester hydrolase; glycoprotein
 F;1-23/Domain: (or 4-23) signal sequence #status predicted <SIG>
 F;24-745/Product: triacylglycerol lipase, bile salt-activated
 F;53-536/Domain: cholinesterase homology <CHE>
 F;210/Binding site: carbohydrate (Aem) (covalent) #status predicted
 F;217,459/Active site: Ser, His #status predicted

Query Match 18.4%; Score 828.5; DB 2; Length 745;
 Best Local Similarity 30.6%; Pred. No. 2.3e-43;
 Matches 253; Conservative 98; Mismatches 288; Indels 187; Gaps 34;

QY 44 VNTAYGRVGRVRELNNILGPVQ-FLGVYATPPLGARRFQPEAPASWPGVNRATTL 102
 DB 29 VYTEGGFVEGVNKKLG--LLGDSVDIFKGIFFAAP---TKALENPQHPGQGTAKNF 83
 QY 103 PPACQNLHGALPATMLPVWFTDNLAAATVQNS---EDCLYINLYVPTEDGPTKKR 159
 DB 84 KKRLQ-----ATITQDSTYGDDECLYINWVP--QGRKQVSR 119
 QY 160 DEATLNPPDTRDQPKKPMFLHGGSYMEGTN-----MFDGSVLAAGNVIAT 211
 DB 120 D-----LPNWIYGAFLMGSHGANGFNLNLYDGEETATGNVIWT 163
 QY 212 LNYRLVGLGFSTGDAQAGNYGLDQTQALRWLSENIAHFGDPERITTFGSGAGASCV 271
 DB 164 FNYRVGLCLSTGDANLPNGYLRDQHMALAWKRNIAAFGDPNNITLFGSAGASV 223
 QY 272 NLLILSHSEGLFQKATAQSTALSSVSNVQPKYTRLLAAKVGCDREDSAEVCLRR 331
 DB 224 SLQTLSPYKGLIRRAISQSGVALSPVVIQKNPLFWAKVAEKVCGCPVGDAAARMAQCLKV 283
 QY 332 KPSREL-----VDQVQPARYHIAFGPVVDGWDVDDPEILMQCEFLNYDMLIGVQ 384
 DB 284 TDPRALTAYKVPAGLEYPMLHYGVFPVIDGDFIADFINLYANAADIDY--IAGTNN 341
 QY 385 GEGLEK--VEDSAESDQVSASADF--TVSNF--VDNLYGPEGKDVLRETIKFMYTDW 438

Db 342 MDGHIFASIDWPAINKGNKKVTEEDFYKLVSFETITKGLGAKTTPFDVYTES-----W 394
 QY 439 ADRDNGEMRKTLLALFTDQHWAPA-VATAKLEADYQS-PVYFYFHHQAGREPEWA 496
 Db 395 AQPDSQENKKTVVDFDVLVFTETIAQAHRNAKSAKTYAYLFSHPSRMEVPYKWW 454
 QY 497 DAAGDELPLYVFGVPMVGATDLFPFCNFKNDVMSAVVMYTNFAKTGDPN---QVPQ 553
 Db 455 GADHADDIQVFGKPF--AI---PTGYRPODRIVSKAMIAYTNFAKTGDPNWDGSAVPT 509
 QY 554 DTFEHTKPNRPREVWVSKNSKEKYLHIGLK--PRVDNRYRANKVAFWELVPHLHN 610
 Db 510 H-----WEPTYTENSGLYLETIKWSSMKRSLRTNLFRTW--TLTYL-A 551
 QY 611 LHTELEFTTTRLPPYA-TRWPPRPAGAGQTRRRPPPPATLPPPEPEPGPRAVDRPGDS 669
 Db 552 LPTVTDQEAFTVPTGDSSEATVPVPTGDSATAPVPTGSGAPVPP-----TGDS 602
 QY 670 RDISTELSVTVAVGASLLFINILAFALYYKRRDRQELRCRLSPFGSGSGVPGGGLL 729
 Db 603 -----GAPFV-----PPTGD-SGAP---PVP 619
 QY 730 PAAAGRELPPBEELVSLQKKGSGVGADPAELARPACPPDYTLALRRAPDDVLLARQALT 789
 Db 620 PTGDSGAPP-----VPTGDSGAPPV-----PPTGDSG---APPVPTGDSGAPP 661
 QY 790 LLPSG-LGPPPPPP-----PPSLHPFGPPPPPPPTATSHNLTLPHP 829
 Db 662 VPPTGDAGPPVPPTGDSGAPPVPTGDSGAPPVPTGDSATAPV 707

RESULT 9
 A39256
 acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human
 C;Species: Homo sapiens (man)
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1999
 C;Accession: A39256; S03959
 R;Soreg, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Ghatt, A.; Neville, L.; Lieman-Hurw
 Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990
 A;Title: Molecular cloning and construction of the coding region for human acetylcholine
 A;Reference number: A39256; MUID:91088577; PMID:2263619
 A;Accession: A39256
 A;Molecule type: mRNA; DNA
 A;Residues: 1-614 <SOR>
 A;Cross-references: GB:M55040; NID:gl77974; PIDN:AAA68151.1; PID:gl77975
 A;Note: this sequence represents composite of clones including clone ABGACHE from adult
 ice should represent an authentic brain splice form
 R;Chhajlani, V.; Derr, D.; Earles, B.; Schmeil, E.; August, T.
 FEBS Lett. 247, 279-282, 1989
 A;Title: Purification and partial amino acid sequence analysis of human erythrocyte acet
 A;Reference number: S03959; MUID:89232136; PMID:2714437
 A;Accession: S03959
 A;Molecule type: protein
 A;Residues: 256-266,'Y',268-273;306-308,'X',310-313,'X',315-316,'D',318-323,'D',325-326;
 Y,532-551 <CH>
 A;Experimental source: erythrocytes
 A;Note: this form was a disulfide-linked homodimer
 C;Genetics:
 A;Gene: GDB:ACHE; YT
 A;Cross-references: GDB:118746; OMIM:100740
 A;Map position: 7q22-7q22
 C;Superfamily: cholinesterase, cholinesterase homology
 C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphatidy
 F;63-569/Domain: cholinesterase homology <CHE>

Query Match 18.4%; Score 827.5; DB 2; Length 614;
 Best Local Similarity 32.2%; Pred. No. 2.1e-43;
 Matches 201; Conservative 96; Mismatches 238; Indels 89; Gaps 16;

QY 30 GIGLSLGEERFPVNTAY-GRVGRRELNNILGPVQFLGVYATPPLGARRFOPPE 88
 Db 26 GGVGAEGREDAELLIVTGRGLRGLRKTPG---GPVSAFLGIPFAEPMPGRFLPPE 82

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Db      44  -FTQPVAVFLGVPPAKPLGSLRFAPPQPAEPWSSVKNATSPYPMCFQDPVTGQIVNDLL 102
QY      120  -----PWFTDNLEAAATVYQNSEBCLYNLYVPTDEGPLTKKRDEATLNPDDTDIR 172
Db      103  TNRKEKIPLOF-----SEDCLYNIYTPAD---LTKS-----131
QY      173  DPGKKPVMLFLHGGSYMEGTGNMFDGSLAAYGNVIVATLNYRLGVLGPLSGDQAAKN 232
Db      132  --DRLPVMMVHGGGLVLGASATYDGLVSLTHENVVVVVVYQRLGIWGFSGDEHSRN 189
QY      233  YGLDQIQALRWLSENTIAHFQGDPERITFGSGAGACVNNLLILSHSEGLFKQIAQSG 292
Db      190  WGHLDQVAALHWQDNTAKFGDPCGSVTIFGESAGGESVVLVLSPLAKNLFQRAISEG 249
QY      293  TAISWSVNYQPLKXTRLLAAKV---CCDREDSNAEVECLRRKPSRELVDQVQ-----343
Db      250  VALTAGLVK----KXNTRPLASKIAVISECKNNTSAAMVHCLQRKTEBELLGTLKLNLPK 305
QY      344  ----PARYHTIAFGP-VVDGDPWDDPPEILMQOGEFLNYDMLIGNQGE-----GLKRV 391
Db      306  LD LHGDSRQSPFPFVPTVLDGVLLPKMPEEILAEKNFNTVPVIGINKQEGFGWILPTMNY 365
QY      392  EDSAESDGVSAFDFTVSNFVNDLYXGYPGKQVLRETI-KFMYTDWADRNGEMRRKT 450
Db      366  PPSDVKLQDMTAMSL-LKKSFFLLN---PE--DAIAVAIEKYL---RDKDYTGKNDQ 415
QY      451  LLALFTDQHWAPAVATAKLHADYQSPVYPTFFVH--HCQREGPEWADAAGHDELPLYV 508
Db      416  LLELTGDPVGVPSVTVSRGHRDAGATPYMYEFQYSPFSSEMXPDTVVGHDGDIYGVF 475
QY      509  GVPMV-GATDLFPNCFSKNDVMSAVVMYVWTFNAFKTGDPN-QVPVQDTKTHTKPNRFE 566
Db      476  GAPIRGGT-----SEEEINLSKMMKFWANPARNPNQOGLPH-----515
QY      567  EVWVKNSKSKQVLIHGLKPRVRDNTRANKVAFWLELV--PHLIUHLTEL 615
Db      516  ---WPEYDOKE-GYLIQICATTQQAQKLKEKEVAFWELLAKKOPTHETEL 562

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RESULT 11

JC2447

carboxylesterase (EC 3.1.1.1) ES-3 precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 28-Mar-1995 #sequence_revision 26-May-1995 #text_change 18-Jun-1995

C/Accession: JC2447; S23462

R/Robbi, M.; Beaufay, H.

Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994

A/Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (EGAS)

A/Reference number: JC2447; MUID:95032008; PMID:7945287

A/Accession: JC2447

A/Molecule type: mRNA

A/Residues: 1-561 <R0>

A/Cross-references: GB:X81395; NID:g550146; PIDN:CAA57158.1; PID:g550147

A/Experimental source: liver

R/Medda, S.; Proia, R.L.D.

Eur. J. Biochem. 206, 801-806, 1992

A/Title: The carboxylesterase family exhibits C-terminal sequence diversity

A/Reference number: S23460; MUID:92299008; PMID:1606962

A;Experimental source: liver
R;Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
A;Title: The carboxylesterase family exhibits C-terminal sequence divers
A;Reference number: S23460; MUID:92299008; PMID:1606962
A;Accession: S23462
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 503-554, 'R', 556-561 <MED>
A;Cross-references: EMBL:X65295; NID:575757; PIN:CAA64390.1; PID:957558
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-561/Product: carboxylesterase ES-3 #status predicted <PAT>
F;50-551/Domain: cholinesterase homology <CHE>
F;79,407,489/Binding site: carboxylate (Asn) (covalent) #status predicted
F;221,466/Active site: Ser, His #status predicted

Cross-references: EMBL: X65295; NID: G57557; PIDN: CA46390.1; P
Superfamily: cholinesterase; cholinesterase homology
Keywords: carboxylic ester hydrolase; glycoprotein
1-18/Domain: signal sequence #status predicted <SIG
19-561/Product: carboxylesterase ES-3 #status predicted <WAT>
50-551/Domain: cholinesterase homology <CHE>
79,107,489/Binding site: carbohydrate (Asn) (covalent) #status
221,466/Active site: Ser, His #status predicted
18.2%; Score 819; DB 2; Length 561.
Query Match

Best Local Similarity 33.9%; Pred. No. 6.1e-43;
Matches 218; Conservative 102; Mismatches 213; Indels 110; Gaps 23;

QY 1 MWLLALCLVLAGAQRGGGPGGAPGGGLGLSGLEERFFVNTAYGRVGRVRLNN 60
Db 1 MCLYLALILVFLA-AFTAGGHPS- -LPVDTLQKVLGKVSLEG 42

QY 61 EILGPVVQFLGVYATPPPGARRFQPEAPASPGVGNATTLPPACPN-LHALPALM 119
Db 43 -FTQPVAVFLGVFAKPPGLSRLFAPQPAEPWFSVNTTSYPPMCSQDPVAGQIVNDLL 101

QY 120 PVFTDLNLEAAATVYQNSDECLYLNLVFTEDGPTKKRDEATLNPDPDIRDPGKPPV 179
Db 102 TNW-BENISL-----QFSEDCLYLNIYTPAD--LTKR-----DRLPV 135

QY 180 MLFLHGSYMEGNGNMFDSVLAAYGNVIVATNLRLVGLSTGDDQAAKNYGLLQI 239
Db 136 MWIHGGGLVGLGASTYDGLALSTHENVVVIQVRLGIWGFSGFDSHSGRNWHLDOV 195

QY 240 QALRWLSENIAHFGDPPEIRITIFGSGAGASCYNLILSHHSEGLFOKALQSGTAISWS 299
Db 196 AALHWYQDNI DNFQDPGSGVTIFGESAGGESVSLVSLAKNLFHKAISSGVALTAGL 255

QY 300 VNYQPKYTRLLAAKY-----GQREDSABAVCLRRKPSRELVDQDVQ-----PA 345
Db 256 VR-----KNTRPLAEKIAVYSGCKSTTSASNVHCLRQKTEELLETLLKLNLFSLDLHGD 311

QY 346 RYHIAFGP-VVDGVDVDPDEILMOGGEFLNYDMLIGVNOGS-----GLKFEVDSASE 398
Db 312 RQSYPPVPTVLQGVLPKXPEILAEKDNTPVYIVGINKQFEGWILPTMNYPPSDMKL 371

QY 399 DGVSASAFPTVSNFVDNIYGYPEGKQVRLRETIKMYTMDADRNGEMRRKTLALFTDH 458
Db 372 DPMATSL-LKSSFFLNL---PEEAIPVAVEKYLRLHTDDPRNDQ-----LLELIGD 422

QY 459 QWVAPAVATAKLHADYQSPVYFVTH--COAEGRPWADAAGDELPIYVGVPMV-CA 515
Db 423 IFGVPSVIVSRGHRDAGATYMEFYQRPSPSKMKPSTVVDGHDGEIYVSFGAPILGG 482

QY 516 TDLFPNCFKNDVMSAVVMTYWTNFAKTGDPN-QPVQDTKFIHTKENREVEVWVKFN 574
Db 483 T-----SKEINLSKMMKFWANFARNGNPGQLPH-----WPEYD 519

QY 575 SKEQVHLHGLKPRVDRDYNRANKVAFWLEL--VPHLNLHTEL 615
Db 520 QXE-GYLQIGATTQQAQKKEKVAFWSELLAMKPLHAGHTEL 561

RESULT 12
A41010
N;Alternate names: carboxylesterase, hepatic; monocyte/macrophage serine esterase
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 08-Dec-2000
C:Accession: A41010; JH0327; A47376; A49816; PS0280; I61085; A48809; I57004
R:Munger, J.S.; Shi, G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A.
J. Biol. Chem. 266, 18832-18838, 1991
A:Title: A serine esterase released by human alveolar macrophages is closely related to
A:Reference number: A41010; MUID:92011649; PMID:1918003
A:Accession: A41010
A:Molecule type: mRNA
A:Residues: 1-567 <MUN>
A:Cross-references: GB:M73499; NID:q179927; PIDN:AAA35649.1; PID:gl179928
A:Note: Parts of this sequence, including the amino end of the mature protein, were conf
R:Long, R.M.; Calabrese, M.R.; Martin, B.M.; Pohl, L.R.
Life Sci. 48, PL43-PL49, 1991
A:Reference number: JH0327; MUID:91148424; PMID:1997784
A:Accession: JH0327
A:Molecule type: mRNA
A:Residues: 61-567 <LON>
A:Cross-references: GB:M55509; NID:gl179929; PIDN:AAA35650.1; PID:gl179930
R:Shibata, F.; Takagi, Y.; Kitajima, M.; Kuroda, T.; Omura, T.

Genomics 17, 76-82, 1993
A:Title: Molecular cloning and characterization of a human carboxylesterase gene.
A:Reference number: A47376; MUID:94010913; PMID:8406473
A:Accession: A47376
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA; DNA
A:Residues: 1-53, PALV, 8-11, 'A', 13-567 <SHI>
A:Cross-references: GB:D21088; NID:G455476; PIDN:BA04650.1; PID:G458470
A:Note: sequence extracted from NCBI backbone (NCBI:137630) and corrected to correspond
R:Zschunke, F.; Salmassi, A.; Kreipe, H.; Buck, F.; Farwarsch, M.R.; Radzun, H.J.
Blood 78, 506-512, 1991
A:Title: cDNA cloning and characterization of human monocytic/macrophage serine esterase.
A:Reference number: A49816; MUID:91300111; PMID:2070086
A:Accession: A49816
A:Molecule type: mRNA
A:Residues: 'G', 65-185, 'G', 187-361, 363-567 <ZSC>
A:Cross-references: GB:X52973; NID:G36421; PIDN:CAA37147.1; PID:gl1335304
R:Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.
Gene 108, 289-292, 1991
A:Title: Cloning and analysis of a cDNA encoding a human liver carboxylesterase.
A:Reference number: PS0280; MUID:92084150; PMID:1748313
A:Accession: PS0280
A:Molecule type: mRNA
A:Residues: 114, 'H', 116-280, 'A', 282-300, 'IGNSYLTWYRETQREST', 318-336, 'R', 338-382, 'GSP', 384-392
A:Cross-references: GB:M5261; NID:gl87028; PIDN:AAA83932.1; PID:gl87029
A:Experimental source: liver
A:Note: differences between this sequence and other reports appear to be due to frameshi
R:Koeztz, D.L.; McBride, O.W.; Gonzalez, F.J.
Biochemistry 32, 11606-11617, 1993
A:Title: Glycosylation-dependent activity of baculovirus-expressed human liver carboxyle
A:Reference number: A48809; MUID:94032283; PMID:8218228
A:Accession: I61085
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-55, 'G', 57-361, 363-535, 'G', 537-567 <KRO1>
A:Cross-references: GB:L07765; NID:gl80949; PIDN:AAA35711.1; PID:gl80950
A:Accession: A48809
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-17, 'A', 18-55, 'G', 57-535, 'G', 537-567 <KRO2>
A:Cross-references: GB:L07764; NID:gl80947; PIDN:AAA16036.1; PID:gl80948
A:Gene: GDB:CES1; HMSC
A:Cross-references: GDB:128044; OMIM:114835
A:Map position: 16q13-16q22.1
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; liver
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-145/Domain: propeptide #status predicted <PRO>
F:50-533/Domain: cholinesterase homology <CHE>
F:146-567/Product: carboxylesterase #status experimental <MAT>
F:564-567/Region: endoplasmic reticulum retention signal #status atypical
F:221,468/Active site: Ser, His #status predicted

Query Match 18.1%; Score 817; DB 1; Length 567;
Best Local Similarity 32.6%; Pred. No. 8.2e-43;
Matches 210; Conservative 93; Mismatches 206; Indels 136; Gaps 22;

QY 1 MWLLALCLVLAGAQRGGGPGGAPGGGLGLSGLEERFFVNTAYGRVGRVRLNN 60
Db 1 MWLRAFILATLSAS-----AAWGHPSF-----PVVDVHGKVLGKFSLEG 42

QY 61 EILGPVVQFLGVYATPPPGARRFQPEAPASPGVGNATTLPPACPNLHAGLPAIMLP 120
Db 43 -FAQPVAVFLGIPFAKPPGLRFPPLRFPQPAEPWFSVKNATSYPPMCTQDPKAGQ---LLS 98

QY 121 VWFTDLNLEAAATVYQNSDECLYLNLVFTEDGPTKKRDEATLNPDPDIRDPGKPPV 180
Db 99 ELFTNRKENIPLKL---SDECLYLNIYTPAD--LTKK-----NRLPWM 136

QY 181 LFLHGSYMEGNGNMFDPGSLVLAAYGNVIVATNLRLVGLSTGDDQAAKNYGLLQIQ 240
Db 137 VMIHGGGLMVGAASTYDGLALAHENVVVVTIQLYRLGIWGFSTGDSHSGRNWHLDOVA 196

A;Note: parts of this sequence, including the amino and carboxyl ends of the mature protein.
 R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; Fed. Proc. 45, 2976-2981, 1986
 A;Title: Primary structure of acetylcholinesterase: implications for regulation and function.
 A;Reference number: A60820; MUID:87054662; PMID:3536598
 A;Accession: A60820
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 22-596 <SC2>
 R;Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.
 J. Biol. Chem. 263, 18979-18987, 1988
 A;Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase.
 A;Reference number: A92701; MUID:89056695; PMID:3198606
 A;Accession: A31962
 A;Molecule type: mRNA
 A;Residues: 1-23 <SC3>
 A;Cross-references: EMBL:X03439; NID:G64389
 A;Experimental source: Clones AChE-11 and AChE-18
 A;Note: revision to sequence A00773
 A;Accession: B31962
 A;Molecule type: DNA; mRNA
 A;Residues: 499-565 <SC4>
 A;Cross-references: GB:X03439; NID:G64389
 A;Experimental source: Clone AChE-1
 R;MacPhee-Quigley, K.; Taylor, P.; Taylor, S.
 J. Biol. Chem. 260, 12185-12189, 1985
 A;Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase.
 A;Reference number: A23902; MUID:86008285; PMID:3900071
 A;Accession: A23902
 A;Molecule type: protein
 A;Residues: 22, 87, 24-45, 214-237 <MAC>
 A;Note: active site Ser identification
 R;Kreienkamp, H.J.; Weisse, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo aequicinctum.
 A;Reference number: A41117; MUID:91296772; PMID:2068091
 A;Accession: B41117
 A;Molecule type: protein
 A;Residues: 100-108 <KRE>
 A;Note: substrate binding site
 R;Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.
 Neuron 4, 289-301, 1990
 A;Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinesterase.
 A;Reference number: P80113; MUID:90166618; PMID:2306366
 A;Accession: S15677
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 557-596 <MAU>
 A;Cross-references: EMBL:X56516
 R;MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.
 J. Biol. Chem. 261, 13565-13570, 1986
 A;Title: Profile of the disulfide bonds in acetylcholinesterase.
 A;Reference number: A43099; MUID:87008586; PMID:3759980
 A;Contents: annotation; disulfide bonds
 R;Sussman, J.L.; Harel, M.; Silman, I.
 submitted to the Brookhaven Protein Data Bank, October 1991
 A;Reference number: A50061; PDB:1ACE
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of Torpedo californica
 R;Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.
 Science 253, 872-879, 1991
 A;Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic serine protease.
 A;Reference number: A43098; MUID:91343928; PMID:1678899
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of Torpedo californica
 C;Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a holoenzyme occurs on the outer surfaces of cell membranes, including those of erythrocytes.
 C;Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of 11S subunits.
 A;Description: hydrolyzes acetylcholine to choline and acetate
 A;Pathway: neurotransmitter degradation
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane protein
 F;1-21/Domain: signal sequence #status predicted <Sig>
 F;22-596/Product: acetylcholinesterase, 11S form #status experimental <Mat>

F;51-551/Domain: cholinesterase homology <CH>
 F;80-478,554/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;88-115,275-286,423-542/Disulfide bonds: #status experimental
 F;105/Binding site: substrate (Trp) #status experimental
 F;221/Active site: Ser #status experimental
 F;348, 461/Active site: Glu, His #status predicted
 F;437/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;593/Disulfide bonds: interchain #status experimental

Query Match 18.0%; Score 813; DB 1; Length 596;
 Best Local Similarity 32.5%; Pred. No. 1.5e-42;
 Matches 198; Conservative 94; Mismatches 238; Indels 80; Gaps 16;

QY	43	VNTAYGRVGRVRELNNEILGPVQFLGVYATPPIGARRFPQPPAPASWPGVRRNATL	102
DB	28	LVNTKSGKVMGTRVPV---LSSHISAFILGIPFAEPVGNMFRFRPEPKPKWSGVWNA	84
QY	103	PPACPQNLHGALPAIMLPVMTDNLEAAATVQNSQEDCLYLNLYPTDGLTKKDEA	162
DB	85	PNNCOQVVDQEPFGFSQSEMNPKE-----MSQCLYLNWVSP-----	125
QY	163	TLNPPDTDIRDPKPKVWFLHGGSYWEG--TGNMFDGSLAAAYGNVIVATLNYRLGVLG	220
DB	126	-----RPKSTTVMWYGGFVSGSSTLDVYNGKYLAYTEEVLSVLSYRVGAFG	175
QY	221	FLST-GDQAAKNGVLLDQIQALRWLSENIAHFGGDPERITIEGSGAGASCYNLLILSHH	279
DB	176	FLAHGQEPAGNVGLDDQMALQWHDNIQPPGGDKTITIFGESAGGASVGMHILSPG	235
QY	280	SEGLFQKAIAGSCTAISW-SVNYQFLKYTRL-LAAKVGCDREDSAAVECLRRKPSREL	337
DB	236	SRDLFRRAILQSGSPCPWASVSAEGRRAVELGRNLNCLNSDELEHCLREKPKQEL	295
QY	338	VQOD--VQP--AYHIAFGVVDGVDVDPPEILMQGDFLNDYMLGVNQEGELKVF--	391
DB	296	IDVENVLPDSIFRSFVFDGFEPTSLSEMLNSGNFKTKTQILLGVNKDEGSFFLLY	355
QY	392	---EDSAESGDSASAFDTVSNFVDNLYGYPEGKDLRETIFKMYTDWDRDNCMER	448
DB	356	GAPFSGKDSKISREDFNSGVKLSV-----PHANDLGLDAVTLQYTDWDDNGIKVR	409
QY	449	KILLALFTDHWVAPAVATAKLHADYQSVYPTFYHHCQASGRPEWADAAGDELFPYVF	508
DB	410	DGLDDITVGDHNVICPLMHFVNKYTKFGNGTYLYFFNHRASNLVWPEWGMVIEGYE	469
QY	509	GVPMVGATDLFCNFSKNDVMSAVMTYMTWTFKTDGPDNQVPQDTKFIHTKPNRFEV	568
DB	470	GLPLVK-----ELNYTAEEALSRRIMHYWATFATGNPNEPHSQESK-----	512
QY	569	VMSKFSKEQYLHGLKFP-RVRDNYRANKVAFWLELVPHLHNLHLELF-----TTT	619
DB	513	-WPLFTTKEQKIDILNTEPMKVQRLRVQMCVFWNQFLPKLNA-TETIDEAERQWKTEF	570
QY	620	TLPLPYATEW 629	
DB	571	HRWSSIMMEW 580	

RESULT 15

S48724

acetylcholinesterase - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 07-May-1995 #sequence revision 21-Jul-1995 #text_change 14-Nov-1997

C;Accession: S48724

R;Jbilo, O.; L'Hermite, Y.; Talsala, V.; Toutant, J.P.; Chatonnet, A.

Eur. J. Biochem. 225, 115-124, 1994

A;Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissue

A;Reference number: S48724; MUID:95010096; PMID:7925428

A;Accession: S48724

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-584 <JBI>

C;Superfamily: cholinesterase; cholinesterase homology

C/keywords: glycoprotein
F/32-539/Domain: cholinesterase homology <CHE>

Query Match 18.0%; Score 811.5; DB 2; Length 584;

Best Local Similarity 32.3%; Pred. No. 1.9e-42;
Matches 196; Conservative 91; Mismatches 239; Indels 81; Gaps 15;

Qy 43 VVNTAYGRVRGRRRLNNEILGPVQFLGVPYATPPIGARREQPPPEAPASWPQVRNATTL 102
 : |||:|||: | | | |: | | | |: | | | | | | | |
Dd 9 LVTVRGKLRGLRKLAFG---GPSVAELGIPEEPVPQRRLFPPEPKRPWAGVLDTAF 65

Qy 103 PPACPQLHGALPAIMLPVWFTDNLEAAATVVQNQSEDCLYLNLYVTEDGPIKKRDEA 162
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 66 QSVCYQVDTLPGFGEGTEMNPNREL-----SDCLYLNWTVTPV----- 106

QY 163 TLNPPDTRDPCKPWLFIHGGSMEGTGNN---FDGSVLAAYGNIVATINRYLGVL 219
| : : : : | : : : :
Db 107 -----RPSPTPLVLTWYGGGYSGASSIDVVGRTVOAEGFTVAMHNVRVCAP 157

[illegible]

279 HSEGLFQKAIQSGTAISSWS-----VNYQLKYTRLLAAKVGCDREDSAEAVECURLRK 332

QY 333 PSRELYDQD-----VQPARYHIAFGPVVDGDVVDPDDPEILMQOGEFLNYDMLIGVNOGEG 388

QY 389 KFVEDSA-----ESEDGVSASAFDFTVSNFVDNLYGPEGKDVLRITKPMYTDWADRDN 443

336 IFLVIGAFGRKDNESFLSRQFLWAGVK-----VGVPQASDLAAEAVVLHITDMLHPEF 391

444 GEMRRKTLALFTDHWVAPAVATAKLHADYQSPVVFYTFYVHHCQAFGRPEWADAAHGE 503

[illegible]

DB	452	IEFI	FG	PLEPS----	LN	YEE	ER	IP	AQ	RL	MY	AN	FAR	GP	NE--	PR	AK----	AP	Q	500																							
QY	564	RFE	VV	WS	KF	NS	KE	QY	LH	IG	KP-	R	Y	R	D	N	Y	R	A	N	K	V	A	F	W	L	E	V	P	H	L	N	L	H	E	L	F	T	T	T	R	L	622

Db	501	-----WPPTYAGAQYVSLNLRPLEVRGRGIRACAFWNREL	-----KLISATDTL 547
Qy	623	PPYATRW 629	

Db 548 DEAEQW 554

Search completed: February 13, 2004, 13:14:15
Job time : 28 secs

Search completed: February 13, 2004, 13:14:15
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 13, 2004, 13:13:42 ; Search time 39 Seconds

(without alignments)
4482.928 Million cell updates/sec

Title: US-09-934-323-2

Perfect score: 4508

Sequence: 1 MWLLALCLVGLAGAQGGGG.....PPTAISHNNTLPHPHSTTRV 835

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PTCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	4508	100.0	835	10	US-09-934-323-2
2	4415.5	97.9	836	10	US-09-934-323-5
3	4075.5	90.4	801	12	US-10-274-694-12
4	2986	65.2	550	10	US-09-934-323-6
5	2746	60.9	848	10	US-09-875-353-5
6	2731	60.6	816	10	US-09-978-295A-375
7	2731	60.6	816	10	US-09-978-697-375
8	2731	60.6	816	10	US-09-978-192A-375
9	2731	60.6	816	10	US-09-999-832A-375
10	2731	60.6	816	11	US-09-978-189-375
11	2731	60.6	816	11	US-09-978-608A-375
12	2731	60.6	816	11	US-09-978-585A-375
13	2731	60.6	816	11	US-09-978-191A-375
14	2731	60.6	816	11	US-09-978-403A-375
15	2731	60.6	816	11	US-09-978-564A-375

16	2731	60.6	816	11	US-09-999-833A-375	Sequence 375, App
17	2731	60.6	816	11	US-09-981-915A-375	Sequence 375, App
18	2731	60.6	816	11	US-09-978-824-375	Sequence 375, App
19	2731	60.6	816	11	US-09-918-585A-375	Sequence 375, App
20	2731	60.6	816	11	US-09-978-423A-375	Sequence 375, App
21	2731	60.6	816	11	US-09-978-193A-375	Sequence 375, App
22	2731	60.6	816	11	US-09-999-830A-375	Sequence 375, App
23	2731	60.6	816	11	US-09-978-757A-375	Sequence 375, App
24	2731	60.6	816	11	US-09-978-187B-375	Sequence 375, App
25	2731	60.6	816	11	US-09-978-643A-375	Sequence 375, App
26	2731	60.6	816	12	US-09-978-375A-375	Sequence 375, App
27	2731	60.6	816	12	US-09-978-188A-375	Sequence 375, App
28	2731	60.6	816	12	US-09-978-298A-375	Sequence 375, App
29	2731	60.6	816	12	US-10-143-031A-375	Sequence 375, App
30	2731	60.6	816	12	US-10-002-967A-375	Sequence 375, App
31	2731	60.6	816	12	US-10-017-083A-375	Sequence 375, App
32	2731	60.6	816	12	US-10-143-030A-375	Sequence 375, App
33	2731	60.6	816	12	US-10-145-128A-375	Sequence 375, App
34	2731	60.6	816	12	US-10-017-191A-375	Sequence 375, App
35	2731	60.6	816	12	US-10-143-028A-375	Sequence 375, App
36	2731	60.6	816	12	US-10-143-029A-375	Sequence 375, App
37	2731	60.6	816	12	US-10-145-089A-375	Sequence 375, App
38	2731	60.6	816	12	US-10-013-926A-375	Sequence 375, App
39	2731	60.6	816	12	US-10-145-017A-375	Sequence 375, App
40	2731	60.6	816	12	US-10-164-728A-375	Sequence 375, App
41	2731	60.6	816	12	US-10-165-067A-375	Sequence 375, App
42	2731	60.6	816	12	US-10-145-124A-375	Sequence 375, App
43	2731	60.6	816	12	US-10-160-502A-375	Sequence 375, App
44	2731	60.6	816	12	US-10-165-247A-375	Sequence 375, App
45	2731	60.6	816	12	US-09-978-194A-375	Sequence 375, App

ALIGNMENTS

RESULT 1
US-09-934-323-2
; Sequence 2, Application US/09934323
; Patent No. US20020150910A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLSTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-081001
; CURRENT APPLICATION NUMBER: US/09/934,323
; CURRENT FILING DATE: 2001-08-21
; PRIOR FILING DATE: 2001-08-21
; PRIOR FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 835
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-323-2

Query Match	100.0%	Score 4508;	DB 10;	Length 835;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches	835;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
QY	1	MWLLALCLVGLAGAQGGGGGPGGPGGLGSLGSEPFVNTAYGRVGRVRELN	60	
Db	1	MWLLALCLVGLAGAQGGGGGPGGPGGLGSLGSEPFVNTAYGRVGRVRELN	60	
QY	61	ETLGPVQFLGVPYATPPLGARRFQPPAPASWPGVRNATLPPACPNLHGALPAIMLP	120	
Db	61	ETLGPVQFLGVPYATPPLGARRFQPPAPASWPGVRNATLPPACPNLHGALPAIMLP	120	
QY	121	VNFTDNLEAAATYVQNSDCILYLNLYPTDGPPTKKRDEATLNPPDTDIRDPCKKPM	180	
Db	121	VNFTDNLEAAATYVQNSDCILYLNLYPTDGPPTKKRDEATLNPPDTDIRDPCKKPM	180	
QY	181	LFHGGSYMEGTGNNFDGSLVLAAYGNVIVATLNYLGLVGLFSLTGDAQAKNGYLLDQIQ	240	

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181 LFLHGSYMEGTGNMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAGNYGLDQIQ 240
241 ALRWLSENIAHFGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQAQSGTAISSWSV 300
241 ALRWLSENIAHFGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQAQSGTAISSWSV 300
301 NYOPLKYRTELAAKVCDEDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDDV 360
301 NYOPLKYRTELAAKVCDEDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDDV 360
361 PDDPEILMOQGEFLNYDMLIGVNOQEGLEKFEVDSAESEDSGVSASAFDFTVSNFVNDLYGY 420
361 PDDPEILMOQGEFLNYDMLIGVNOQEGLEKFEVDSAESEDSGVSASAFDFTVSNFVNDLYGY 420
421 PEGKOVLRITIKFMTYTDWADRDNGEMRRKTLIALFTDQWVAPAVATAKLHADIQSPVYF 480
421 PEGKOVLRITIKFMTYTDWADRDNGEMRRKTLIALFTDQWVAPAVATAKLHADIQSPVYF 480
481 YTFYHHCQAEGRPEWADAAGDELPLYFVGPVMVGATDLPCNFSKNDVMSAVVMTYWTN 540
481 YTFYHHCQAEGRPEWADAAGDELPLYFVGPVMVGATDLPCNFSKNDVMSAVVMTYWTN 540
541 FAKTGDNPQVPQDQTKFIHTKPNRFEVVMVSKFNSKEKQYLIHGLKPRVRDNYRANKVAF 600
541 FAKTGDNPQVPQDQTKFIHTKPNRFEVVMVSKFNSKEKQYLIHGLKPRVRDNYRANKVAF 600
601 WLELVPHLNHLHTELTFTTTTLPVYATRWPPRPPAGAGTTRPPPPATLPPEPEPEGPR 660
601 WLELVPHLNHLHTELTFTTTTLPVYATRWPPRPPAGAGTTRPPPPATLPPEPEPEGPR 660
661 AYDRFPGDSRDYSTELSVTVAVGASLLFNILAFALYKEDRQELRCRLSPPGSGS 720
661 AYDRFPGDSRDYSTELSVTVAVGASLLFNILAFALYKEDRQELRCRLSPPGSGS 720
721 GVPGGGPIIPAAAGRELPEEELVSLQKRGCGVGADPAEALRPACPPDYTLALRAPDDV 780
721 GVPGGGPIIPAAAGRELPEEELVSLQKRGCGVGADPAEALRPACPPDYTLALRAPDDV 780
781 PLLAPGALTLLPSGLGPPPPPPPSLHPFGPPPPPTATSHNNTLPHPHSTTRV 835
781 PLLAPGALTLLPSGLGPPPPPPPSLHPFGPPPPPTATSHNNTLPHPHSTTRV 835

RESULT 2
US-09-934-323-5
; Sequence 5, Application US/09934323
; Patent No. US20020150910A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
; FILE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-081001
; CURRENT APPLICATION NUMBER: US/09/934,323
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,774
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 836
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-934-323-5

Query Match 97.9%; Score 4415.5; DB 10; Length 836;
Best Local Similarity 98.3%; Pred. No. 4.2e-312;
Matches 822; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 1 MWLLALCLVLAGAGQGGGPGGAGPGGGLGSLGEERFPVNTAYGRVGRRELNN 60
Db 1 MWLLALCLVLAGAGQGGGPGGAGPGGGLGSLGEERFPVNTAYGRVGRRELNN 60

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QY 61 EILGPVVQFLGVYATPLGARRFQPEAPAGWPGVNRATTLPPACFQNLHGALPAIMLP 120
Db 61 EILGPVVQFLGVYATPLGARRFQPEAPAGWPGVNRATTLPPACFQNLHGALPAIMLP 120
QY 121 WFTDNLAAATVQNOSEDCIYLNLYVPTDGLTKKDEATLNPDDTDIDRPGKKPYM 180
Db 121 WFTDNLAAATVQNOSEDCIYLNLYVPTDGLTKKDEATLNPDDTDIDRPGKKPYM 180
QY 181 LFLHGSYMEGTGNMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAGNYGLDQIQ 240
Db 181 LFLHGSYMEGTGNMFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAGNYGLDQIQ 240
QY 241 ALRWLSENIAHFGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQAQSGTAISSWSV 300
Db 241 ALRWLSENIAHFGGDPERITIFGSGAGASCNLLILSHHSEGLFQKAIQAQSGTAISSWSV 300
QY 301 NYOPLKYRTELAAKVCDEDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDDV 360
Db 301 NYOPLKYRTELAAKVCDEDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDDV 360
QY 361 PDDPEILMOQGEFLNYDMLIGVNOQEGLEKFEVDSAESEDSGVSASAFDFTVSNFVNDLYGY 420
Db 361 PDDPEILMOQGEFLNYDMLIGVNOQEGLEKFEVDSAESEDSGVSASAFDFTVSNFVNDLYGY 420
QY 421 PEGKOVLRITIKFMTYTDWADRDNGEMRRKTLIALFTDQWVAPAVATAKLHADIQSPVYF 480
Db 421 PEGKOVLRITIKFMTYTDWADRDNGEMRRKTLIALFTDQWVAPAVATAKLHADIQSPVYF 480
QY 481 YTFYHHCQAEGRPEWADAAGDELPLYFVGPVMVGATDLPCNFSKNDVMSAVVMTYWTN 540
Db 481 YTFYHHCQAEGRPEWADAAGDELPLYFVGPVMVGATDLPCNFSKNDVMSAVVMTYWTN 540
QY 541 FAKTGDNPQVPQDQTKFIHTKPNRFEVVMVSKFNSKEKQYLIHGLKPRVRDNYRANKVAF 600
Db 541 FAKTGDNPQVPQDQTKFIHTKPNRFEVVMVSKFNSKEKQYLIHGLKPRVRDNYRANKVAF 600
QY 601 WLELVPHLNHLHTELTFTTTTLPVYATRWPPRPPA-GAPGTRRRPPPPATLPPEPEPEGPR 659
Db 601 WLELVPHLNHLHTELTFTTTTLPVYATRWPPRPPGTSRPPPPATLPPESEDIDLP 660
QY 660 RAYDRFPGDSRDYSTELSVTVAVGASLLFNILAFALYKEDRQELRCRLSPPGSGS 719
Db 661 RAYDRFPGDSRDYSTELSVTVAVGASLLFNILAFALYKEDRQELRCRLSPPGSGS 720
QY 720 SGVPGGGPIIPAAAGRELPEEELVSLQKRGCGVGADPAEALRPACPPDYTLALRAPDD 779
Db 721 SGVPGGGPIIPAAAGRELPEEELVSLQKRGCGVGADPAEALRPACPPDYTLALRAPDD 780
QY 780 VPLLAPGALTLLPSGLGPPPPPPPSLHPFGPPPPPTATSHNNTLPHPHSTTRV 835
Db 781 VPLLAPGALTLLPSGLGPPPPPPPSLHPFGPPPPPTATSHNNTLPHPHSTTRV 836

RESULT 3
US-10-274-694-12
; Sequence 12, Application US/10274694
; Publication NO. US20030143589A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BRUNS, Christopher M.
; APPLICANT: DAS, Debopriya
; APPLICANT: DING, Li
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: KHAN, Farrah A.
; APPLICANT: LAL, Preeti G.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: LU, Yan
; APPLICANT: NGUYEN, Damiel B.
; APPLICANT: PATTERSON, Chandra S.

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; APPLICANT: RANKUMAR, Jayalaxmi
 ; APPLICANT: RING, Huijun Z.
 ; APPLICANT: SANJANWALA, Madhusudan M.
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: THANGAVELU, Kavitha
 ; APPLICANT: THORNTON, Michael B.
 ; APPLICANT: TRIBOULEY, Catherine M.
 ; APPLICANT: WALIA, Narinder K.
 ; APPLICANT: XU, Yuming
 ; APPLICANT: YANG, Junming
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: YUE, Henry
 ; TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
 ; FILE REFERENCE: PI-0151 USA
 ; CURRENT APPLICATION NUMBER: US/10/274,694
 ; CURRENT FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: 60/221,837
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: 60/220,037
 ; PRIOR FILING DATE: 2000-07-21
 ; PRIOR APPLICATION NUMBER: 60/218,948
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: US01/21324
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: 60/216,804
 ; PRIOR FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 12
 ; LENGTH: 801
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030143589A1 7473875CD1
 US-10-274-694-12

Query Match 90.4%; Score 4075.5; DB 12; Length 801;
 Best Local Similarity 95.1%; Pred. No. 2e-287;
 Matches 770; Conservative 3; Mismatches 18; Indels 19; Gaps 3;

QY 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGEBRFPVNTAYRGVRELN 60
 DB 1 MWLLALCLVGLAGAQGGGPGGAPGGGLGSLGEBRFPVNTAYRGVRELN 60
 QY 61 EILGPVVQFLGVYATPPLGARRFQPPAPASPGVGRNATLLPACPNLHGALPAILP 120
 DB 61 EILGPVVQFLGVYATPPLGARRFQPPAPASPGVGRNATLLPACPNLHGALPAILP 120
 QY 121 VFTDNLAAATVQNSDCLYLNLYVPTDGLTKKREATLNPDPDTRDPPGKFPV 180
 DB 121 VFTDNLAAATVQNSDCLYLNLYVPTDGLTKKREATLNPDPDTRDPPGKFPV 180
 QY 181 LFLHGGSYNEGTMNFDGSLAAYGNVIVATLNYRLVGLSTGDAAGNYGLDQIQ 240
 DB 181 LFLHGGSYNEGTMNFDGSLAAYGNVIVATLNYRLVGLSTGDAAGNYGLDQIQ 240
 QY 241 ALRWLSANIHFPGDPERITIFGSGAGASCVNLLILSHSEGLFQKAIAGSGTAISMSV 300
 DB 241 ALRWLSANIHFPGDPERITIFGSGAGASCVNLLILSHSEGLFQKAIAGSGTAISMSV 300
 QY 301 NTQPLKYTHLLAAKVCDBEDSAEVECLRRKPSRELVDQVQARYHIAFGPVVDG 360
 DB 301 NTQPLKYTHLLAAKVCDBEDSAEVECLRRKPSRELVDQVQARYHIAFGPVVDG 360
 QY 361 PDDPEILMQQGEFLNYDMLIGNVQGEGLKFVEDSAESDGSASAFDFTVNFVDNLYG 420
 DB 361 PDDPEILMQQGEFLNYDMLIGNVQGEGLKFVEDSAESDGSASAFDFTVNFVDNLYG 420
 QY 421 PGKQVLRBTIKFMTYTDWADRDNGEMRRKTLALFTDHWAPAVATAKLHADYQSPVY 480
 DB 421 PGKQVLRBTIKFMTYTDWADRDNGEMRRKTLALFTDHWAPAVATAKLHADYQSPVY 480

QY 481 YTFYHHCQAEGRPEWADAAGHDELPPYVGVPMVGATDLFPCNFSKNDVMSAVVMTYWTN 540
 DB 481 YTFYHHCQAEGRPEWADAAGHDELPPYVGVPMVGATDLFPCNFSKNDVMSAVVMTYWTN 540
 QY 541 FAKTGDPNQVPQDTKFTHTKPNRFEVWWSKFNKSKQYLIHGLKPRVRNRYANKVAF 600
 DB 541 FAKTGDPNQVPQDTKFTHTKPNRFEVWWSKFNKSKQYLIHGLKPRVRNRYANKVAF 600
 QY 601 WLELVPHLNLHTLFTTTTLRPPYATRWPPRPAGAPGTRRRPPATLPEPEPEPGPR 660
 DB 601 WLELVPHLNLHTLFTTTTLRPPYATRWPPRPAGAPGTRRRPPATLPEPEPEPGPR 660
 QY 661 AYDRPGDSRDYSTELSVTVAVGASLLFLNLTAALYYKDRQELRCRLSPGSGS 720
 DB 661 AYDRPGDSRDYSTELSVTVAVGASLLFLNLTAALYYKDRQELRCRLSPGSGS 720
 QY 721 GVPGGPPLLPAAGRELPEBELVSLQKRGGVGADPAEALRPACPDYTLALRAPDDV 780
 DB 721 GVPGGPPLLPAAGRELPEBELVSLQKRGGVGADPAEALRPACPDYTLALRAPDDV 780
 QY 781 PLLAPGALTLLPSGLGPPPPPPPSLHPFG 810
 DB 776 -----LSSLGPDQRP-----HPWG 791
 RESULT 4
 US-09-934-323-6
 ; Sequence 6, Application US/09934323
 ; Patent No. US20020150910A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Rory A. J.
 ; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
 ; FILE OF INVENTION: FAMILY MEMBER AND USES THEREOF
 ; FILE REFERENCE: 10448-081001
 ; CURRENT APPLICATION NUMBER: US/09/934,323
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: US 60/226,774
 ; PRIOR FILING DATE: 2000-08-21
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 550
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-934-323-6
 Query Match 66.2%; Score 2986; DB 10; Length 550;
 Best Local Similarity 100.0%; Pred. No. 1.8e-208;
 Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 286 KATAQSGTAISSNSVNYQPLKYTRLLAAKVCDBEDSAEVECLRRKPSRELVDQVQPA 345
 DB 1 KATAQSGTAISSNSVNYQPLKYTRLLAAKVCDBEDSAEVECLRRKPSRELVDQVQPA 60
 QY 346 RYHIAFGPVVDGVDPPDPEILMQQGEFLNYDMLIGNVQGEGLKFVEDSAESDGSASA 405
 DB 61 RYHIAFGPVVDGVDPPDPEILMQQGEFLNYDMLIGNVQGEGLKFVEDSAESDGSASA 120
 QY 406 FDTVSNFVDNLYGYEGKDVLRBTIKFMTYTDWADRDNGEMRRKTLALFTDHWAPAV 465
 DB 121 FDTVSNFVDNLYGYEGKDVLRBTIKFMTYTDWADRDNGEMRRKTLALFTDHWAPAV 180
 QY 466 ATAKLHADYQSPVYFTFYHHCQAEGRPEWADAAGHDELPPYVGVPMVGATDLFPCNFSK 525
 DB 181 ATAKLHADYQSPVYFTFYHHCQAEGRPEWADAAGHDELPPYVGVPMVGATDLFPCNFSK 240
 QY 526 NDVMSAVVMTYWTNFAKTGDPNQPQDTKFTHTKPNRFEVWWSKFNKSKQYLIHGL 585
 DB 241 NDVMSAVVMTYWTNFAKTGDPNQPQDTKFTHTKPNRFEVWWSKFNKSKQYLIHGL 300
 QY 586 KPRVRNRYANKVAFWLELVPHLNLHTLFTTTTLRPPYATRWPPRPAGAPGTRRRPP 645
 DB 301 KPRVRNRYANKVAFWLELVPHLNLHTLFTTTTLRPPYATRWPPRPAGAPGTRRRPP 360

QY 646 PATLPPEPPEPGRAYDRPGRSRYSTELSVTVAVAGSLLFLNLAFAALYYKDRRQ 705
Db 361 PATLPPEPPEPGRAYDRPGRSRYSTELSVTVAVAGSLLFLNLAFAALYYKDRRQ 420
QY 706 ELRCRLSPGGSGVPGGGPLPAAGRELPEBELVSLQKRGSGVADPAEALRPAC 765
Db 421 ELRCRLSPGGSGVPGGGPLPAAGRELPEBELVSLQKRGSGVADPAEALRPAC 480
QY 766 PPDYTLALRRADDVLLAPGALTLLPSGLPPPPPPPSLHPGFPFPPPTATSHNT 825
Db 481 PPDYTLALRRADDVLLAPGALTLLPSGLPPPPPPPSLHPGFPFPPPTATSHNT 540
QY 826 LPHPHSTTRV 835
Db 541 LPHPHSTTRV 550

RESULT 5
US-09-875-353-5
; Sequence 5, Application US/09875353
; Patent No. US20020168713A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 46960, A NOVEL HUMAN NEUROLOGIN FAMILY
; FILE REFERENCE: 10448-058001
; CURRENT APPLICATION NUMBER: US/09/875,353
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,949
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 848
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-875-353-5

Query Match
Best Local Similarity 60.9%; Score 2746; DB 10; Length 848;
Matches 538; Conservative 101; Mismatches 138; Indels 104; Gaps 18;

QY 1 MWLLALCLVGLAGARGGGGPGGAPGGGLGSLGEERFPVNTAYGRVGRRLN 60
Db 26 LWFLSLVL--RSTQ-----APA-----PTVNTHFGKLGARVELPS 60
QY 61 ELTGVVQFLGVYATPPLGARRFOPPEAPASWPGVRNATLBPACPNLHGALPAIMP 120
Db 61 ELTGVVQFLGVYATPPLGARRFOPPEAPASWPGVRNATLBPACPNLHGALPAIMP 120
QY 121 VFTNLEAAATYVQNSDECLYNLYPTED-----GPLTKRD 160
Db 121 VFTNLEAAATYVQNSDECLYNLYPTED-----GPLTKRD 160
QY 161 EATLN---PPDTIDPCKKPMFLHGGSYMEGTGMFGSVLAAGNVIVATLNRLG 217
Db 161 EATLN---PPDTIDPCKKPMFLHGGSYMEGTGMFGSVLAAGNVIVATLNRLG 217
QY 218 VLGLSTGDAQAKNGYLLDQIALRWLSENIAHFGGDPERITIFGSGAGASCNNLLLS 277
Db 241 VLGLSTGDAQAKNGYLLDQIALRWLSENIAHFGGDPERITIFGSGAGASCNNLLLS 300
QY 278 HHSEGLFQKATQSTALSSWSVNYQPKYTRLLAAKVGCDREDSABVCLRKPSREL 337
Db 301 HHSEGLFQKATQSTALSSWSVNYQPKYTRLLAAKVGCDREDSABVCLRKPSREL 360
QY 338 VQDQVQARYHAFQPVVDGWDVDPPEILMQOGEFLNYDMLGVNGEGIKFVEDSAES 397
Db 361 VQDQVQARYHAFQPVVDGWDVDPPEILMQOGEFLNYDMLGVNGEGIKFVEDSAES 420
QY 398 EDGVSASAFDTVSNFVNDLYGYPEGKDTLRETIKFMYTDWADRDNGEMRRTLLALFTD 457
Db 457 EDGVSASAFDTVSNFVNDLYGYPEGKDTLRETIKFMYTDWADRDNGEMRRTLLALFTD 457

Db 421 EDGVSAGTDFDYSVSNFVNDLYGYPEGKDTLRETIKFMYTDWADRDNGEMRRTLLALFTD 480
QY 458 HQWAPAVATAKLHADYQSPVYFTFYHCOASGRPEWADAAGDELPHYVGVPMYGATD 517
Db 481 HQWAPAVATAKLHADYQSPVYFTFYHCOASGRPEWADAAGDELPHYVGVPMYGATD 540
QY 518 LFCNFSKNDVMSLVAVMTYTNFAKTGDDNQVPQDTKFIHTKPNRFEVYVWSKFNSE 577
Db 541 LFCNFSKNDVMSLVAVMTYTNFAKTGDDNQVPQDTKFIHTKPNRFEVYVWSKFNSE 600
QY 578 KOYLHIGLKPRVDNTRANKVAFWLELVHNLHTELF---TTTTLPP---YATRW 630
Db 601 KOYLHIGLKPRVDNTRANKVAFWLELVHNLHTELF---TTTTLPP---YATRW 630
QY 631 PRPPAGAPGTRRPPPPATLPPEPEPPGPRAYDRFFGDS-----RDYSTELESTV 680
Db 660 PRPPAGAPGTRRPPPPATLPPEPEPPGPRAYDRFFGDS-----RDYSTELESTV 712
QY 681 AVGASLLFLNLAFAALYYKRCRBLRCLRCLRCLRCLRCLRCLRCLRCLRCLRCLRCL 740
Db 713 AVGASLLFLNLAFAALYYKRCRBLRCLRCLRCLRCLRCLRCLRCLRCLRCLRCLRCL 761
QY 741 ELVSLQKRGSGV-----GADPAEALRPACPPDYTLALRRAPDDVLLAPGALTLLPSGL 795
Db 762 ELAALQL---GPTHHECEAGPPHDTLRLTALPDYTLILRSPPDIPLMTPTNITMIPNSL 818
QY 796 GPPPPPPPSLHPGFPFPPPTATSHNT-LPHPHSTTRV 835
Db 819 GPPPPPPPSLHPGFPFPPPTATSHNT-LPHPHSTTRV 848

RESULT 6
US-09-978-295A-375
; Sequence 375, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249

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68	PRIOR FILING DATE: 1998-05-13

; PRIOR FILING DATE: 1998-05-15
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 50.6%; Score 2731; DB 10; Length 816;
 Best Local Similarity 64.2%; Pred. No. 1e-189;
 Matches 527; Conservative 97; Mismatches 147; Indels 50; Gaps 15;

QY	38	ERFPVNTAYGRVGRVRELNNELGPVQVGLVGYATPPLGARRFOPPEAPASWPCVR	97
DB	23	QAQYVWNTYKIRGLRTPLENEILGPVEQVGLVGYASPTGERFQPPPPSWTIGIR	82
QY	98	NATTLPPACPNL-HGALPAIMLVWFTDNLEAAATVYQNSEDCYLNLYVPTDGLPT	156
DB	83	NTTQFAVCPCHLDRSLHDMPLWFTANLDTLMTYVQDQNECDCLYLNIVPTDGANT	142
QY	157	KKG-DEATINP--PTDIEDP-GKKPVMLFEGGSYMEGTGNTGDSVLAAYGNVIVATL	212
DB	143	KKNADITISNDRGEDHIDQNSKPKVMVYIHGGSYMEGTGNTGDSVLAAYGNVIVIT	202
QY	213	NYRLVGLSTGDOAAKNGYGLLDQIQALRWLSENIAHFGDGPDRITIFGSGAGASCVN	272
DB	203	NYRLGILGLSTGDOAAKNGYGLLDQIQALRWLSENIAHFGDGPDRITIFGSGAGASCVS	262
QY	273	LLILSHHSEGLFOKAIASGTASVSNVYQPLKTRILLAAKVGCDREDSABAVECLRRK	332
DB	263	LTLSHYSEGFLQKAIOSGTALSSWAVYQPKYTRILADKVCNMLDITDMVECLRNK	322
QY	333	PSREIVDDQVOPARYHIAFGVPVGDVVDPPDPEILMQGGEFLNYDMLIGVNOGSLKFEV	392
DB	323	NYKELIQTITPATVHIAFGVIGDGVIPDDPQILMEGGEFLNYDMLIGVNOGSLKFEVD	382
QY	393	DSASEDGVASADFTVSNFVNLGYPEGKVLRETIFKMYTDWADRNGEMRRKTL	452
DB	383	GIVNEDGVTPNDFSVSNFVNLGYPEGKVLRETIFKMYTDWADRNGEMRRKTLV	442
QY	453	ALFTDQWVAPAVATAKLHAYQSPVYTYFHHQCAEGRPEWADAAGDELPIVFGVPM	512
DB	443	ALFTDQWVAPAVA-ADLHAYQSPVYTYFHHQCAEGRPEWADAAGDELPIVFGVPM	501
QY	513	VGATDLFCNFSKNDVMSAVVMTYWTNFAKTGDPNQPVPQDTKFIHTKPNRPEEVVWSK	572
DB	502	IGTPELFCNFSKNDVMSAVVMTYWTNFAKTGDPNQPVPQDTKFIHTKPNRPEEVVWSK	561
QY	573	PNSEKQVHLHGLKPRVDNVRANKYAFWELVPHLNLHTELF---TTTTRLP-----	623
DB	562	YNPKQQLYHLHGLKPRVDNVRANKYAFWELVPHLNLHTELF---TTTTRLP-----	620
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DB	678	TVAVGASLLFLNLAALYKRRDRRELRCRLSPGGSGSGVPGGGLPAAAGRELPP	725
QY	739	EEELVSLQKLR---GGVGADPAEARPACPDYTLALRRAPDDYVPLAPGALTLLPSG	794
DB	726	NEETMSLQKLEHDEHCELSQADHTLRLTCPDYTLRLRRSPDDIPLMTPTNTIMPNT	785
QY	795	LGPPPPPPPSLHPFGFPFPPPPPTATSHNNLPLPHPHSTTRV	835

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 ; Sequence 375, Application US/09978697
 ; Patent No. US20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gottlieb, Mary E.
 ; APPLICANT: Goddard, Audrey
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 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
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 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tamas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C27
 ; CURRENT APPLICATION NUMBER: US/09/978,697
 ; PRIOR FILING DATE: 2001-10-16
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Qy	38	ERFPVNTATGVRVGRVRELNNEILGVPVQVPTLGVPIATPPLGARFPQPEAPASWPGVVR	97
Db	23	QAYVPPVNTATGVRVGRVRELNNEILGVPVQVPTLGVPIATPPLGARFPQPEAPASWPGVVR	82
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RESULT 8

US-09-978-192A-375
 ; Sequence 375, Application US/09978192A
 ; Patent No. US20020177553A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Destrochers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Fingaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
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 ; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
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 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630P1C9
 CURRENT APPLICATION NUMBER: US/09/978,192A
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 PRIOR FILING DATE: 1997-10-17
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 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PlC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
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PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
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PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
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PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558

Db 263 LLTSLHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRI LADKVGCNMLD TTD MVECLRNK 322

Db 263 LLTSLHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRI LADKVGCNMLD TTD MVECLRNK 322

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; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 375
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-375

Query Match      60.6%; Score 2731; DB 11; Length 816;
Best Local Similarity 64.2%; Pred. No. 1e-189;
Matches 527; Conservative 97; Mismatches 147; Indels 50; Gaps 15;

Qy 38 EERFPVNTAYGVRGVRRELNEILGPVVQFLGVYATPPLCARFQPPPEAPASWPGVR 97
Db 23 QAGYFVNTNYGKIRGLRPLNEILGPVEQVLGVYASPTTGERRFQPPPEPSSWTGIR 82
Qy 98 NATLPPACPQNL-HGALPAIMLPVWFTONLEAAATYVQNSQEDCLYLNLYPTEDGFLT 156
Db 83 NTTQFAAVCPQHLDERSLLHDLPIWFTANLDTLMTYVQDQEDCLYLNLYPTEDGANT 142
Qy 157 KKR-DEATLNP--PDTDIRDP-GKPEVMLFLHGGSYMEGTGMFGSVLAAYGNVIVATL 212
Db 143 KKNADITNSDRGEDDEIDHONSKKPVVYIHGGSYMEGTGMFGSVLAAYGNVIVITI 202
Qy 213 NYRLGVLGFLSTGDAQAKNGYGLLDQIQALRWLSNIAHFHFGDPERITIFSGAGASCYN 272
Db 203 NYRLGILGFLSTGDAQAKNGYGLLDQIQALRWTEENVGAFGDPKRVITIFSGAGASCVS 262
Qy 157 KKR-DEATLNP--PDTDIRDP-GKPEVMLFLHGGSYMEGTGMFGSVLAAYGNVIVATL 212
Db 143 KKNADITNSDRGEDDEIDHONSKKPVVYIHGGSYMEGTGMFGSVLAAYGNVIVITI 202
Qy 213 NYRLGVLGFLSTGDAQAKNGYGLLDQIQALRWLSNIAHFHFGDPERITIFSGAGASCYN 272
Db 203 NYRLGILGFLSTGDAQAKNGYGLLDQIQALRWTEENVGAFGDPKRVITIFSGAGASCVS 262
Qy 273 LLTSHSHSGLFQKATAQSGTAISSWSVNYQPKYTRLLAAKVGCDREDSAEVCLRRK 332
Db 263 LLTSHYSGLFQKATIQSGTALSSWAVNYQPAKYTRILADKVCNMLDITDMVECLRNK 322
Qy 333 PSRELVDQVQFARYHIAFGPVVDGVPDDPEILMQQGEFLNYDMLIGVNGQEGFLKFE 392
Db 323 NYKELIQQTITPATYHIAFGPVVDGVPDDPEILMQQGEFLNYDMLIGVNGQEGFLKFE 382
Qy 393 DSAESDGVSAFADFTVSNFVNDLYGYPEGKDVLRRTIKFMYTDWADNCGEMRKILL 452
Db 383 GIVDNEGVTNPDDFVSFNFDNLYGYPEGKDTLRRTIKFMYTDWADNCGEMRKILL 442

; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 375
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-375

Query Match      60.6%; Score 2731; DB 11; Length 816;
Best Local Similarity 64.2%; Pred. No. 1e-189;
Matches 527; Conservative 97; Mismatches 147; Indels 50; Gaps 15;

Qy 38 EERFPVNTAYGVRGVRRELNEILGPVVQFLGVYATPPLCARFQPPPEAPASWPGVR 97
Db 23 QAGYFVNTNYGKIRGLRPLNEILGPVEQVLGVYASPTTGERRFQPPPEPSSWTGIR 82
Qy 98 NATLPPACPQNL-HGALPAIMLPVWFTONLEAAATYVQNSQEDCLYLNLYPTEDGFLT 156
Db 83 NTTQFAAVCPQHLDERSLLHDLPIWFTANLDTLMTYVQDQEDCLYLNLYPTEDGANT 142
Qy 157 KKR-DEATLNP--PDTDIRDP-GKPEVMLFLHGGSYMEGTGMFGSVLAAYGNVIVATL 212
Db 143 KKNADITNSDRGEDDEIDHONSKKPVVYIHGGSYMEGTGMFGSVLAAYGNVIVITI 202
Qy 213 NYRLGVLGFLSTGDAQAKNGYGLLDQIQALRWLSNIAHFHFGDPERITIFSGAGASCYN 272
Db 203 NYRLGILGFLSTGDAQAKNGYGLLDQIQALRWTEENVGAFGDPKRVITIFSGAGASCVS 262
Qy 273 LLTSHSHSGLFQKATAQSGTAISSWSVNYQPKYTRLLAAKVGCDREDSAEVCLRRK 332
Db 263 LLTSHYSGLFQKATIQSGTALSSWAVNYQPAKYTRILADKVCNMLDITDMVECLRNK 322
Qy 333 PSRELVDQVQFARYHIAFGPVVDGVPDDPEILMQQGEFLNYDMLIGVNGQEGFLKFE 392
Db 323 NYKELIQQTITPATYHIAFGPVVDGVPDDPEILMQQGEFLNYDMLIGVNGQEGFLKFE 382
Qy 393 DSAESDGVSAFADFTVSNFVNDLYGYPEGKDVLRRTIKFMYTDWADNCGEMRKILL 452
Db 383 GIVDNEGVTNPDDFVSFNFDNLYGYPEGKDTLRRTIKFMYTDWADNCGEMRKILL 442

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RESULT 12

US-09-978-585A-375

; Sequence 375, Application US/09978585A

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QY 453 ALFTDHOWAPAVATAKLHADYOSPVYFTFYHHCQAEGRPEWADAAGDELPHYVGVPM 512
; PRIOR FILING DATE: 1997-11-13
Db 443 ALFTDHOWAPAVA-ADLHAQYGSPTFYAFYHHCQSEMKSADSAHGEVPHYVGVPM 501
; PRIOR FILING DATE: 1997-11-21
QY 513 VGATDLPFCNFSKNDVMSLVAVNTYTNFAKTGDPNQPVQDTKFTHTKXNRFEEVYVWSK 572
; PRIOR FILING DATE: 1998-03-10
Db 502 IGTTELFCNFSKNDVMSLVAVNTYTNFAKTGDPNQPVQDTKFTHTKXNRFEEVYVWSK 561
; PRIOR FILING DATE: 1998-03-11
QY 573 FNSKEQYLIHLGKPRVDNRANKVAFWLELVPHLNLHTELF---TTTTLPL----- 623
; PRIOR FILING DATE: 1998-03-11
Db 562 YNFDQYLIHLGKPRVDNRANKVAFWLELVPHLNLHTELF---TTTTLPL----- 620
; PRIOR FILING DATE: 1998-03-11
QY 624 -PYATRRPPPPAGA-PGTRRRPPPPATLPEPEPEP---GPRAYDRFPQDSRDSYSTELSV 678
; PRIOR FILING DATE: 1998-03-12
Db 621 FPYGTR---RSPAKIWPTTKRPAITPANPNPKSKDPKGTGPDTTVLITKDYSTELSV 677
; PRIOR FILING DATE: 1998-03-13
QY 679 TVAVGASLLFLNLAAALYKEDRQELRCRLSPGSGSGVPGGGLLPAAGRELP 738
; PRIOR FILING DATE: 1998-03-20
Db 678 TVAVGASLLFLNLAAALYKEDRQELRCRLSPGSGSGVPGGGLLPAAGRELP 725
; PRIOR FILING DATE: 1998-03-20
QY 739 EELVSLQKLR-----GGVGADPAEALRPACPPDYTLALRRAPDDVPLIAPGALTLLPSG 794
; PRIOR FILING DATE: 1998-03-20
Db 726 NEEIMSLQKLEHDECSLQAHDTLRLTCLPDYTLRLRRSPDDIPLMTPTITWINT 785
; PRIOR FILING DATE: 1998-03-20
QY 795 LGPPPPPPPSLHPPGFPFPPPPPTATSHNNTLPHPHSTTRV 835
; PRIOR FILING DATE: 1998-03-25
Db 786 LTMQGP-----LHTFNTF-----SGQONSTNLPHGHSTTRV 816
; PRIOR FILING DATE: 1998-03-25

RESULT 13
US-09-978-191A-375
; Sequence 375, Application US/09978191A
; Publication No. US2003050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bosstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Luo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918595
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03

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RESULT 14

US-09-978-403A-375
Sequence 375, Application US/09978403A
Publication No. US2003050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/518585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495

APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC25
 CURRENT APPLICATION NUMBER: US/09/978,564A
 CURRENT FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
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 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 17:13:07 ; Search time 4890.86 Seconds
(without alignments)
12463.166 Million cell updates/sec

Title: US-09-934-323-3

Perfect score: 2508

Sequence: 1 atgtggctctggcgtgtg.....actccaccactgggtatag 2508

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hctc:*
9: gb_est1:*
10: gb_est2:*
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16: em_estom:*
17: em_gss_hum:*
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19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	991.8	39.5	3853	11 AK039018	AK039018 Mus muscu
2	740	29.5	1884	11 BC028738	BC028738 Homo sapi
3	733.6	29.3	1157	12 BM477185	BM477185 AGENCOURT
4	699.8	27.9	790	14 CA324321	CA324321 UI-M-FY0-

5	682.8	27.2	981	13	BU542698	AGENCOURT
6	674.6	26.9	919	13	BQ891968	AGENCOURT
7	667.2	26.6	735	10	BF058856	7k35609.x
8	661.8	26.4	879	13	BQ947939	AGENCOURT
9	656.4	26.2	708	14	CD349431	UI-M-FY0-
10	652.6	26.0	739	13	BQ769293	UI-M-FY0-
11	645.8	25.7	755	14	CD348520	UI-M-FY0-
12	643.4	25.7	1155	13	BQ278029	AGENCOURT
13	636.8	25.4	784	14	CD526398	UI-M-FY0-
14	636.6	25.4	807	14	CD348683	UI-M-FY0-
15	629.4	25.1	729	13	BQ771190	UI-M-FY0-
16	628.4	25.1	795	14	CA316129	UI-M-FY0-
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18	626.2	25.0	1066	13	BQ920779	AGENCOURT
19	621.2	24.8	804	14	CD355788	UI-M-FY0-
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22	618.2	24.6	770	12	BM944282	UI-M-EHOP
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26	613.4	24.5	780	14	CA316667	UI-M-FW0-
27	606.2	24.2	692	10	BE952199	UI-M-CD0-
28	602.8	24.0	727	14	CB526164	UI-M-FY0-
29	597.8	23.8	689	13	BU708515	UI-M-FY0-
30	595.2	23.3	735	14	CB249514	UI-M-EXO-
31	593.6	22.9	679	14	CB248107	UI-M-FY0-
32	593.2	22.9	733	14	CA316458	UI-M-FW0-
33	567.2	22.6	714	12	BM963021	UI-M-EQ0-
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35	549.6	21.9	680	14	CD355677	UI-M-FY0-
36	549	21.9	709	12	BM951227	UI-M-EH0-
37	546	21.8	788	12	BI687443	603315171
38	545.6	21.8	699	14	CA324959	UI-M-FY0-
39	537.2	21.4	647	14	CB524511	UI-M-FY0-
40	530.8	21.2	766	14	CA749282	AI337820 qt329e04.x
41	526	21.0	528	9	AI337820	qt329e04.x
42	524.8	20.9	627	13	BQ769413	UI-M-FY0-
43	524.6	20.9	612	13	BU057485	UI-M-FY0-
44	510	20.3	658	13	BQ443270	UI-M-EV0-
45	508	20.3	580	9	AW291374	UI-H-BI2-

ALIGNMENTS

RESULT 1
AK039018
LOCUS
DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length
enriched library, clone:A230085M13 product:NEUROLIGIN 3 ISOFORM
HNL3 homolog [Homo sapiens], full insert sequence.
ACCESSION AK039018
VERSION AK039018.1 GI:26332978
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, N., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, N., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159

QY 483 -----GGGACGCTCAATCCGCCAGACACAGATATCCGTGACCCCTGGGAAAGACCTGTGCA 538
Db TAGCGGATAATGACGGGATGAAGATGAAGACATCCGAGACAGTGTGCTAAACCTGTCA 825
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QY 599 TCCTGGCTGCTATGGCAACGCTCATTTGATAGCAGCTCAACTACCGTCTTTGGGGTCTCG 658
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Db 1846 CTTCAACTTCTCCAGAAATGATGTTATGTCTAGTGTGCTCATGACCTATTGGACCA 1905
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QY 1961 AGCCGAGCCCGGCCCAAGGGCTATGA-----CCGTTCCCGGGGACTCAGGG 2011
Db CCGCTGGGTCTGGAATGGGACCAAGATGCGGGGCCACTCTCTGGTTGAGAACCTCGAG 2325
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QY 2072 TCCTGGCCTTTGCTGCCCTCTTACTACAAAGGGGACCGCGCAGAGCTGCGGTGACGGC 2131
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QY 2252 GTGGCTGCGGGGAGACCTCGCCGAGGCTGTGCGCCCTGCTGCGCGCCGACTACACCC 2311
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Db TTCTTAATTCCTG 2673

RESULT 2

BC028738
LOCUS 1884 bp mRNA linear HTC 01-MAY-2002
DEFINITION Homo sapiens, Similar to neurologin 3, clone IMAGE:526328, mRNA.
ACCESSION BC028738
VERSION BC028738.1 GI:20380993
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1884)
AUTHORS Strausberg, R.


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RESULT 3
LOCUS BM477185 1157 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_64848.4 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5553956
5', mRNA sequence.
ACCESSION BM477185
VERSION BM477185.1 GI:18526227
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1157)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM12271 row: 1 column: 21
High quality sequence start: 2
High quality sequence stop: 606.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cdones="IMAGE:5553956"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_85"
/notes="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 215 a 420 c 322 g 198 t 2 others
ORIGIN
Query Match 29.3%; Score 733.6; DB 12; Length 1157;
Best Local Similarity 93.6%; Pred. No. 2.5e-126;
Matches 876; Conservative 0; Mismatches 44; Indels 16; Gaps 10;
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Db 13 GCTTCGGGAGACCATCAAGTTATGTATGATACAGACTGGCGGACCGGACCAATGGCGAAAT 72
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Qy 1758 GCACGCGTGGTGTGACAACTACCGCGCCAAACAAAGTGGCTTCTGGCTGGAGCTCGTGCC 1817
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Qy 2053 TCCCTCTCTC-TTCCTCAACATCCTGGCC---TTTCTGCTCCCTCTACTACAGCGGG--AC 2106
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Qy 2107 CCGCGCGGAGGAGT-GCGGTGCGAGCGGCTTAGCCACACTG--CGGCTCAGGCTCTGG- 2162
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Qy 2163 -CGTCCCTGGTGGGGCCCCCTGCTCCCGCGCGGG 2197
Db 913 CCGGCGCTGGGGGGGGCCCCCTGCTCCCGCGCGG 948
RESULT 4
CA324321 790 bp mRNA linear EST 26-NOV-2002
LOCUS UI-M-FY0-ccp-g-21-0-UI_r1 NIH_BMAP_FY0 Mus musculus cDNA clone
DEFINITION IMAGE: 6822670 5', mRNA sequence.
ACCESSION CA324321
VERSION CA324321.1 GI:24542419
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 790)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 21-63, >GC_rich#low_complexity (matched complement)
Seq primer: PYX-5.
Location/Qualifiers
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FEATURES
source

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found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1CM2561 row: f column: 18
High quality sequence start: 14
High quality sequence stop: 486.

FEATURES

Location/Qualifiers
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/issue_type="neuroblastoma, cell line"
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/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 187 a 290 c 275 g 167 t
ORIGIN

Query Match 26.9%; Score 674.6; DB 13; Length 919;
Best Local Similarity 98.0%; Pred. No. 2.2e-115; Indels 0; Gaps 0;
Matches 683; Conservative 0; Mismatches 14;

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DB 61 GAGGACTGCTGTACCTCACTTACGTGCGCCACGAGGACGCTCGCTCAGAAAAA 120
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DB 181 GTGATGTGTTTCCATATGCGGCTCTTATGAGGAGGACCGGAAACATGTTTGGTGGC 240
QY 595 TCAGTCTGCTGCTATGCGCAAGTCAATGAGTACGCTCAACTACCGTCTTGGGGTG 654
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QY 1970 CCGG 1973
DB 853 CCGG 856

RESULT 6
BO891968
LOCUS BO891968 919 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8695255 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6377489
5', mRNA sequence.
ACCESSION BO891968
VERSION BO891968.1 GI:22283982
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 919)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 171 a 315 c 240 g 153 t

ORIGIN

Query Match 26.4%; Score 661.8; DB 13; Length 879;
Best Local Similarity 89.3%; Pred. No. 5.1e-113; Indels 4; Gaps 4;
Matches 758; Conservative 0; Mismatches 87; Indels 4; Gaps 4;

QY 1166 AGTTCGTGGAGACTCTGCAGAGCGAGGACGGTGTGTCTGCCAGCGCCTTTGACTTCA 1225
DB 12 AGTTCGTGGAGACTCTGCAGAGCGAGGACGGTGTGTCTGCCAGCGCCTTTGACTTCA 71
QY 1226 CTGTCTCCAACTTTGTGACAACTGTATGCTACCCGGAAGGCAAGATGTGCTTCGGG 1285
DB 72 CTGTCTCC-AC TTTGTGACAACTGTATGCTACCCGGAAGGCAAGATGTGCTTCGGG 130
QY 1286 AGACCATCAAGTTTATGACACAGACTGGGCGGACCGGCAATGGCGAAATGGCGCGCA 1345
DB 131 AGACCATCAAGTTTATGACACAGACTGGGCGGACCGGCAATGGCGAAATGGCGCGCA 190
QY 1346 AAACCTCTCGCGCTTTTACTGACCAACCAATGGGTGGCAACAGCTGTGGCCACTGCCA 1405
DB 191 AAACCTCTCGCGCTTTTACTGACCAACCAATGGGTGGCAACAGCTGTGGCCACTGCCA 250
QY 1406 AGCTGACGCGGACTACCACTCTCCGCTACTTTTACACCTTCTACCACTGCGCCAGG 1465
DB 251 AGCTGACGCGGACTACCACTCTCCGCTACTTTTACACCTTCTACCACTGCGCCAGG 310
QY 1466 CGAGGGCGCGCTCAGTGGGACAGTGGGCGGACCGGGGATGAAGTGCCTTATCTTTTG 1525
DB 311 CGAGGGCGCGCTCAGTGGGACAGTGGGCGGACCGGGGATGAAGTGCCTTATCTTTTG 370
QY 1526 GGTGTCCTATGGTGGGTGCGACCGACCTTTCCTGCTGTAATCTTCCAGNATGACGTCA 1585
DB 371 GGTGTCCTATGGTGGGTGCGACCGACCTTTCCTGCTGTAATCTTCCAGNATGACGTCA 430
QY 1586 TGCTCAGTGCCGTGTGATGACCTACTGAGCAACTTCGCAAGACTGGGACCCCAACC 1645
DB 431 TGCTCAGTGCCGTGTGATGACCTACTGAGCAACTTCGCAAGACTGGGACCCCAACC 490
QY 1646 AGCCGGTCCGCGAGATACCAAGTTTATCCACACCAAGCCCAATGCTTGGAGAGTGG 1705
DB 491 AGCCGGTCCGCGAGATACCAAGTTTATCCACACCAAGCCCAATGCTTGGAGAGTGG 550
QY 1706 TGTGAGCAAAATTCACAGCAGGAGAGAGTATCTGCATAGGCTGAAGCCACGCG 1765
DB 551 TGTGAGCAAAATTCACAGCAGGAGAGAGTATCTGCATAGGCTGAAGCCACGCG 610
QY 1766 TCGTGACAACTACCGCGCCCAACAGGTGG-CTTTCTGGCTGGAGCTGTGCCCCCA-CCT 1823
DB 611 TCGTGACAACTACCGCGCCCAACAGGTGGCTTTCTGGCTGGAGCTGTGCCCCCACT 670
QY 1824 GCACAACTGACACGG-AGCTTTCACACACACAGCGGCTGTGCTTCTACGCCAGC 1882
DB 671 GCACAACTGACACGGAGCTTTCACACACACAGCGGCTGTGCTTCTACGCCAGC 730
QY 1883 GTGTGCGGCTGTGCTTCCCGCTGTGCGGCGCGGCGACACGCGGCGCGGCGCTGCGCA 1942
DB 731 AGCGCTGCGGCTGTGCTTCCCGCTGTGCGGCGCGGCGCGGCGCGGCGCGGCGG 790
QY 1943 CCTGCTCCCGAGCCCGAGCCCGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 2002
DB 791 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 850
QY 2003 ACTCAGGG 2011
DB 851 GCGCCAGG 859

RESULT 9
CD349431
LOCUS

DEFINITION

ACCESSION
CD349431
VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD349431 708 bp mRNA linear EST 29-MAY-2003
UI-M-F10-cfq-b-14-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone
IMAGE: 6854415 5', mRNA sequence.

CD349431.1 GI:31140946
EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 708)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousef1.html>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

The following repetitive elements were found in this cDNA

sequence: 16-58, >GC_richLow_complexity (matched complement)

Seq primer: pYX-5.

Location/Qualifiers

1..708

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE: 6854415"

/tissue_type="whole brain"

/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"

/db_host="PH108 (T1 phage resistant)"

/clone_lib="NIH BMAP_FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according

Bonafide, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is ACGGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

BASE COUNT 126 a 242 c 222 g 117 t

ORIGIN

Query Match 26.2%; Score 656.4; DB 14; Length 708;
Best Local Similarity 95.5%; Pred. No. 5e-112;
Matches 675; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 40 GCTCAACGGGGGGGGGGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 99
DB 1 GCTCAACGGGGGGGGGGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 60
QY 100 GGCAGCCTCGGAGAGAGCGCTTCCCGGTGGTGAACACACGCGCTACGGGAGTGGCGGT 159
DB 61 GGCAGCCTCGGAGAGAGCGCTTCCCGGTGGTGAACACACGCGCTACGGGAGTGGCGGT 120
QY 160 GTGCGGCGGAGCTCAACACGAGATCCTGGGCGCGCGCGCGCGCGCGCGCGCGCTTC 219

Db 661 CCCCCGTCTATTTTACACTTTTACCACTCCAGGAGAGGGCGGCGAGAGTGGG 720
QY 1487 CAGATCGCGGCGACGGGAGTGAACCTGCCTATGCTTCTTGGCGTCCCATGTGG 1540
Db 721 CAGACGACGACGCGGAGGACGAGTGCCTACGCTCTTGGTGGCCCCCATGGTG 774

RESULT 11
CD348520 755 bp mRNA linear EST 29-MAY-2003
LOCUS UI-M-FY0-cfo-g-15-0-UI_r1 NIH_BMAP_FY0 Mus musculus cDNA clone
DEFINITION IMAGE: 6853768 5', mRNA sequence.
ACCESSION CD348520
VERSION CD348520.1 GI:31140035
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 755)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: nih.gov
cDNA Library Preparation: Dr. Jim Lin, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.
Location/Qualifiers
1. 755
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6853768"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 156 a 213 c 214 g 170 t 2 others
ORIGIN

Query Match 25.7%; Score 645.8; DB 14; Length 755;
Best Local Similarity 90.9%; Pred. No. 4.7e-110;
Matches 686; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 508 GATATCCGTGACCTCGGAGAACGCTGTGATGCTGTTTCCATGCGGCTCCTACATG 567
Db 1 GATATCCGGACTCTGGGAGAAACCGGTGATGCTGTTTCTACACGGGCTCCTACATG 60
QY 568 GAGGGGACCGGAACATGTTTCGATGGCTAGTCTGCTGCTCCTATGCAACGTCATTGTA 627

Db 61 GAAGGCACCGGAACATGTTTACGGCTCAGTCTCGCTGCCCCATGCAATGTCATGTA 120
QY 628 GCACGCTCAACTACCGTCTTGGGGTGTCTCGTTTTCTCAGCACCGGAGCAGGCTGCA 687
Db 121 GTCACACTCACTACCGTCTTGGGGTGTCTCGTTTTCTCAGCACTGGTGACCGGCTGCA 180
QY 688 AAAGGCAACTATGGGCTCTGGACAGATCCAGGCGCTCGCTGGCTCAGTGAAGAACATC 747
Db 181 AAAGGCAACTATGGGCTCTGGACAGATCCAGGCGCTCGCTGGCTCAGTGAAGAACATC 240
QY 748 GCCCACTTTGGGGCGACCCCGAGCGTATCACCATCTTTGGTTCCGGGGCAGGGCCCTCC 807
Db 241 GCCCACTTTGGAGGTGACCCCTGAACGATCACTATCTTTGGGTCTGGTGACGGGCTCC 300
QY 808 TCGTCAACCTTTCTGATCTCTCCCACTCCAGAGGGCTGTTCCAGAAGGCCATCGCC 867
Db 301 TGTGTCACTCTGCTGATCTCTTCCCACTCCAGAGGACTGTTCCAGAAGGCCATTTGCT 360
QY 868 CAGAGTGGACCGCCATTTCCAGCTGGTCTGTCACTACCACTACCGCCCTCAAGTACACGGG 927
Db 361 CAAAGTGGTACTGCCATTTCCAGCTGGTCTGTCAACTACCACTACCGCCCTCAAGCACACGGG 420
QY 928 CTGCTGGCAGCCCAAGTGGGCTGTGACCGAGAGGACAGTGTGAAGCTGTGGAGTGTCTG 987
Db 421 CTGCTGGCGGCCAAAGTGGGCTGTGACCGAGAGACAGCACTGAAGCTGTGGAGTGTCTG 480
QY 988 CCGCGAAGCCCTCCCGGAGCTGGTGACAGAGAGCTGCGACCTGCGCTGACACATC 1047
Db 481 CCGCGAAGTCTTCCCGGAGCTAGTGACAGAGATGTACAGCTGCGCGCTACCCACTT 540
QY 1048 GCCTTTGGGCGGTGGTGGAGCGACCTGCTCCCGATGACCTGAGATCTCTCATGCAG 1107
Db 541 GCCTTTGGGCGGTGGTGGAGCGGACGTANTCCCTGATGACCGCGAGATCTCTCATGCA 600
QY 1108 CAGGAGAAATTCCTCACTACGATGCTCATCGCGCTCAACACCGGAGAGGCGCTCAAG 1167
Db 601 CAGGCGGAATTCCTCACTACGATGCTCATCGCGCTCAACACCGGAGAGGCTCTCAAG 660
QY 1168 TTCGTGGAGGACTCTGGAGAGCGGAGCGGTGTGTGTCGAGCGCTTTGACTTCACT 1227
Db 661 TTCGTGGAGGACTCTGGAGAGGAGTGAAGACGCTGTGCTGCCGCGCTTTGACTTCACT 720
QY 1228 GTCCTCAACTTTGTGCAACACTGTGATGGCTACCC 1262
Db 721 GTCCTCAACTTTGTGCAACACTTTGTACGGGTACCC 755

BQ278029 1155 bp mRNA linear EST 07-MAY-2002
AGENCOURT 7061669 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:5804959
5', mRNA sequence.
BQ278029
VERSION BQ278029.1 GI:20488237
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1155)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ruben Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

RESULT 12
BQ278029
LOCUS
DEFINITION
ACCESSION BQ278029
VERSION BQ278029.1 GI:20488237
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1155)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ruben Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

300 CACCTTCCCGCCGCTGCGCAGAACCTGACGGGGCGCTCCCGCCCATCATGCTGCC 359
 Db 121 CACCTTCCCGCCGCTGCGCAGAACCTGACGGGGCGCTCCCGCCCATCATGCTGCC 180
 Qy 360 TGTGTGTTTACCGAACAATGAGGCGCGCCCACTAGCTGAGAACAGAGGAGGA 419
 Db 181 TGTGTGTTTACCGAACAATGAGGCGCGCCCACTAGCTGAGAACAGAGGAGGA 240
 Qy 420 CTGCTCTACTCACTCTACCTGCTGCGCCACCGAGGAGCGTCCGCTCACAAAAACGTGA 479
 Db 241 CTGCTCTACTCACTCTACCTGCTGCGCCACCGAGGAGCGTCCGCTCACAAAAACGTGA 277
 Qy 480 CGAGGAGCGCTCAATCCGCGACACAGATATCCGTGACCCCTGGGAAGAGCCTGTGAT 539
 Db 278 -----GATATCCGGGACTCTGGGAGAAACCGGTCTAT 309
 Qy 540 GCTGTTTCTCCATGGGGCTCTACATGGAGGAGCGGGAACATGTTGATGGCTCACT 599
 Db 310 GCTGTTTCTACAGCGGGCTCTACATGGAGGAGCGGGAACATGTTGATGGCTCACT 369
 Qy 600 CTTGGCTGCTATGGCAACCTGATGAGCAGCGCTCAACTACCGTCTTGGGGTGTCTCG 659
 Db 370 CTTGGCTGCTATGGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 429
 Qy 660 TTTTCTCAGCAGCGGAGCAGCGCTGCAAAAGGCAATGAGGCTCTCTGGACAGATCCA 719
 Db 430 TTTTCTCAGCAGCGTGTGACGAGGCTGCAAAAGGCAATGAGGCTCTCTGGACAGATCCA 489
 Qy 720 GGCCTCTGCTGCTGATGAGTAAACATCGCCCACTTTGGGGGCGACCCGAGCGTATCAC 779
 Db 490 GGCCTCTGCTGCTGATGAGTAAACATCGCCCACTTTGGGGGCGACCCGAGCGTATCAC 549
 Qy 780 CATCTTTGTTCCGGGCGAGGGCTCTCTGCGTCAACTCTTCTGATCTCTCCACCATTC 839
 Db 550 TATCTTTGGGCTGTGTCAGCGGGCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 609
 Qy 840 AGAGGGCTTTCCAGAGGCGCATCGCCAGAGTGCACGCGGCAATTTCCAGCTGTCTGT 899
 Db 610 AGAGGAGCTTTCCAGAGGCGCATCGCCAGAGTGCACGCGGCAATTTCCAGCTGTCTGT 669
 Qy 900 CAATACAGCGCTCAAGTACACGCGGCTGCTGGCAGGCAAGGTGGGCTGTGACCGAGA 959
 Db 670 CAATACAGCGCTCANGTACACGCGGCTGCTGGCAGGCAAGGTGGGCTGTGACCGAGA 729
 Qy 960 GGACAGTGTGAGCTGTGAGTGTGTGCGCCGGAAGCCCTCCCGGAGCTGGTG 1014
 Db 730 AGACAGCACTGAAGCTGTGAGTGTGTGCGCCGGAAGCTCTCCCGGAGCTAGTG 784

RESULT 14
 LOCUS CD348683
 DEFINITION UI-M-FYO-cfs-c-19-0-UI.r1 NIH BMAP_FYO Mus musculus cDNA clone
 IMAGE: 6855212 5', mRNA sequence.
 ACCESSION CD348683
 VERSION CD348683.1 GI:31140198
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 807)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-t@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: pYX-5.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE: 6855212"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_FYO"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGAGCAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
 BASE COUNT 162 a 236 c 238 g 170 t 1 others
 ORIGIN

Query Match 25.4%; Score 636.6; DB 14; Length 807;
 Best Local Similarity 89.6%; Pred. No. 2.4e-108;
 Matches 706; Conservative 0; Mismatches 80; Indels 2; Gaps 2;
 Qy 753 CTTTGGGGGCGACCCGAGCGTATCACATCTTTGGTTCGGGGCAGGGGCTCTGGGT 812
 Db 1 CTTTGGAGGTGACCTGAACGCATCATATCTTTGGGTCTGGTGCAGGGGCTCTGTGT 60
 Qy 813 CAACCTCTGATCTCTCCACCATTCAGAGGGCTGTTCAGAGGCGCATCGCCAGAG 872
 Db 61 CACTTGTGATCTCTTCCACCACTCAGAGGACTGTTCAGAGAGCCATTTGCTCAAG 120
 Qy 873 TGGCAGCCGCAATTCAGCTGTGTCTCAACTACACGCGCTCAAGTACACGCGGTGCT 932
 Db 121 TGGTACTGCCATTTCCAGCTGTCTGTCAACTACACGCGCTCAAGTACACGCGGTGCT 180
 Qy 933 GGCAGCCAAAGTGGGCTGTGACGAGAGGACAGTGTGAGCTGTGAGTGTCTGCGCCG 992
 Db 181 GCGGCGCAAGTGGGCTGTGACCGAGAGACAGCACTGAAGCTGTGAGTGTCTGCGCCG 240
 Qy 993 GAAGCCCTCCCGGAGCTGTGGACAGGACGTGCAGCTTCGCGGCTACCCACATCGCCTT 1052
 Db 241 GAAGTCTTCCCGGAGCTGTGGACAGGATGTACAGCTTCGCGGCTACCCACATTCGCTT 300
 Qy 1053 TGGCCCGCTGTGTGATGCGACAGTGTCCCGATGACCTGAGATCTCTATGACGAGGG 1112
 Db 301 TGGCCCTGTGTGATGCGACAGCTGTAGTCCCTGATGACCCCGAGATCTCTATGCAACAGGG 360
 Qy 1113 AGAATTCCTCAACTACACATGCTCATCGCGCTCAACAGGAGAGGGCTCAAGTTCGT 1172
 Db 361 GGAATTCCTCAACTACACATGCTCATTTGTTGTCACACGAGAGGGTCTCAAGTTCGT 420
 Qy 1173 GGAGGACTCTGCAGAGAGCGAGCGGTGTGTCTGTCAGCGCTTTGACTTCACTGTCTC 1232
 Db 421 GGAGGACTCTGCAGAGAGTGCAGGACGGTGTGTCTGTCAGCGCTTTGACTTCACTGTCTC 480
 Qy 1233 CAATCTTGTGACAACTGCTGTATGCTACCCGAGAGGCAAGATGTGCTTCGGAGAGCAT 1292
 Db 481 CAATCTTGTGACAACTGCTGTATGCTACCGGAGGCAAGGAGGAGGAGCTGTCTTCAGAGAGCAT 540

QY 1293 CAAAGTTATGATACAGAGCTGGCGCCGACCGGACAAATGGCGAAATGGCGCGCAAAACCCCT 1352
 Db 541 CAAAGTTATGATACAGAGCTGGCGCCGACCGGACAAATGGCGAAATGGCGCGCAAAACCCCT 600
 QY 1353 GTGGGCGCTCTTACTGACACCAATGGGTGGGACCAAGCTGTGGCACTGCCAAGCTGCA 1412
 Db 601 GTGGGCGCTCTTACTGACACCAATGGGTGGGACCAAGCTGTGGCACTGCCAAGCTGCA 660
 QY 1413 CGCGGACTACAGCTGCCGCTGTCTTACTTACACCTTCTACCACTTCTACCACTGCGAGCGGAGG 1472
 Db 661 TGGCGACTACAGCTGCCGCTGTCTTACTTACACCTTCTACCACTTCTACCACTGCGAGCGGAGG 719
 QY 1473 CGCGGCTGAGTGGGAGAGTGGCGGACCGGAGTGAAGTCCCTAATGCTTTGGCGTGC 1532
 Db 720 CGCGGAGAGTGGGAGAGTGGCGGACCGGAGTGAAGTCCCTAATGCTTTGGTGTGCC 778
 QY 1533 CATGGTGG 1540
 Db 779 ATGGTGGG 786

RESULT 15
 BQ771190
 LOCUS
 DEFINITION
 UI-M-F10-byx-f-03-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone
 IMAGE:6400514 5', mRNA sequence.
 BQ771190
 BQ771190.1 GI:21979666
 EST.
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 REFERENCE
 1 (bases 1 to 729)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pyX-5.
 Location/Qualifiers
 1..729
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6400514"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_hosts="DRI0B (11 phage resistant)"
 /clone_lib="NIH_BMAP_F10"
 /note="Organ: Brain; Vector: pyX- Asc; Site 1: Ecor I;
 Site 2: Not I; The library was constructed according
 to the protocol of Benton and Davis, Molecular Cloning, 2nd ed.,
 Cold Spring Harbor, New York, 1988. The library was
 size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with Not I and then cloned
 directionally into pyX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CAGCCAGCAG. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
 Developing Mouse Nervous System, supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."
 BASE COUNT 149 a 205 c 206 g 168 t 1 others
 ORIGIN
 Query Match 25.1%; Score 629.4; DB 13; Length 729;
 Best Local Similarity 91.8%; Pred. No. 5.2e-107; Indels 0; Gaps 0;
 Matches 666; Conservative 62; Mismatches 62;
 QY 535 GTGATGCTGTTTCTCCATGCGCGCTCTACATGAGGAGGACCGGAAACATGTTTCGATGGC 594
 Db 1 GTCATGCTGTTTCTACACGCGGCTCTACATGAGGAGGACCGGAAACATGTTTCGATGGC 60
 QY 595 TCAGTCTGCTGCTATGAGCAACGTCATGTTAGCAGCAGCTCAACTACCGTCTTGGGTG 654
 Db 61 TCAGTCTGCTGCTATGAGCAATGTATCGTAGTCACACTCAACTACCGTCTTGGGTG 120
 QY 655 CTGGTCTTCTCAGCACCGGGGACCGAGCTGCAAAAGGCAACTATGGGCTCTCTGGACCG 714
 Db 121 CTGGTCTTCTCAGCACTGTGTGACCGAGCTGCAAAAGGCAACTATGGGCTCTCTGGACCG 180
 QY 715 ATCCAGCCCTGCGCTGCTCAGTGAACATCGCCCACTTTTGGGGGCGACCCCGAGCGT 774
 Db 181 ATCCAGCCCTGCGCTGCTCAGTGAACATTTGCCCACTTTTGGAGGTGACCCCTGAACGC 240
 QY 775 ATCACCATCTTTGGTTCGGGGGAGGGGCTCTCGGTCAACCTTCTGATCTCTCCAC 834
 Db 241 ATCACCATCTTTGGTTCGGGGGAGGGGCTCTCGGTCAACCTTCTGATCTCTCCAC 300
 QY 835 CATTACAGAGGCTGTTTCCAGAAAGGCGCATCGCCAGAGTGGCACCCGCAATTTCCAGCTGG 894
 Db 301 CACTCAGAGGACTGTTTCCAGAAAGGCGCATTTGCTCAAAGTGGTACTGCAATTTCCAGCTGG 360
 QY 895 TCTGTCAACTACAGCCGCTCAAGTACACCGGCTGCTGCGCAGCAGCTGGAGTGGGTGAC 954
 Db 361 TCTGTCAACTACAGCCGCTCAAGTACACCGGCTGCTGCGCAGCAGCTGGAGTGGGTGAC 420
 QY 955 CGAGAGCAGTGTCTGAAGCTGTGGAGTGTCTGCGCGGAGGCGCTCCCGGAGCTGGT 1014
 Db 421 CGAGAGCAGTGTCTGAAGCTGTGGAGTGTCTGCGCGGAGGCGCTCCCGGAGCTGGT 480
 QY 1015 GACAGAGCTGACAGCTGCGCGCTACACATCGCTTTGGGCGCGTGGTGGATGGCGAC 1074
 Db 481 GACAGAGTGTACAGCTGCGCGCTACACATTTGCTTTGGGCGCTGGTGGAGCGGCGAC 540
 QY 1075 GTGGTCCCGATGACCTGAGATCTCATGACGAGGAGAAATTCCTCAACTACGACATG 1134
 Db 541 GTANTCTCTGATGACCCCGAGATCTCATGACAGGAGGAAATTCCTCAACTACGACATG 600
 QY 1135 CTCATCGGCTCAACACGAGGAGGCGCTCAAGTTCGTGAGGAGCTCTGAGAGAGCGAG 1194
 Db 601 CTCATGCTGTCAACACGAGGAGGCGCTCAAGTTCGTGAGGAGCTCTGAGAGAGTGTGAG 660
 QY 1195 GACGCTGTGTGCGAGGCGCTTTGACTTCACTGTCTCCAACTTTGGGCAACCTGTAT 1254
 Db 661 GACGCTGTGTGCGAGCGCTTTGACTTCACTGTCTCCAACTTTGGGCAACCTGTAT 720
 QY 1255 GGCTACCC 1262
 Db 721 GGGTACCC 728

Search completed: February 19, 2004, 04:51:21
 Job time : 4894.86 secs

181	Db	GAGATCCTGGGCCCCGTCGTGCAGTTCCTTGGGCGTGCCTTACGCCACGCCGCCCTCGGGC	241
241	Qy	GCCGCGCGCTTCCAGCCGCTTGAGCGCGCCGCTCGTGGCCCGGCGTGCACGCGCCACC	300
241	Db	GCCGCGCGCTTCCAGCGCGCTTGAGCGCGCCGCTCGTGGCCCGGCGTGCACGCGCCACC	300
301	Qy	ACCTGCGGCGCGCTGCCCGGAGAACTGTGACGGGGCGCTGCCGCCCATCATGCTGCCT	360
301	Db	ACCTGCGGCGCGCTGCCCGGAGAACTGTGACGGGGCGCTGCCGCCCATCATGCTGCCT	360
361	Qy	GTGTGGTTACCGCAAACTTGGAGCGGCGCCACCTACGTGCAGAAACACAGGCGAGGAC	420
361	Db	GTGTGGTTACCGCAAACTTGGAGCGGCGCCACCTACGTGCAGAAACACAGGCGAGGAC	420
421	Qy	TGCCTGTACTCAACCTCTA	480
421	Db	TGCCTGTACTCAACCTCTA	480
481	Qy	GAGCGGCGCTCAATCCGCCAGACACAGATATCCGTGACCTCGTGGAGAGACGCTGTGATG	540
481	Db	GAGCGGCGCTCAATCCGCCAGACACAGATATCCGTGACCTCGTGGAGAGACGCTGTGATG	540
541	Qy	CTGTCTTCTCATTGCGGCTCCTACATGAGGGGACCGGAAACATGTTTGCATGGCTCAATC	600
541	Db	CTGTCTTCTCATTGCGGCTCCTACATGAGGGGACCGGAAACATGTTTGCATGGCTCAATC	600
601	Qy	CTGGCTGCTATGCAACGTCATTTGTAGCAGCGTCACTACCGTCTTGGGGTGCCTGGT	660
601	Db	CTGGCTGCTATGCAACGTCATTTGTAGCAGCGTCACTACCGTCTTGGGGTGCCTGGT	660
661	Qy	TTTCTCAGCACCGGGACCGAGCTGCAAAAGGCAACTATGGGCTCCTGGACAGATCCAG	720
661	Db	TTTCTCAGCACCGGGACCGAGCTGCAAAAGGCAACTATGGGCTCCTGGACAGATCCAG	720
721	Qy	GCCCTGCGCTGCTCAGTGAACAACTATGCGCCCACTTTGGGGGCGACCCGAGCGTATCAC	780
721	Db	GCCCTGCGCTGCTCAGTGAACAACTATGCGCCCACTTTGGGGGCGACCCGAGCGTATCAC	780
781	Qy	ATCTTTGGTTCGGGGCAGGGGCTCCTGGCTCAACCTTCTGATCTCTCCACCATTTCA	840
781	Db	ATCTTTGGTTCGGGGCAGGGGCTCCTGGCTCAACCTTCTGATCTCTCCACCATTTCA	840
841	Qy	GAAAGGCTGTTCCAGAGGCGCATCGCCAGAGTGGCACCGCCATTTCCAGTGTGCTGTC	900
841	Db	GAAAGGCTGTTCCAGAGGCGCATCGCCAGAGTGGCACCGCCATTTCCAGTGTGCTGTC	900
901	Qy	AACATACAGCCGCTCAAGTACACCGGCTGTGCGACGACAGTGGGCTGTGACGAGAG	960
901	Db	AACATACAGCCGCTCAAGTACACCGGCTGTGCGACGACAGTGGGCTGTGACGAGAG	960
961	Qy	GACAGTGTGAAGCTGTGGAGTGTCTGCGCCGGAAGCCCTCCCGGAGCTGGTGGACAG	1020
961	Db	GACAGTGTGAAGCTGTGGAGTGTCTGCGCCGGAAGCCCTCCCGGAGCTGGTGGACAG	1020
1021	Qy	GACGTGACGCTGCCCGCTACACATCGCTTTGGGCCGCTGGTGGATGGCGACGTGCTC	1080
1021	Db	GACGTGACGCTGCCCGCTACACATCGCTTTGGGCCGCTGGTGGATGGCGACGTGCTC	1080
1081	Qy	CCCGATGACCTTGAGATCCTCATGACGAGGAGAAATTCCTCAACTACGACATGCTCATC	1140
1081	Db	CCCGATGACCTTGAGATCCTCATGACGAGGAGAAATTCCTCAACTACGACATGCTCATC	1140
1141	Qy	GGCGTCAACAGGAGAGGGGCTCAAGTTCGTGAGGACTCTGACAGAGCGGAGCGGT	1200
1141	Db	GGCGTCAACAGGAGAGGGGCTCAAGTTCGTGAGGACTCTGACAGAGCGGAGCGGT	1200
1201	Qy	GTGTCTGCGAGGCTTTGACTTCACTGTCTCCAACTTTGGGACACCTGTATGGGTAC	1260
1201	Db	GTGTCTGCGAGGCTTTGACTTCACTGTCTCCAACTTTGGGACACCTGTATGGGTAC	1260
1261	Qy	CCGGAAGGCAAGGATGTGCTTCGGGAGACCACTAAGTTTATGTATACAGACTGGGCGGAC	1320

1261	CCGGAAGCGCAAGGATGTGCTTTGGGAGACCATCAAGTTTATGTACACAGACTCGGGCGGAC	1321
1321	CGGGACAAATGGCGAAATTCGCGCGCAAAACCTCTGCTGGCGCTCTTTACTGACCAACCAATGG	1381
1321	CGGGACAAATGGCGAAATTCGCGCGCAAAACCTCTGCTGGCGCTCTTTACTGACCAACCAATGG	1380
1381	GTGGCACAGCTGTGGCCACTGCCAGCTGCAGCGCCGACTACCAAGTCTCCCGTCTACTTT	1440
1381	GTGGCACAGCTGTGGCCACTGCCAGCTGCAGCGCCGACTACCAAGTCTCCCGTCTACTTT	1440
1441	TACACCTTTTACCACCACTGCCAGCGGGAGGCGCGCTGAGTGGGAGATGGCGGCAC	1500
1441	TACACCTTTTACCACCACTGCCAGCGGGAGGCGCGCTGAGTGGGAGATGGCGGCAC	1500
1501	GGGATGAACTGCCCTATGTCTTTGGCGTGCCTATGTGTGGTGGTGCACCGGACCTCTTCCCC	1560
1501	GGGATGAACTGCCCTATGTCTTTGGCGTGCCTATGTGTGGTGGTGCACCGGACCTCTTCCCC	1560
1561	TGTAACCTTCTCAAGAATGACGTCAATGCTCAGTGGCGGTGTCATGACTACTGGACCAAC	1620
1561	TGTAACCTTCTCAAGAATGACGTCAATGCTCAGTGGCGGTGTCATGACTACTGGACCAAC	1620
1621	TTGCGCAAGACTGGGAGCCCAACACAGCGGTTGCCAGGATACCAAGTTTCATCCACACC	1680
1621	TTGCGCAAGACTGGGAGCCCAACACAGCGGTTGCCAGGATACCAAGTTTCATCCACACC	1680
1681	AAGCCCAATCGCTTCGAGGAGGTGGTGTGAGCAAAATCAACAGCAGGAGAGACAGTAT	1740
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1741	CTGCACATPAGGCTGAAGCCACGCGTGCCTGACAACTACCGCGCCCAACAAGGTGGCTTC	1800
1741	CTGCACATPAGGCTGAAGCCACGCGTGCCTGACAACTACCGCGCCCAACAAGGTGGCTTC	1800
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1801	TGGCTGAGAGCTGTGCCCACTGTGCACAACTGTGCACACGAGCTCTTCAACACCAACACG	1860
1861	CGCCTGCTCCTACGCGACGCGTGCCTGCTGCTCCCGCGCTGGCGGCCCGGGGACCA	1920
1861	CGCCTGCTCCTACGCGACGCGTGCCTGCTGCTCCCGCGCTGGCGGCCCGGGGACCA	1920
1921	CGCGCGCCCGCGCGCTGTGCCACCTTGCTCCGAGCCGAGCCGAGCCGCGCCCAAGG	1980
1921	CGCGCGCCCGCGCGCTGTGCCACCTTGCTCCGAGCCGAGCCGAGCCGCGCCCAAGG	1980
1981	GCCTATGACCGCTTCCCGGGGACTACGGGACTACTCTCAACGAGCTGACGCTCACCGTG	2040
1981	GCCTATGACCGCTTCCCGGGGACTACGGGACTACTCTCAACGAGCTGACGCTCACCGTG	2040
2041	GCCGTGGTGCCTCCCTCTTTCCTCAACATCCTGGCCTTTGCTGCCCTCTACTACAAG	2100
2041	GCCGTGGTGCCTCCCTCTTTCCTCAACATCCTGGCCTTTGCTGCCCTCTACTACAAG	2100
2101	CGGACCGGGCAGGAGCTGCGGTGCAGCGGCTTAGCCACCTCGCGGCTCAGGCTCT	2160
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2161	GGCGTGCCTGGTGGGGCCCCCTGCTCCCGCGCGGGCGCTGAGCTGCCACACAGAGGAG	2220
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2221	GAGCTGTGTCTCATGCACTGAAGCGGGGTGTGGGTGTGGGCGGACCTTCCCGAGGCT	2280
2221	GAGCTGTGTCTCATGCACTGAAGCGGGGTGTGGGTGTGGGCGGACCTTCCCGAGGCT	2280
2281	CTGGCGCCTGTGCTGCCCGCCGACTACACCTGGCCCTTGGCGCGGGCAACCGACGATGTG	2340
2281	CTGGCGCCTGTGCTGCCCGCCGACTACACCTGGCCCTTGGCGCGGGCAACCGACGATGTG	2340
2341	CCTCTTTGGCCCCCGGGGCCCTTGACCTGTGCTGCCAGTGGCTGTGGGCGACCGCCACCC	2400
2341	CCTCTTTGGCCCCCGGGGCCCTTGACCTGTGCTGCCAGTGGCTGTGGGCGACCGCCACCC	2400

QY 1621 TTCCGCAAGACTGGGAGCCCAACACGCGGCTGCGCAGGATACCAAGTTTCATCCACACC 1680
Db 2040 TTCCGCAAGACTGGGAGCCCAACACGCGGCTGCGCAGGATACCAAGTTTCATCCACACC 2099
QY 1681 AAGCCCAATCGCTTCGAGGAGTGGTGTGAGCAAAATTCACAGCAGGAGGAGAGTAT 1740
Db 2100 AAGCCCAATCGCTTCGAGGAGTGGTGTGAGCAAAATTCACAGCAGGAGGAGAGTAT 2159
QY 1741 CTGCACATAGCGCTGGAAGCAACGCGTGGTGAACAATTCACCGCCCAACAGGTGGCTTC 1800
Db 2160 CTGCACATAGCGCTGGAAGCAACGCGTGGTGAACAATTCACCGCCCAACAGGTGGCTTC 2219
QY 1801 TGGCTGAGCTCGTGGCCCACTGACAACTGACAGCAGGAGTCTTCACACACGAG 1860
Db 2220 TGGCTGAGCTCGTGGCCCACTGACAACTGACAGCAGGAGTCTTCACACACGAG 2279
QY 1861 CGCTGCTCTCCACGACGCGTGGCGCGCTGCTCCCGCCGCTGCGCGCCCGGACACA 1920
Db 2280 CGCTGCTCTCCACGACGCGTGGCGCGCTGCTCCCGCCGCTGCGCGCCCGGACACA 2339
QY 1921 CGCGGCGCGCGCGCTGACACCTGCTCCGAGCCGAGCCGAGCCCGCCCAAGG 1980
Db 2340 CGCGGCGCGCGCGCTGACACCTGCTCCGAGCCGAGCCGAGCCCGCCCAAGG 2399
QY 1981 GCCTATGACGCTTCCCGGGGACTCACGGGACTACTCCACGAGCTGAGCGTCACCGTG 2040
Db 2400 GCCTATGACGCTTCCCGGGGACTCACGGGACTACTCCACGAGCTGAGCGTCACCGTG 2459
QY 2041 GCGTGGGTGCTCCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
Db 2460 GCGTGGGTGCTCCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2519
QY 2101 CGGACCGCGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2160
Db 2520 CGGACCGCGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2579
QY 2161 GGGTGTCTGTGGGGGCCCCCTCTCTCCCGCGCGCGCGTGGTGGTGGTGGTGGTGGTGGT 2220
Db 2580 GGGTGTCTGTGGGGGCCCCCTCTCTCCCGCGCGCGCGTGGTGGTGGTGGTGGTGGTGGT 2639
QY 2221 GAGCTGTGTCTGTGAGCTGAGCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2280
Db 2640 GAGCTGTGTCTGTGAGCTGAGCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2699
QY 2281 CTGCGCCTGCTGCGCGCGCGCTACACCTGCGCGCGCGCTGCGCGCGCGCTGCGCGCGCG 2340
Db 2700 CTGCGCCTGCTGCGCGCGCGCTACACCTGCGCGCGCGCTGCGCGCGCGCTGCGCGCGCG 2759
QY 2341 CTTCTTTGGGCGCGCGCGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2760 CTTCTTTGGGCGCGCGCGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2819
QY 2401 CCACCGCGCGCGCGCGCTTCTGCGCGCGCTTCTGCGCGCGCTTCTGCGCGCGCTTCTGCG 2460
Db 2820 CCACCGCGCGCGCGCGCTTCTGCGCGCGCTTCTGCGCGCGCTTCTGCGCGCGCTTCTGCG 2879
QY 2461 AGCCACAACACGCTTACCCCAACCCCACTCCACCACTCCGCTATAG 2508
Db 2880 AGCCACAACACGCTTACCCCAACCCCACTCCACCACTCCGCTATAG 2927

RESULT 3
US-10-274-694-30
; Sequence 30, Application US/10274694
; Publication No. US20030143589A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BRUNS, Christopher M.
; APPLICANT: DAS, Debopriya
; APPLICANT: DING, Li
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: GANDHI, Ameera R.
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APPLICANT: WALIA, Narinder K.
APPLICANT: XU, Yuming
APPLICANT: YANG, Junming
APPLICANT: YAO, Monique G.
APPLICANT: YUE, Henry
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0151 USA
CURRENT APPLICATION NUMBER: US/10/274,694
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 60/221,837
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/220,037
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/218,948
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US01/21324
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/216,804
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL Program
SEQ ID NO 30
LENGTH: 2663
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030143589A1 7473875CB1
US-10-274-694-30

Query Match 90.3%; Score 2265.4; DB 13; Length 2663;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ATGTGGCTCTCTGGCGCTGTGTCTGTGGGCTGGCGGGGCTCAACGCGGGGAGGGGGT 60
Db 177 ATGTGGCTCTCTGGCGCTGTGTCTGTGGGCTGGCGGGGCTCAACGCGGGGAGGGGGT 236
QY 61 CCCGGCG 120
Db 237 CCCGGCG 296
QY 121 TTCCCGGTGGTGAACACGCGCTACGCGCGAGTGCCTGTGGCGCGCGAGCTCAACAAC 180
Db 297 TTCCCGGTGGTGAACACGCGCTACGCGCGAGTGCCTGTGGCGCGCGAGCTCAACAAC 356
QY 181 GAGATCTGGGCG 240
Db 357 GAGATCTGGGCG 416
QY 241 GCCCGCGCTTCCAGCGCGCTGAGGGCGCGCGCTCGTGGCGCGCGCGCGCGCGCGCGCGCG 300
Db 417 GCCCGCGCTTCCAGCGCGCTGAGGGCGCGCGCTCGTGGCGCGCGCGCGCGCGCGCGCGCG 476
QY 301 ACCCTGCGCGCGCGCTGCCCGCAGAACCTGACGCGCGCGCTGCCCGCGCATGCTGCTGCT 360
Db 477 ACCCTGCGCGCGCGCTGCCCGCAGAACCTGACGCGCGCGCTGCCCGCGCATGCTGCTGCT 536

QY 361 GTGTGTTTCAACGCAAACTTGGAGCGCGCCACCTACTAGTGCAGAACAGAGCGAGAC 420
 Db 537 GTGTGTTTCAACGCAAACTTGGAGCGCGCCACCTACTAGTGCAGAACAGAGCGAGAC 596
 QY 421 TGCCTGTACTCAACTCTACCTGTCGCCACGAGGAGCGTCCGCTCACAAAACAGTGCAC 480
 Db 597 TGCCTGTACTCAACTCTACCTGTCGCCACGAGGAGCGTCCGCTCACAAAACAGTGCAC 656
 QY 481 GAGGCGACGCTCAATCCGCGACAGACAGATATCCGTGACCCCTGGGAAGAAGCCTGTGATG 540
 Db 657 GAGGCGACGCTCAATCCGCGACAGACAGATATCCGTGACCCCTGGGAAGAAGCCTGTGATG 716
 QY 541 CTGTTTCTCCATGGCGGCTCTACATGAGGAGGAGCCGGAACATGTTGATGGCTCAGTC 600
 Db 717 CTGTTTCTCCATGGCGGCTCTACATGAGGAGGAGCCGGAACATGTTGATGGCTCAGTC 776
 QY 601 CTGGGTGCTTATGGCAACGCTCATTTAGCCACGCTCAACTACCGTCTTTGGGCTGCTCGGT 660
 Db 777 CTGGGTGCTTATGGCAACGCTCATTTAGCCACGCTCAACTACCGTCTTTGGGCTGCTCGGT 836
 QY 661 TTTCTCAGACCCGCGGACCCAGGCTGCAAAAGCAACTATGGGCTCTTGGAACAGATCCAG 720
 Db 837 TTTCTCAGACCCGCGGACCCAGGCTGCAAAAGCAACTATGGGCTCTTGGAACAGATCCAG 896
 QY 721 GCGCTGCGCTGCTCAGTGAACCAATCCGCCACCTTTGGGCGGACCCCGAGCGTATCACC 780
 Db 897 GCGCTGCGCTGCTCAGTGAACCAATCCGCCACCTTTGGGCGGACCCCGAGCGTATCACC 956
 QY 781 ATCTTTGGTTCCGCGGCGAGGCGCTCTCTGCGTCAACCTTTCTGATCTCTCCACCAATCA 840
 Db 957 ATCTTTGGTTCCGCGGCGAGGCGCTCTCTGCGTCAACCTTTCTGATCTCTCCACCAATCA 1016
 QY 841 GAAGGCTGTTCCAGAGGCCATCCGCCAGAGTGCACCGGCATTTCCAGTGTGTCTGTC 900
 Db 1017 GAAGGCTGTTCCAGAGGCCATCCGCCAGAGTGCACCGGCATTTCCAGTGTGTCTGTC 1076
 QY 901 AACTACCGACCGCTCAAGTACACGCGGCTGTGGCAGCAAGTGGGCTGTACCGAGAG 960
 Db 1077 AACTACCGACCGCTCAAGTACACGCGGCTGTGGCAGCAAGTGGGCTGTACCGAGAG 1136
 QY 961 GACAGTGTGAAGCTGTGAGTGTCTGCGCGGGAAGCCCTCCCGGAGCTGGTGGACAG 1020
 Db 1137 GACAGTGTGAAGCTGTGAGTGTCTGCGCGGGAAGCCCTCCCGGAGCTGGTGGACAG 1196
 QY 1021 GACGTGACGCTGCCCGCTACACATCCGCTTTGGGCGCGGTGGTGGAGCGAGTGTGTC 1080
 Db 1197 GACGTGACGCTGCCCGCTACACATCCGCTTTGGGCGCGGTGGTGGAGCGAGTGTGTC 1256
 QY 1081 CCCGATGACCCCTGAGATCCTCATGACGAGGAGAAATTCCTCAACTACGACATGCTCATC 1140
 Db 1257 CCCGATGACCCCTGAGATCCTCATGACGAGGAGAAATTCCTCAACTACGACATGCTCATC 1316
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 Db 1317 GCGTCAACCGAGGAGAGGCGCTCAAGTTCGTGGAGGACTCTGACGAGAGGAGAGCGGT 1376
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 Db 1377 GTGTGTCCAGCGCTTTGACTCTACTGTCTCCAACTTTGTGGCAACCTGTATGGGTAC 1436
 QY 1261 CCGGAAGCGAGAGGATGTGCTTCGGGAGACCAATCAAGTTTATGTACACAGACTGGCGCGAC 1320
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Db 1617 TACACCTTCTTACCACTGCCAGCGGAGCGCGCTGAGTGGCAGATGCGGCGCAC 1676
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 QY 1561 TGTAACTTCTCCAAAGATGACGCTCATGCTCAGTGGCGTGGTCTATGACCTACTCGACCAAC 1620
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 QY 1621 TTGCGCAAGACTGGGAGACCCCAACAGCGGCTGCCAGGATACCAAGTTTCTATCCACACC 1680
 Db 1797 TTGCGCAAGACTGGGAGACCCCAACAGCGGCTGCCAGGATACCAAGTTTCTATCCACACC 1856
 QY 1681 AAGCCCAATCGCTTCAGGAGGAGTGGTGTGAGCAAAATTCAAAGAGGAGAGAGCAGTAT 1740
 Db 1857 AAGCCCAATCGCTTCAGGAGGAGTGGTGTGAGCAAAATTCAAAGAGGAGAGCAGTAT 1916
 QY 1741 CTGCAATAGGCTGAAGCCACGCGTGGCTGAGCAACTACCGCGCCAAAGTGGGCTTC 1800
 Db 1917 CTGCAATAGGCTGAAGCCACGCGTGGCTGAGCAACTACCGCGCCAAAGTGGGCTTC 1976
 QY 1801 TGGCTGAGCTGCTGCCACCTGCAACACTGCAACGAGAGCTCTTCAACACCAACAG 1860
 Db 1977 TGGCTGAGCTGCTGCCACCTGCAACACTGCAACGAGAGCTCTTCAACACCAACAG 2036
 QY 1861 CGCTGCTCTCCCTAAGCCACGCGCTGGCGCTCTGCTCCCGCCCTGCGCGCCCGGSCACA 1920
 Db 2037 CGCTGCTCTCCCTAAGCCACGCGCTGGCGCTCTGCTCCCGCCCTGCGCGCCCGGSCACA 2096
 QY 1921 CGCGGCGCGCGCGCGCTGCCACCTGCTCCGAGCGCGAGCGCGCGCGCGCGCAAG 1980
 Db 2097 CGCGGCGCGCGCGCGCTGCCACCTGCTCCGAGCGCGAGCGCGCGCGCGCGCGCAAG 2156
 QY 1981 GCCTATGACCGCTTCCCGCGGAGACTCACGCGAGTACTTCCACGAGAGTGCAGCGTCAAC 2040
 Db 2157 GCCTATGACCGCTTCCCGCGGAGACTCACGCGAGTACTTCCACGAGAGTGCAGCGTCAAC 2216
 QY 2041 GCGTGGGTGCTCCCTCTCTTCTCAACATCTGCGCTTTGCTGCGCTCTTACTACAAG 2100
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 QY 2101 CGGAGCGCGCGGAGAGCTGGTGCAGCGGCTTAGCCACCTGCGCGGCTCAGGCTCT 2160
 Db 2277 CGGAGCGCGCGGAGAGCTGGTGCAGCGGCTTAGCCACCTGCGCGGCTCAGGCTCT 2336
 QY 2161 GCGTGGCTGGTGGGCGCGCTGCTCCCGCGCGGCGCGTGAAGTGCACACAGAGGAG 2220
 Db 2337 GCGTGGCTGGTGGGCGCGCTGCTCCCGCGCGGCGCGTGAAGTGCACACAGAGGAG 2396
 QY 2221 GAGTGGTCTCACTGCAGCTGAAGCGGCTGGTGGCTGGGCGGAGACCTGCGG 2275
 Db 2397 GAGTGGTCTCACTGCAGCTGAAGCGGCTGGTGGCTGGGCGGAGACCTGCGG 2451

RESULT 4

US-09-978-295A-374
 ; Sequence 374, Application US/09978295A
 ; Patent No. US20020156006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: KJavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 36.4%; Score 912.2; DB 10; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2.5e-206;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

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 Qy 465 CACAAAAAAGCTGACGAGGCG-----ACGCTCAATCCGCCAGACACAGATATCCG 515
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RESULT 5

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 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Shexman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
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 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C27
 ; CURRENT APPLICATION NUMBER: US/09/978,697
 ; CURRENT FILING DATE: 2001-10-16
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 ; PRIOR FILING DATE: 2001-07-30
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Best Local Similarity 64.7%; Pred. No. 2.5e-206;

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 DB 112 CAGCCAGCACAGTATCCAGTTGTCAACACAAATATGCAAAATCCGGGGCTAAGAAC 171
 QY 168 CGAGCTCAACACGAGATCTCGGGCCCGGTCTGTGAGTCTTTGGGGTGGCTACGCCAC 227
 DB 172 ACCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCCTC 231
 QY 228 GCGGCCCTGGGGCGCGCGCTTCCAGCGCTGAGGCGCGCGCTCGTGGCCCGGGGT 287
 DB 232 ACCCCCACTGGAGAGAGCGGTTTCAGCCCCCAGAACCCCGTCTCTGTGACTGGAT 291
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 QY 345 GCGCATCATGCTGCTGT 404
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Qy 1233 CAATTTTGGACAACTGTATGCTACCGGAGGCAAGATGTGCTTCGGAGACCAT 1292
Db 1252 CAACCTTCGTGACAACTTTACGGCTACCTGAAAGGGAAGACACTTTTGGGGAGACTAT 1311
Qy 1293 CAAGTTTATGATACAGACTGGGCGGACCGGGAATGGGGAATGGCGGCAAAACCCCT 1352
Db 1312 CAAGTTTATGATACAGACTGGGCGGATAGGAATAACCGGAGACGCGGGAACCCCT 1371
Qy 1353 GCTGGCGCTCTTTACTGACCAACAAATGGTGGGACAGCTGTGGCCACTGCGCAAGTGA 1412
Db 1372 GGTGGCTCTTTACTGACCAACAGTGGTGGGCGGCGCGCTGGCC---GCCGACCTGCA 1428
Qy 1413 CGCGGACTACAGTCTCCGCTCTACTTTTACACCTTCTACACCTGCTACACCACTGCCAGGCGAGGG 1472
Db 1429 CGCGGAGTACGGCTCCCCCACTACTTCTATGCTTGTGAGTCCCTATGCTTCGGGAT 1488
Qy 1473 CCGGCTCAGTGGGAGATGGGGGCAAGGGGATGAACCTGCTTATCTTTTGGCGTGC 1532
Db 1499 GAAGCCAGCTGGGAGATTCGGGCCATGGTGTGAGTCCCTATGCTTCGGGATCC 1548
Qy 1533 CATGTGGTGGACCGGACCTTTCCCTGTAACTTCTCCAGATGACGCTCATGCTCAG 1592
Db 1549 CATGATCGTCCGACCGAGCTCTTCACTGTGAACTTTTCCAGAAACGAGCTCATGCTCAG 1608
Qy 1593 TGCGGTGTGATGACTACTGACCACTTCGCAAGACTGGGAGCCCAACAGCGGCT 1652
Db 1609 CGCGGTGTGATGACTACTGACCACTTCGCAAGACTGGTGTATCCAAATCAACAGT 1668

Qy 1653 GCCCAGGATACCAAGTTTCATCCACCAAGCCCAATCGCTTCGAGAGGTGGTGGAG 1712
Db 1669 TCCTCAGGATACCAAGTTTCATCCACCAAAACCCCAACCGCTTTGAAGAAGTGGCTGGTC 1728
Qy 1713 CAATTCACACAGCAGAGAGAGTATCTGCAATAGGCTGAAGCCAGCGCTGCTGGA 1772
Db 1729 CAAGTATATCCAAAGACCAAGCTCTATCTGATATTTGGCTTGAACCCAGAGTGAGAGA 1788
Qy 1773 CAATACCGGCCCAACAAAGTGGCTTCTGGCTGGAGCTCGTGCCCACTGCAACCT 1832
Db 1789 TCACTACCGGCAAGAAAGTGGCTTCTGGTTGAACTCGTTCTCTCATTTGCAACACT 1848
Qy 1833 GCA-----CAGGAGCTCTTCAACCAACCAACCGGCTGCTCCCTACGCCACGCG 1883
Db 1849 GAACGAGATATTCAGTATGTTTCAACCAACCAAGGTTCTCTCAACAGACATGACATC 1908
Qy 1884 CTGGCGGCTCGTCCCGGCTGGCGCCCGGCGCACAGCGGCGCCCGCGCTGCGCAC 1943
Db 1909 ATTTCCCTATGACACCGGCGATCTCCCGCAAGATATGGCCAAACCAACCGCCAGC 1968
Qy 1944 CTGGCTCCGAGCGCGAGCCGAGC-----CGGCCCCAAGGC 1982
Db 1969 AATCACTCTCTCCCAACATCCCAAACTCTAAGGACCCCTCAAAAACAGGCGCTGAGGA 2028
Qy 1983 CTATGACCGCTTCCCGGAGCTCAAGGAGTCTCCACGAGCTGAGCGTCAACGTTGC 2042
Db 2029 CACAACTGCTCTCATTTGAACCAACAGATTTATCCACCGAATTAAGTGTCAACATTGC 2088
Qy 2043 CGTGGTGGCTCCCTCTCTTCTTCAACATCTCGGCTTCTGCTGCTCTTACTACAGCG 2102
Db 2089 CGTGGGCGCTCGCTCTCTCTTCTTCAACATCTTCTTCTTCTGCGGCTGTACTACAAA 2148
Qy 2103 GGACCGGCGGAGGAGCTGCGGTGAGCGGCTTACCGGCTTACCGGCTCAGGCTCTGG 2162
Db 2149 GGACAGAGGCGGAGGAGTCAAGGAGTCAAGCGGCGGCTGAGGAGAACACCAATGA 2208
Qy 2163 CGTGGCTGGTGGGCGGCTCTCTCCCGCGCGCGGCGTGTGAGTGCACAGAGGAGGA 2222
Db 2209 TATCGCTCACATCCAGAACGAGAGATCATGCTCTGAGATGAAGCAGCTGGAACAGA 2268
Qy 2223 GCTGTGTCTACTGACGCTGAAGCGGGTGGTGGCGTGGGCGGACCTGCGGAGGCTCT 2282
Db 2269 TCACAGAGTGTGAGTGGTGGAG-----GCACAGCACACT 2304
Qy 2283 GCGGCTCTGCTGCGGCGGCTACACCTGCGGCTGCGGCGGCGACCGGAGCTGTGCC 2342
Db 2305 GAGGCTGACCTGCGGCGGCGGAGTACACCTCAAGTGGCGGCTGCGGAGATGATCC 2364
Qy 2343 TCTCTTGGCGGCGGCGGCTGAGCCCTGCTGCGGAGGCGCTG 2385
Db 2365 ACTTATGAGCGCAACACCATCATCATGATTCCAAACACACTG 2407

RESULT 6

US-09-978-192A-374
; Sequence 374, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06

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QY 1653 GCGGAGGATACCAAGTTTCATCCACACCAAGCCCAATCGTTTCGAGGAGGTGGTGGAG 1712
 Db 1669 TCTCAGGATACCAAGTTTCATCCACACCAAGCCCAATCGTTTCGAGGAGGTGGTGGAG 1728
 QY 1713 CAAATTCACACAGCAAGGAGAGCAGTATCTGCACATAGCCTGAGCCACCGGTGGTGA 1772
 Db 1729 CAAATTCACACAGCAAGGAGAGCAGTATCTGCACATAGCCTGAGCCACCGGTGGTGA 1788
 QY 1773 CAACTACCGGCAACAGAGTGGCTTCTGGGTGAGTCTGGTGGTGGTGGTGGTGGTGG 1832
 Db 1789 TCACCTACCGGCAACAGAGTGGCTTCTGGGTGAGTCTGGTGGTGGTGGTGGTGGTGG 1848
 QY 1833 GCA-----CAGGAGCTCTTCCACACCAAGCCCAATCGTTTCGAGGAGGTGGTGGAG 1893
 Db 1849 GACGAGATATTCAGTATGTTTCAACCAACCAAGGTTCTTCCACGAGCATGACATC 1908
 QY 1884 CTGGCGGCTCTGCTCCCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1943
 Db 1909 ATTCCCTATGCAACCGGCGGATCTCCGCGCAAGATATGGCCAAACCAACCGGCGGCG 1968
 QY 1944 CTGGCTCCGAGCGGAGCCCGGAG-----CCGCGCCCAAGGCG 1992
 Db 1969 AATCACTCTGTCACCAATCCCAACACTCTAAGGACCTTCAACAAACAGGCGGCTGAGGA 2028
 QY 1983 CTATGACCGCTTCCCGGCGGACTCACGGGACTTCTCCACGAGCTGAGCGTCAACGGTGC 2042
 Db 2029 CACAACTGCTCTATTGAAACCAACGAGATATTTCCACCAATTAAGTGTACCATGTC 2088
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 Db 2089 CTGGGTGCT 2148
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RESULT 7

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 ; Sequence 374, Application US/09999832A
 ; Publication No. US20020192706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
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 ; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C63
 ; CURRENT APPLICATION NUMBER: US/09/999,832A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
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Query Match 36.4%; Score 912.2; DB 10; Length 3113;

Best Local Similarity 64.7%; Pred. No. 2.5e-206; Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGGCGAGGAGCGCTTCCCGGTGGTGAACACCGCGCTACGGGCGAGTGC CGCGGTGTGCGCGC 167
 DB 112 CAGCCAGCACAGTATCCAGTTGTCAACACAAATATGGCAAATCCGGGCGCTAAGAAC 171
 QY 168 CGAGCTCAACACGAGATCTTGGGCGCGCTCGTGCAGTCTTTGGGCGTGCCTACGCCAC 227
 DB 172 ACCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCCTC 231
 QY 228 GCGGCGCGCTGGGCGCGCGCGCTTCCAGCGCGCTGAGGCGCGCGCTGCTGCGCGCGGT 287
 DB 232 ACCCGCCACTGGAGAGGCGGTTTACGCCCCCAGAACCCCGCTCTCTGGACTGGCAT 291
 QY 288 GCGCAACGCCACCCCTGCGCGCGCGCTGCGCGCAACCTGCAACG ---GGGCGCTGCC 344
 DB 292 CGGAATACTACTCAGTTTGTCTGTGTGTGTCGCCCGCAGCACCTGATGAGATCCTTACT 351
 QY 345 CGCCATCATGCTGCTGTGTGTTCACCGCAAACTTGGAGGGCGCGCGCCACCTACGTGCA 404
 DB 352 GCATGACATGTGCGCCATCTGGTTTACGCGCAATTTGGATACTTTGATGACCTATGTTCA 411
 QY 405 GAAACGAGCGGAGGACTGCTGTACCTCAACCTCTAGTGCCCGCCAGGAGCGGTCCGCT 464
 DB 412 AGATCAAAATGAGACTGCGCTTTACTTTAAACATCTACGTGCCCGGGAAGATGAGCCAA 471
 QY 465 CACAAAAAAGTGCAGGCGG-----ACGCTCAATCCGCGCACACAGATATCCG 515
 DB 472 CACAAAGAAAAACCGCAGATGATATAACGAGTAATGACCGTGTGAAGCAGAGATATTC 531
 QY 516 TGACCCCTG---GGAAGAAGCGCTGTGCTGCTTCTCCATGCGCGCTCTCTACATGAGGG 572
 DB 532 TGATCAGAACAGTAGAAGAGCCGCTCATGCTCTATATCATCGGGGATCTTACATGGAGG 591

573	QY	GACCGGAAA	CATGTT	CGATGGCT	CAGTCT	CGCTGCT	CTATGCGAAC	CGTCA	TTGTAGCCAC	632
592	DB	CACCGGCAA	CATGAT	TGACGGCAGC	ATTTGGCAAG	CTACGGAA	ACGT	TCATCGTGAT	TCAC	651
633	QY	GCTCAACT	ACCGCT	TTTGGG	TGCTCGGTTT	CTCAGCAC	CCGGGAC	CCAGGCT	CGCAAAAGG	692
652	DB	CATTAACT	ACCGCT	CTGGGA	ATCTAGGG	TTTTAAAG	TACCGGT	GAC	CCAGG	711
693	QY	CAACTAT	TGGGCT	CTCGAC	CCAGAT	CCAGCCCT	CGCTGGCT	CAGT	GAAACAT	752
712	DB	CAACTAT	TGGGCT	CCTGAT	CAAGAT	CAAGCAT	CTGGGTGGAT	TGAG	GAGAT	771
753	QY	CTTTGGGGG	CGA	CCCGAG	CGTAT	CAACAT	CTTTGGTT	CCGGGGCA	GGGGCT	812
772	DB	CTTTGGGGG	CGGGA	CCCCAAG	AGAGT	GACCAT	CTTTGGCT	CGGGGGCT	GGGGCT	831
813	QY	CAACCTT	CTGAT	CCTCT	CTCCAC	CAATTC	CAGAAG	GGGTGT	CCAGAAG	872
832	DB	CAGCGT	GTGAC	CTGTGCC	CACTACT	CAAGAG	GTCTCT	CTCCAGAAG	GCCTAT	891
873	QY	TGGCAC	CGCCAT	TTCCAG	CTGGTCT	CTCAACT	ACACAG	CCGCTCAAG	TATCAC	932
892	DB	CGGCAC	CGCCCT	CTGTC	CAAGCT	TGGCAGT	GAATCA	CCAG	CGCCAGT	951
933	QY	GGCAGCA	AGGTGG	GGCTGT	GACCG	AGACAGT	CTGTGA	AGCTGTG	AGATGT	992
952	DB	GGCAGCA	AGAGT	CGGGT	CGCAAC	ATGCTG	GACACCA	CGACAT	TGTAAG	1011
993	QY	GAAGCCCT	CCCGG	AGCTGGT	GGACAG	AGCCTG	CGAGCT	CTGCCGCT	TACCACAT	1052
1012	DB	CAAGAA	CTACA	AGAGCT	CTAT	CTCAG	CAGACCAT	CA	CCCGCCACCT	1071
1053	QY	TGGSCCG	GTGGTGG	CGAGCT	GTGCTCCCG	CATGACCT	CAGATCT	CATGAC	CGAGG	1112
1072	DB	CGGGCGG	TGAT	CGACGG	CGAGCT	CA	TCCACAG	CGACCC	CAGATCT	1131
1113	QY	AGAA	TTCTCA	ACTA	CGA	ATGCTCAT	CGGCTCA	AC	CAGGGAG	1172
1132	DB	CGAGT	TTCTCA	ACTAG	CAATCAT	GTCTGGG	CGCTCA	ACCAAGG	GAAGG	1191
1173	QY	GGAGGA	CTCTG	CAGAG	AGCGAG	CGGTGT	CTGCCAG	CGCTTT	GACTT	1232
1192	DB	GGACGG	CATCGT	GGATA	ACGAG	CGGTGT	GACGCC	CAACGAC	TTTGACT	1251
1233	QY	CAACTTT	GTGGAC	CAACTGT	TATGGCT	CTACCG	GAAGG	CAAGAT	GTGCT	1292
1252	DB	CAACT	CTGGGAC	CAACCTTT	ACGCTAC	CCCTCGA	GGGAA	AGGCT	CTGAGT	1311
1293	QY	CAAGTTT	ATGTAT	CACAG	CTGGCC	CGACCGG	ACAATGG	CGAAAT	CGCCG	1352
1312	DB	CAAGTT	CATGTAT	CACAG	CTGGCC	CGCAT	TAAGG	AAACCGG	AGACG	1371
1353	QY	GCTGGG	CGCTTT	TACT	TGAC	CAACCA	ATGGGTGG	CAAC	AGCTGG	1412
1372	DB	GGTGGCT	CTCTTT	TACT	TGAC	CAAC	CAAGTGG	GTGG	CCCCCG	1428
1413	QY	CGCGCAT	CTACAGT	CTCCG	CTACTTTT	TACACCTT	CTAC	CAAC	CACTT	1472
1429	DB	CGCGCAT	CTACAGT	CTCCG	CACTTCT	CTATGCC	TTCTCT	CAT	CAC	1488
1473	QY	CCGGC	CTGAGT	GGG	CGAGAT	CGCGG	CACTG	GCCTT	ATGTCT	1532
1489	DB	GAAGCC	CAGCTGGG	CGAGAT	TCGGGCC	CAATGGT	GTATGAG	GTGCC	CTATGT	1548
1533	QY	CATGGT	GGGTGG	CCAC	CGACCT	CTTCCCT	GTAACTT	CTCC	AGAA	1592
1549	DB	CATGAT	CGGTCC	CAAC	CGAGCT	CTCT	CAGTGT	TAATCTTT	CC	1608
1593	QY	TGGCGT	GTGTAT	AG	CTAT	CTG	AGCA	CACTT	CGCC	1652
1609	DB	CGCCGT	GGTCT	AT	CTG	AGCA	CACTT	CGCC	CA	1668
1653	QY	CGCCGAG	GAT	ACCA	AGTT	CA	CA	CCCAAG	CGCAAT	1712

[illegible]

APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuc, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
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Best Local Similarity 64.7%; Pred. No. 2,5e-206;
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112 CAGCAAGCACAGTATCCAGTTGTCACACAAATATGGCAAAATCCGGGGCTAAGAAC 171
168 CGAGCTCAACACAGAGATCTCGGCGCGCTGCGAGTCTTGGGGGTGCGCTACGCCAC 227
172 ACGTTACCAATGAGATCTTGGGTCAATGAGAGAGTACTTAGGGGTCCCTTATGCTC 231
228 GCGGCCCTCGGGCGCGCGCTTCCAGCGCTTCCAGCGCGCGCGCGCTCGTGGCGCGGT 287
232 ACCCCCACTGGAGAGAGGGGGTTTCAGCCCCCAGAAACCCCGCTCCTCGACTGGCAT 291
288 GCGCAAGCCACACCTCGCGCGCGCTGCGCGAGAACCTGCAGC---GGGCGGTGCC 344
292 CCGAAATACATCACTAGTTCGTGTGCGCGCGCGCGCGCTGAGATGAGATCTTACT 351
345 CGCCATCATGCTGCTGTGGTTTCAACGACAACTTGGAGCGCGCGCGCGCTTACGTGCA 404
352 GCATGACATGCTGCCATCTGGTTTACCGCCAATTTGGATACCTTGTGATGACCTATCTCA 411
405 GAACGAGGAGGAGTCTGCTGTACCTCACTTACCTGCTGCGCGCGCGCGCGCGGTCCGT 464
412 AGATCAAAATGAGACTGCTTACTTAAACATCATAGTGTGCGCGCGCGCGCGAGATGAGCCAA 471
465 CACAAAAAACGTCAGAGGGG-----ACGCTCAATCCCGCAGACACAGATATCCG 515
472 CACAAAGAAACACAGATGATATACAGAGTATGACCGTGGTGAAGACAGATATCA 531
516 TGACCTCTG---GGAAGAGCGTGTGATGCTGTTTCTCCATGGCGGTCTCTACATGAGGG 572
532 TGATCAGAAACAGTAAAGACCGGTCAATGCTCTATATCCATGGGGGATCTTACATGAGGG 591
573 GACCGAAACATGTTGATGCTCAGTCTCGTGGCTGCTATGCGCAACGTCATTGTAGCCAC 632

Db 592 CACCGGCACACATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTATCGTGTATCAC 651
Qy 633 GCTCAACTACCGTCTTGGGGTGTCTCGTTTCTCAGCACCGGGGACCAAGGCTCAAAAGG 692
Db 652 CATTAACCTACCGTCTGGATATCTAGGGTTTAACTACCGGTGACCGGACGACAAAGG 711
Qy 693 CAACATATGGCTCTCTGGAACAGATCCAGGCGCTCGCGTGGCTCAGTGAAACATCGCCCA 752
Db 712 CAATATGGGCTCTCTGATCAGATTCAAGCACTCGCGTGGATTGAGGAGAAATCGGAGAC 771
Qy 753 CTTTGGGGGACCCCGAGCGTATCACCATCTTTGGTTCCGGGCGCAGGGGCTCTCTCGCT 812
Db 772 CTTTGGCGGGGACCCCAAGAGAGTACCATCTTTGGCTCGGGGCTCGGGGCTCTCTGTGT 831
Qy 813 CAACCTTCTGATCTCTCCACCATTCAGAAAGGCTGTTCCAGAGGCCATCGCCACAG 872
Db 832 CAGCCTGTTGACCTGTCTCCACTACTCAGAAGGTCTCTCCAGAAGGCCATCATTTACAG 891
Qy 933 GGCAGCCAAAGGTGGGCTGTCAACGAGAGACAGTGTCTGAAGCTGTGGAGTGTCTGCGCCG 992
Db 952 GGCAGACAAAGTGGCTGTGCAACATCTGGGACACACAGACATGCTAGATGCTCTGCGGAA 1011
Qy 993 GAAGCCCTCCGGGAGCTGTGGACAGAGAGTGTGACGCTGCGCGTACACACATCGGCTT 1052
Db 1012 CAAGAATCTAAGAGAGCTCATCCAGCAGACCATCACCCCGGCCACCTTACACATAGCCTT 1071
Qy 1053 TGGCCCGTGTGATGGCGACGCTGTCGCCGATGACCTCTGAGATCTCTATGACGAGGG 1112
Db 1072 CGGGCGGTGATCGACGGCGAGCTTATCCAGAGAGCCCGCCAGATCTGTAGAGCAAG 1131
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Db 1312 CAAGTTTATGACAGACTGGGCGGATAGGGAACCCCGAGACGCGGCGGAAACCCCT 1371
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Db 1429 CCGCAGTACGCTCCCGCACTTCTATGCTTCTATCATCTGCTGCAAGGAAAT 1498
Qy 1473 CCGGCTCAGTGGGCGAGTGGGCGGACCGGGATGAACTGCGCTTATGTTCTTGGCGTGC 1532
Db 1499 GAAGCCAGCTGGGCGAGATTCGGCCCATGGTGTAGTGTGCTTCTTCTGCGCATCCC 1548
Qy 1533 CATGTGGGTGGCGACCGGACTCTTCCCGCTTAACTTCTCCAGAGATGACGTCATGCTCAG 1592
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Qy 1653 GCGCAGGATACCAAGTTTATCCACCAAGCCCAATCGCTTCGAGGAGGTGTGTGAG 1712

1669 TCCTCAGGATCAAGTTTCATTACACAAACCCCAACCGCTTTGAAGAGTGGCGCTGGTC 1728
 1713 CAAATTCACAGCAGAGAGAGAGTATCTGCATAGGCTGAGCCACGCGTGGTGA 1772
 1729 CAAGTATAATCCCAAGACAGCTCTATCTGCATATGGCTTGAACCCAGAGTGAGAGA 1788
 1773 CAACTACCGCGCCCAACAAAGGTGGCTTCTGGGTGGAGCTCGTGGCCCACTGCAACCT 1832
 1789 TCACCTACCGGGCAACGAAAGTGGCTTCTGGTGGAACTCGTCTCTCATTTGCACAACT 1848
 1833 GCA-----CAGGAGCTTTCACACACACAGCGCTGCTCTCTAGCCAGCG 1883
 1849 GAACGAGATATTCAGATATTTTCAACACCAACAAAGGTTCCTCCACGACATGATC 1908
 1884 CTGGCGCGCTCGTCCCGCGCTGGCGCCCGGACACAGCGCGCCCGCGCGCTGGCCAC 1943
 1909 ATTTCCTATGACACCGCGGATCTCCCGCCAGATATGGCCACCAACCAACCGCCAGC 1968
 1944 CTGCTCTCCGAGCCGAGCCGAGC-----CCGCCCCAAGGGC 1982
 1969 AATCACTCTGCGCAACAATCCCAACACCTTAAGGACCTTCACAAACAGGGCCCTGAGGA 2028
 1983 CTATGACCGCTTCCCGGGAGCTCAGGAGTACTCCAGGAGCTGAGCGTCACCGTGGC 2042
 2029 CAACTGCTCTATTAACCAACAAAGAGATTTCCACCGNATTAAGTGTACCAATTC 2088
 2043 CGTGGGTGCTCTCTCTCTCTCAACATCTGGCTTGTGCTGCTCTCTCTCTCTCTCTCT 2102
 2089 CGTGGGGGCTCGCTCTCTCTCTCAACATCTAGCTTTTGGCGGCTGTACTACAAAA 2148
 2103 GACCGGGGAGGAGCTGGGTGAGCGGCTTACGCCACTGCGGCTCAGGCTCTGG 2162
 2149 GGAACAGAGGCGCATGAGACTCACAGGCGCCCACTGCTCCCGAGAAACACCAAAATGA 2208
 2163 CGTGCCTGTGGGGGCGCCCTGCTCCCGCGCGCGCTGAGCTGCCACAGAGGAGGA 2222
 2209 TATCGTCTACATCCAGAAAGAGATCATGCTCTGAGAGTGAAGAGCTGGAACAGA 2268
 2223 GCTGGTGTCACTGAGCTGAGCGGGTGGTGGCTGGGGGCGGACCTTGGCGAGCTCT 2282
 2269 TCAGGAGTGTAGTCTCGAG-----GCACAGACACACT 2304
 2283 GCGCCCTGCTGCGCCCGCGAGCTACACCTGCTGCTGCGCGCGGACCGGAGATGTGCC 2342
 2305 GAGGCTCACTGCGCCGCGAGACTACACCTCAGCTGCGCGGCTGGCCAGATGACATCC 2364
 2343 TCTCTTGGCCCGCGGGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2385
 2365 ACTTATGCGCCAAACACCATCACCATGATTTCCAAACACACTG 2407

RESULT 9

US-09-978-608A-374
 ; Sequence 374, Application US/09978608A
 ; Publication No. US20030045462A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Geritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: 2630P1C22
 ; CURRENT APPLICATION NUMBER: US/09/978,608A
 ; NUMBER OF SEQ ID NOS: 624
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 374
 ; LENGTH: 3113
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-978-608A-374

Query Match 36.4%; Score 912.2; DB 11; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2.5e-206;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGCGGAGGAGCGCTTCCCGTGTGAGACAGCGCTACGGGCGAGTGCAGGCTGTGCGGCG 167
 DB 112 CAGCCAAGCACATATCCAGTTGTCAACAAATTTATGGCAAAATCCGGGCGCTAAGAAC 171
 QY 168 CGAGCTCAACACAGAGATCTGGGCGCGCTCGTGCAGTTCTTTGGGCGTGCCTTACGCCAC 227
 DB 172 ACCTTACCAATGAGATCTTGGTCCAGTGGAGCAGTACTTAGGGGTCCCTTATGCCTC 231
 QY 228 GCGCGCCCTGGGCGCGCGCTTTCAGCGCTGAGGCGCCCGCTCTGTGGCCCGCGCT 287
 DB 232 ACCCGCCACTGAGAGAGGCGGTTTTCAGCGCGCGCGCGCGCGCTCTCTGTGGACTGCGCAT 291
 QY 288 GCGCAACGCCACACACCTGCGCGCGCGCTGCGCGCGAGAACCTGACG---GGGCGGTGCC 344
 DB 292 CCGAATATCTACTCAGTTTCTGCTGTGTGCTCCCGCGCGCTGATGAGAGATCTTACT 351
 QY 345 CGCCATCATCTGCTGTGTGTTCACCGAACAATTTGGAGGCGCGCGCGCTACCTGAGTGA 404
 DB 352 GCATGACATCTGCGCATCTGCTTTACCGCAATTTGGATCTTTGATGACCTTATGTTC 411
 QY 405 GAACGAGCGAGGAGTGCCTGTACCTCACTCTAGTGCCTCCACCGAGGACGCTCGCT 464
 DB 412 AGATCAAAATGAAGACTGCTTTTACTTTAAACATCTAGTGCCTCCACCGAAGTGGACCA 471
 QY 465 CACAAAAAACGTGACGAGGCG-----ACGCTCAATCCCGCGAGACACAGATATCCG 515
 DB 472 CACAAAGAAAACGACATGATATACGAGTAAATGACCGTGTGAAGACGAAGATATTC 531
 QY 516 TGACCTTG---GGAGAGCGCTGTGCTGTCTTCATGGGCGCTCTTACATGGAGGG 572
 DB 532 TGATCAGAACAGTAAAGAGCGCGTCTATCTATCCATGGGGGATCTTACATGGAGGG 591
 QY 573 GACCGGAAACATGTTCCATGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
 DB 592 CACCGGCAACATGATTCAGCGGACATTTTGGCAAGCTACGGAACCTCATCTGATCAC 651
 QY 633 GCTCAACTACCGTCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
 DB 652 CATTAACCTACCGTCTGGGAATCTAGGGTCTTTTAAAGTACCGGTGACCGAGCGCAAGG 711
 QY 693 CAACCTATGGCTCTCTGAGCAGATCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
 DB 712 CAACCTATGGCTCTCTGATCAGATTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
 QY 753 CTTTGGGGCGGACCGCGAGCTATCAACATCTTTGGTTCGGGCGAGGCGCTCTCTCGT 812

Qy	1884	CTGGCGGCCTGTCTCCCGCCCGTGGCGCCCGGGCACACGCGCGGCCCGCGCGCTGCAC	1943
Db	1909	ATTTCCTATGGCACCGCGGATCTCCGCGAAGATATGGCCAAACCAACCGCCGAGC	1968
Qy	1944	CCTGCCTCCCGAGCCGAGCCCGAGC-----CCGGCCCCAAGGGC	1982
Db	1969	AATCACTCTCTGCCAAACAAATCCCAACACACTAAGGACCCTCACAAACACGGGCTGAGGA	2028
Qy	1983	CTATGACCGCTTCCCGGGGACTCACGGGACTACTCCACGGAGCTGAGCGTCAACCTGGC	2042
Db	2029	CACAACGTCTCTATTGAACCCAAACGAGATTATTCACCGAAATTAAGTGTCAACATTC	2088
Qy	2043	CGTGGGTGCTCCTCTCTCTCTCAACATCTCTGGGCTTTGCTGCCCTCTACTACAAAGC	2102
Db	2089	CGTCGGGGCGTGGTCTCTCTCTCAACATCTTAGCTTTTGGCGCGTGTACTACAAA	2148
Qy	2103	GZACCGGCGCGCAGAGGTGCGGTGCGAGCGCGGTAGCCACCTGGCGGGCTCAGGCTCTGG	2162
Db	2149	GZACAGAGCGCGCATGAGACTCACAGGGCGCCGAGTCCCACAGAGAACACCAAAATGA	2208
Qy	2163	CGTGCCTGTGGGGGCCCCCTGTCCCGCGCGGGCGGTGAGTGCCACACAGAGGAGGA	2222
Db	2209	TATCGCTCACATCCAGNACGAAGAGATCATGTCTCTGCAGATGAAGCAGTGGNACAGA	2268
Qy	2223	GCCTGGTGTACTGAGCTGAAGCGGGGTGGTGGCTGCGGGCGGACCTTCCCGAGGCTCT	2282
Db	2269	TCACGAGTGTGAGTCGGTGCAG-----GCACACGACACACT	2304
Qy	2283	CGCGCTTGCCTGCCCGCGACTACACCTTGGCCCTTGGCGCGGGGACCGGACGATGTGC	2342
Db	2305	GAGGCTCACTGCGCGCGAGACTACACCTTCACGCTGCGCGCGGTGCGCAGTGCATCCC	2364
Qy	2343	TCTTTGGCCCCCGGGGCCCTGACCTGTGTGCCAGTGGCCTG	2385
Db	2365	ACTTATGACGCCAAACACCAATCAACCATGATTCCTCAACACACTG	2407

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RESULT 10
US-09-378-585A-374
; Sequence 374, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Descoviers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivay J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Knapier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William L.
; TITLE OF INVENTION: Secreted and Trans
; TITLE OF INVENTION: Acids Encoding t
; FILE REFERENCE: P2630P1C15

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Query Match	36.4%	Score 912.2	DB 11	Length 3113
Best Local Similarity	64.7%	Pred. No. 2.5e-206		
Matches 1503	Conservative 0	Mismatches 748	Indels	Gaps 72
QY	108	CGCGGAGGAGCGCTTCGCGTGGTGCACACGGCTACAGCGCGAGTGCAGCGGTGTCGGCGG	167	
DB	112	CAGCCAAAGCACAGTATTCAGTTGTTCACACAAATATGCGAAATCCGGGGCTTAAGAAC	171	
QY	168	CGAGCTCAACACAGAGATCCTCGGCGCCCGTGTGCAGTCTTTGGGCGTCCCTACGCGAC	227	
DB	172	ACGGTTACCCAAATGAGATCTTGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCTCTC	231	
QY	228	GGCGGCCCTGGCGGCCCGCTTCGACCGCCTGAGGCGCCCGCTCTGTGCGCCGGCGT	287	
DB	232	ACCCGCCCATGTGAGAGAGCGGTTTCAGCGCCCGCAGAACCCCGCTCTCTCGTGAATGGCAT	291	
QY	288	GGCGAACGCCACACCTCGCGCCCGCTGCGCGCAGAACCTGCACG---GGCGCCTGCC	344	
DB	292	CGGAATACTACTCAGTTTGTCTGTGTGTCGCCCGCAGCCTGGATGAGAGATCCTTACT	351	
QY	345	CGCCATCATGTGCTGTGTGTTTACCGCAAACTTTGGAGGCGGCGCCCACTACGTGCA	404	
DB	352	GCATGACATGCTGCGCCATCTGGTTTACCGCAATTTGGTACTTTTGATGACCTATGTTCA	411	
QY	405	GAAACAGAGGAGGACTGCTGTACTCTCACTCACTGTCGCCACCGAGGAGCGTCCGCT	464	
DB	412	AGATCAAAATGAAGACTGCCCTTACTTTAAACATCTACGTGCCACCGAAAGATGGAGCAA	471	
QY	465	CACAAAAAACGTGACGAGGGG-----AGCTCAATTCGCCACAGACACAGATATCCG	515	
DB	472	CACAAAGAAACGCGAGATGATATACAGGATTAATGACCGTGGTGAAGACGAAGATATCA	531	
QY	516	TGACCTG---GGAAGAGCTGTGATGCTGTTTCTCCATGGCGGCTCTCATCGAGGG	572	
DB	532	TGATCAGAACAGTAAGAACCCCGTCATGGCTATATCCATGGGGGATCTTACATCGAGGG	591	
QY	573	GACCGGAAACATGTTGATGTGCTCAGTCTCGGTGCTATGCGCAAGCTCATTTGTAGCCAC	632	
DB	592	CACCGCAACATGATTTGACGCGAGCATTTGGCAAGCTACGAAAGCTCATGCTGATCAC	651	
QY	633	GCTCAACTACCGTCTTTGGGTGCTCGGTTTTCTCAGCACCGGGAACAGGCTGCAAAAGG	692	
DB	652	CATTAACTACCGTCTGGGAATACTAGGGTTTTTAAAGTACCGGTGACCAAGCAGCAAAAGG	711	
QY	693	CAACTATGGGCTCTGGACAGATCCAGGCGCTGCGTGCCTATGGCAAGCTCATTTGTAGCCCA	752	
DB	712	CAACTATGGGCTCTCTGGATCAGATTCAGCACTGCGGTGATTTGAGAGAGATGTCGGAGC	771	
QY	753	CTTTGGGGGCGACCCCGACGCTATCACCATCTTTTGGTTTCGGGGCGAGGGCCCTCTCGGT	812	
DB	772	CTTTGGCGGGAGCCCAAGAGAGGTGACCATCTTTGGGCTCGGGGGCTCGGGGCTCTCTGTGT	831	
QY	813	CAACCTTCTGATCTCTCCAGCAATTCAGAAGGCTGTTCCAGAGGCGCATCGCCACAGAG	872	
DB	832	CAGCTGTTTACCCCTGTCTCCACTACTCAGAAGTCTCTTCCAGAGGCGCATCATTCAGAG	891	
QY	873	TGGCACCGCATTTTCAGCTGTGTCTGCTCAACTACCGCCGCTCAAGTACACGCGGCTGCT	932	
DB	892	CGGCACCGCCCTGTCCAGCTGGCAGTGAACTTACCGACGCGGCCAAGTACACTCGGATATT	951	
QY	933	GGCAGCAAGGTGGGCTGTGACCGAGAGGACAGTGTGTGAAGCTGTGGAGTGTCTCGCGCG	992	
DB	952	GGCAGCAAGGTGGGCTGTGACATGCTGGACACACAGCAATCGGTAGAAATGCTCGCGAA	1011	

QY 2043 CGTGGTGCTCCTCTCTCTCTCAACATCCCTGGGCTTTGCGCCCTCTACTACAGCG 2102
Db 2089 CGTGGGGCTCCTCTCTCTCTCAACATCTTAGCTTTTGGCGGCTGTACTACAAAA 2148
QY 2103 GGACCGCGGCGAGCTGGGTCAGGGGGCTTACGCCACCTGGGGCTCAGGCTCTGG 2162
Db 2149 GGACAGAGGCGCATGAGACTCAGAGGCGCCCATCTCCAGAGAAACACCAATGA 2208
QY 2163 CGTGGTGCTGAGCTGGGCGCCCTCTCCCGCGCGGCGCTGAGCTGCCACCGAGAGGA 2222
Db 2209 TATCGCTCATACCAAGAACGAGAGATCATGTCTGCGAGATGAAGCAGCTGGAACCA 2268
QY 2223 CGTGGTGCTGAGCTGGGCGGCTGGTGGCTGGGCGGCGGCTGCGGAGGCTT 2282
Db 2269 TCAGAGTGAGTCTGCTGAG-----GCACAGACACT 2304
QY 2283 GCGCCCTGCTGCGCCCGGAGCTACACCTGCGGCGGCGGCGGCGGAGGATGCGC 2342
Db 2305 GAGGCTCACCTGCGCGGAGACTACACCTCAGCTGGCGGCTCGGCGAGATGACATCC 2364
QY 2343 TCTCTGGCGCGGCGGCGGCTGACCTGCTGCGGAGTGGCCTG 2385
Db 2365 ACTTATGAGCGCAACACCATCATCATGATCCAAACACACTG 2407

RESULT 11
US-09-978-191A-374
Sequence 374, Application US/09978191A
Publication No. US2003050239A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1998-05-15
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 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 ;
 Query Match 36.4%; Score 912.2; DB 11; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2.5e-206;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;
 ;
 QY 108 CGCGGAGGAGCGCTTCCCGTGGTGAACACGCGCTACGGCGAGTGGGGTGTGGCGG 167
 DB 112 CAGCCAAGCACAGTATCCAGTTGTCAACACAAATATGGCAAAATCCGGGGCCATAAGAAC 171
 QY 168 CGAGCTCAACACGAGATCCTGGGCCCGCTCGTGCAGTTCTTTGGGGCGTCCCTTACGCCAC 227
 DB 172 ACCGTTACCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTTATGCCTC 231
 QY 228 GCGGCCCTGGGGCGCGCGCTTCCAGCGGCTCAGCGGCTGAGGCGCGCGCTCTGTGGCCCGCGT 287
 DB 232 ACCCGCCACTGGAGAGAGCGGTTTTCAGCCCGCCAGAACCCCGTCTCTCTGGACTGGCAT 291
 QY 288 GCGCAAGCGCCACACCTTCCCGCCCGCTGCCCGCAGAACCTTGCACG---GGCGGCTGCC 344
 DB 292 CCGAATATCTACAGTTTGTCTGTGTGTCGCCCGACCTGGATGAGAGATCTTACT 351
 QY 345 CGCCATCATGCTGCTGTGTGTTTCAACGACAACTTTGGAGGGCGCGCCACCTTACGTGCA 404
 DB 352 GCATGACATGCTGCCCATCTGGTTTACCSCCAATTTGGATATCTTTGATGACCTATGTTCA 411
 QY 405 GAACGAGCGGAGTGGCTGTACCTCAACCTCTACGTGCCCGCAGAGACCGTCCGCT 464
 DB 412 AGATCAAAATGAAGACTGCCCTTTTAAACATCTACGTGCCCGCAGAGATGAGGCCAA 471
 QY 465 CACAAAAAAGCGTGAAGGCGG-----AGCTCAATCCCGCACACAGATATCCG 515
 DB 472 CACAAAGAAAACGAGATGATATAACGAGTATGACCTGGTGAAGAGACAGATATCA 531
 QY 516 TGACCCCTG---GGAAGAGCTGTGATGTGTTCATGCGGCTCTCTACATGAGGG 572
 DB 532 TGATCAGAACAGTAAGAGCGCGTCAATGCTATATCCATGGGGGATCTTACATGAGGG 591
 QY 573 GACCGAAACATGTCAGTGGCTCAGTCTGCTGCTATGTCATGCAACGTCATTTGTATGCCAC 632
 DB 592 CACCGCAACATGATGACGCGAGCATTTTGGCAAGCTACGGAACGTCATCGTATCAC 651
 QY 633 GCTCAACTACCGTCTGGGGTGTCTCGGTTTCTCAGACCGGGGACAGGCTGCAAAAG 692
 DB 652 CATTAACTACCGTCTGGGAATACTAGGGTTTTTAAGTACCGGTGACCCGGCAGCAAAAG 711
 QY 693 CAACTATGGGCTCTGACCCAGATCCAGGCGCTGCGCTCAGTGAAGAAACATCCGCCA 752
 DB 712 CAACTATGGGCTCTGATCAGATTCAAGCATGCGGTGGATTGAGAGAAATGTTGGAGC 771
 QY 753 CTTTGGGGCGACCCCGAGCGTATCAACATCTTTGTTGTTGCGGGGACGGGCTCTCTGCGT 812
 DB 772 CTTTGGCGGGGACCCCAAGAGAGTGAACCATCTTTGGCTCGGGGGCTGGGGCTCTCTGTGT 831
 QY 813 CAACCTTCTGATCTCTCCCAACCATTCAGAGGGCTGTTCCAGAGGCCATCCGCCAGAG 872
 DB 832 CAGCTTGTACCTGTGCCACTACTCAGAAAGTGTCTTCCAGAGGCCATCTTACAGAG 891
 QY 873 TGGCACCGCCATTTCCAGCTGGTCTGTCACTACAGCGCTCAAGTACACGCGGCTGTCT 932
 DB 892 CGGCACCGCCCTGTCCAGCTGGGCGAGTGAACCTACAGCGGCGCCAGTACACTCGGATATT 951
 QY 933 GGCAGCCAAAGTGGGCTGTGACCGAGAGGACAGTGTGAAGCTGTGGAGTGTCTGGCCG 992
 DB 952 GGCAGCAAGGTCGGCTGCAACATGTGGACACCCAGGACATGTTAGAAATGCTCGCGAA 1011

QY 993 GAAGCCCTCCGGAGTGTGTGACAGGACGTGACGCTGCGGCTACACATCCGCTT 1052
 Db 1012 CAAGAACTCAAGAGAGCTATCCAGCAGACCATACCCCGGCCACCTACACATAGCTT 1071
 QY 1053 TGGCCCGTGGTGGATGGGACAGTGGTCCCGGATGACCTGATCTCATGACAGAGG 1112
 Db 1072 CGGCCCGGTGATCGACGGCGAGCTCATCCAGAGACCCCGAGATCTGATGGAGCAGG 1131
 QY 1113 AGAATTCCTCAACTACACATGCTCATCGGCTCAACAGGGAGAGGGCTCAAGTTCTG 1172
 Db 1132 CGAGTTCTCTCAACTACACATGCTGCTGGCGCTCAACAGGGAGAGGGCTGAAGTTCTG 1191
 QY 1173 GGAGGACTCTCGAGAGACGAGAGCGGTGTGTGCGAGCGCTTTGACTTCACTGCTC 1232
 Db 1192 GGACGGGATCGTGATACAGAGACGGTGTGTGCGGACGATTTGACTTCTCCGTGTC 1251
 QY 1233 CAACCTTTGTGGACAACTGTATGGCTACCCGAGGCAAGGATGTGCTTCGGGAGACCAT 1292
 Db 1252 CAACCTCGTGGACAACTTTACGGCTACCTCTGAAGGMAAGACACTTTGCGGAGACTAT 1311
 QY 1293 CAAGTTTATGTACAGACTGGGCGGACCGGACAAATGGGGAATGCGCGCAAAACCTT 1352
 Db 1312 CAAGTTTCATGTACAGACTGGGCGGATAAGGAAACCCCGAGACGCGGGGAAACCTT 1371
 QY 1353 GCTGGCGCTCTTTACTGACCAACAAATGGGTGGCAGCTGTGGCCACTGCCAAGCTGA 1412
 Db 1372 GTTGGCTCTCTTTACTGACCAACAGTGGGTGGCCCGCGTGGCC---GCCACTGCA 1428
 QY 1413 CGCGACTACAGTCTCCGCTACTTTTACACTTCTACCACTGCGAGCGGAGGG 1472
 Db 1429 CGCGAGTACGGTCCCGCACTTCTATGCTTCTATCATCACTGCGCAAAAGCAAT 1488
 QY 1473 CGGCGCTGAGTGGCAGATCGGCGACGGGATGAACTGCCCTATGCTTTGGCGTGC 1532
 Db 1489 GAAGCCGAGTGGCAGATTCGGGCCCATGTGTATGAGTCCCTATGCTTCGGCATCC 1548
 QY 1533 CATGGTGGTGGCCACCGACCTCTTCCCTGTAACCTTCTCCAAAGTGAAGTCACTGCTAG 1592
 Db 1549 CATGATCGTCCACCGAGCTCTTCACTTGTAACTTTCCAAAGACGAGTCACTGCTAG 1608
 QY 1593 TGCGGTGATGACTGAGTGGACCAACTTCCGCAAGACTGGGAGACCCAAACAGCGGT 1652
 Db 1609 CGCGTGGTCACTGACTGAGTGGACCAACTTCCGCAAACTGGTATCCAAATCAACACT 1668
 QY 1653 GCGCAGATACCAAGTTCACTACACCAAGCCCAATCGCTTCGAGAGGTGTGGAG 1712
 Db 1669 TCCTCAGATACCAAGTTCACTACACCAAGCCCAATCGCTTCGAGAGGTGTGGAG 1728
 QY 1713 CAATTCACAGCAAGGAGAGAGTATCTGCATAGGCTGAAGCCACGGTGGCTGA 1772
 Db 1729 CAAGTATAATCCCAAGACCGAGCTCTATCTGCATATTTGGCTTGAACCCAGAGTGAGAG 1788
 QY 1773 CAACCTCGGCGCAACAGGTGGCTTCTGGCTGGAGCTGTCGCCCACTTCACAACT 1832
 Db 1789 TCACCTCGGCGCAACAGGTGGCTTCTGGTGGAACTCTGTTCCCTATTTGACAACTT 1848
 QY 1833 GCA-----CACGAGCTCTTCAACCAACCGCGCTGCTCCCTACGCCACGG 1883
 Db 1849 GAACGAGATATTCAGTATGTTTCAACCAACCAAGAGTTCTCCACAGACATGACATC 1908
 QY 1884 CTGGCGGCTGCTGCTCCCGGCTGGCGGCGGACAGCGCGGCGCGCGCGCTGCCAC 1943
 Db 1909 ATTTCCCTATGGCAGCGCGGATCTCCGCGCAAGATATGGCCCAACCAACCGCGCAG 1968
 QY 1944 CTTGCTCCCGAGCGGAGCGGAGC-----CGGGCCCAAGGCG 1982
 Db 1969 AATCACTCTCTGCCAATATCCCAACACTTAAGGACCTTCAAAACAGGGCTGAGAA 2028
 QY 1983 CTATGACCGTCTCCCGGAGCTACCGGAGTACTCCAGGAGTGAAGGTCAAGGTGCG 2042
 Db 2029 CAAACTGTCTCATTTGAACCAACAGATTTATTCACCGGAATTAAGTGTCACTTGC 2088
 QY 2043 CGTGGGTGCTCTCTCTCTCAACTCTGCGCTTGTGCTGCTCTACTACAAGCG 2102

RESULT 12

US-09-978-403A-374
 ; Sequence 374, Application US/09978403A

; Publication No. US20030050240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Kenneth J.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C17

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

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 QY 2103 GGACCGGCGGAGAGCTGGCGTTCAGGCGCTTAGCCACCTGGCGCTCAGGCTCTGG 2162
 Db 2149 GGACAAGAGGCGCCATGAGACTCAGAGGCGCCAGTCCCGAGAGAAACACCAAAATGA 2208
 QY 2163 CGTGCCTGGTGGGGGCGCCCTGCTCCCGCGCGGGCGGTGAGCTGCCACAGAGGAGGA 2222
 Db 2209 TATCGTCCATCATCCAGAACGAAGAGATCATGTCTCTGAGATGAAGCAGCTGGAAACGA 2268
 QY 2223 GCTGTGTGCTACTGCGAGCTGAAGCGGGTGGTGGCGTGGGGCGGACCTGCGCGAGGCTCT 2282
 Db 2269 TCACGAGTGTGAGTCTGTCGAG-----GCACAGGACACT 2304
 QY 2283 CGGCCCTGCTCCCGCGCGGACTACCTGGCGCTGCGCGGGCACCGGACGATGTGCC 2342
 Db 2305 GAGGCTCACCTGCGCGCGAGACTACCCCTCACGCTGCGCGCGTCCGAGATGACATCCC 2364
 QY 2343 TCTCTTGGCCCCGGGGCGCTGACCTGCTGCCAGTGGCGCTG 2385
 Db 2365 ACTTATGACGCCAAACACCATCATCATGATTTCCAAACACACTG 2407

;	PRIOR FILING DATE: 1998-04-15	
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;	PRIOR APPLICATION NUMBER: 60/085689	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085579	
;	PRIOR FILING DATE: 1998-05-15	

Query Match	36.4%; Score 912.2; DB 11; Length 3113;
Best Local Similarity	64.7%; Pred. No. 2.5e-206;
Matches 1503; Conservative	0; Mismatches 748; Indels 72; Gaps 7;
QY	108 CGCGCAGAGCGCTTCGCGGTGTGTGAACACGGCTACGGCGCAGGTGCGGCTGTGCGCGC 167
DB	112 CAGCCACACACAGTATCAAGTTGTCAACAATAATATGGCAAAATATCCGGGGCCTAAGAAC 171
QY	168 CGAGCTCAACACAGAGATCCTGGGCCCGCTGTGTCAGTTCTTTGGCGGTGCCCTACGCCAC 227
DB	172 ACCGTTATCCCAATAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCTC 231
QY	228 GCGGCCCTTGGCGCCCGCGCTTCAGCCGCTCAGCGCCTGAGGGCGCCGCTGTGTGGCGCGGGT 287
DB	232 ACCGCCCACTCGAGAGAGCGGGTTTACGCCGCCACAGAACCCCGCTCTCTCGACTGGCAT 291
QY	288 GGGCAAAGCCACACCCCTCGCGCCGCTGCCCGCAGAACTGTGCAG--GGGCGCTGCC 344
DB	292 CGAAATACTACTCAGTTTGTCTGTGTGTCGCCCCAGCACCTGGATGAGATCCTTACT 351
QY	345 GCGCATATGCTGCTGTGTGTTTACCAGCAACTTGGAGGCGCGCCACCTACGTGCA 404
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QY	405 GNAACAGAGCAGACTGCTGTGTACCTCAACCTCTACGTGCCACCGAGGACGCTCCGCT 464
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QY	465 CACAAAAAAGCTACAGAGCG-----ACGCTCAATCCGCCAGACACAGATATCCG 515
DB	472 CACAAGAAACCGCAGATGATATACGAGTATGACCGTGGTGAAGACGAAGATTTCA 531
QY	516 TGACCGTG---GGAAGAAGCCTGTGATGTCTTTTCCATGCGGCTCCTACATGAGGG 572
DB	532 TGATCAGAACACGTAAAGACCCGTCATGGTCTATATCCATCGGGGATCTTACATGGAGG 591
QY	573 GACCGGAACATGTTCCGATGGCTCAGTCTCGGCTGCTATGSCAACGTCATTGTAGCCAC 632
DB	592 CACCGGCAACATGATGACCGCAGCAATTTTGGCACTACGAAACGTCATCGTGATCAC 651
QY	633 GCTCAACTACCGTCTTGGGGTGCTCGGTTTTCTCAGCACCGGGACAGGCTGCAAAAGG 692
DB	652 CATTAACCTACCGTCTGGGATCTAGGGTTTTTAAGTACCGGTGACCGGACGACAAAGG 711
QY	693 CAACTATGGGCTCCTGGACAGATCCAGGCCCTGCGCTCGCTCAGTGA AAAACATCGOCCA 752
DB	712 CAACTATGGGCTCCTGGATCAGATTCAAGCACTCGCGTGGATTGAGGAATGTGGGAGC 771
QY	753 CTTTGGGGGCACCCCGAGGGTATCACCATCTTTTGGTTCCGGGCGAGGGGCTCCTCGGT 812
DB	772 CTTTGGCGGGACCCCAAGAGAGTGACATCTTTTGGCTCGGGGGCTGGGGGCTCCTGTGT 831
QY	813 CAACTTCTGTATCTCTCCACCAATCAGAAAGGCTGTTCCAGAAAGGCCATCGGCCAGAG 872
DB	832 CAGCTGTGTACCTGTCTCCACTACTCAGAAAGTCTCTTCCAGAGGCCATCATTTAGAG 891
QY	873 TGGCACCGCCATTTCCAGCTGGTGTGTCAACTACAGCCGCTCAAGTACAACGCGCTGCT 932
DB	892 CGGCACCGCCCTCTCCAGCTGGGCAGTGAATACACAGCGCGGCAAGTACACTCGGATATT 951
QY	933 GGCACGCCAAGTGGGCTGTGACCGAGAGGACAGTGTGTGAAGCTGTGGAGTGTCTGCGCG 992
DB	952 GGCACAGAAGTGCCTGCAACATGCTGGACACCAACCGACATGGTAGAATGCCTGGGAA 1011
QY	993 GAAGCCCTCCCGGAGGTGTGGACAGGACGTCGAGCCTGCCGCTACCAATCCGCTT 1052

Db 2089 CGTCGGGGCGTCGCTCTCTTCTCAACATCTTAGCTTTTGGGGCGGTGTAACAACAAA 2148
QY 2103 GGACCGGGCAGGAGCTGGGTGACGGCGGCTTAGCCACCTGGCGGCTCAGGCTCTGG 2162
Db 2149 GGACAAGAGGGCCATCAGAGCTCAGACGGCGCCCGAGTCCCGAGAGAAACACCAATGA 2208
QY 2163 CGTCCTGTGGGGGGCCCCCTGCTCCCGCGGGCGGTGAGTGGCCACAGAGAGGA 2222
Db 2209 TATCGCTCATCATCAGAACGAAGAGATCATGTCTCTGCAGATGAAGCAGCTGGAACACGA 2268
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QY 2283 GCGCCCTGCTGCGCGCGCGGACATACACCTGGCGCTGGCGCGGACCGGACGATGTGCC 2342
Db 2305 GAGGCTCACCTGCGCGCGGACATACACCTCAGCTGCGCGGTGCGCAGATGACATGCC 2364
QY 2343 TCTCTGCGCGCGCGGCGGCTGACCTGCTGCCAGTGGCGCTG 2385
Db 2365 ACTTATGACGCAACACCATCACCATGATTCAAACACACTG 2407

RESULT 13

US-09-978-564A-374

; Sequence 374, Application US/0978564A

; Publication No US20030050241A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C25
; CURRENT APPLICATION NUMBER: US/09/978,564A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
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; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 Query Match 36.4%; Score 912.2; DB 11; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2.5e-206;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;
 QY 108 CGCGGAGAGCGCTTCCCGGTGGTGAACACACGCGCTACGCGGCGAGTGC CGGGTGTGGCGG 167
 Db 112 CAGCCAGACAGTATCCAGTTGTCAACACAAATATGCAAAATCCGGGGCTTAAGAAC 171
 QY 168 CGAGCTCAACAGAGATCTGGGCGCGGTTCAGCGCGCTCAGCGCGCGCTCGTGGCCCGGGGT 227
 Db 172 ACCGTTACCCAAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCGCTATGCGCTC 231
 QY 228 GCGGCGCTTGGCGCGCGCTTCCAGCGCGCTCAGCGCGCGCGCTCGTGGCCCGGGGT 287
 Db 232 ACCCGCCACTGAGAGAGAGCGGGTTTCAGCGCGCGCGAGAACCGCCGCTCTCTGGACTGGCAT 291
 QY 288 GCGCAACGCCACCAACCTGCGCGCGCGCTGCGCGCGAGAACCTGCAAG---GGCGCTGCC 344
 Db 292 CCGAAATACTACTCACTGTTGCTGTGTCGCCCGCAGCACCTGGATGAGAGATCCTTACT 351
 QY 345 CGCCATCATGTCGCTGTGTGTTTCAACGACAACTTGGAGGCGCGCGCGCTAGTGCA 404
 Db 352 GCATGACATGTCGCCCATCTGGTTTACCGCCAAATTTGGATACTTTTGATGACCTATGTTCA 411
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 Db 412 AGATCAAAATGAAGACTGCCITTTACTTAAACATCTACCTGCGCCACCGAAGATGGAGCAA 471
 QY 465 CACAAAAAAGCTGACGAGGCG-----ACGCTCAATCGCCGACACACAGATATCGG 515
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 QY 516 TGACCCCTG---GGAAGAAAGCTGTGATGCTGTTTCTCCATGCGCGCTCTACATGGAGGG 572
 Db 532 TGATCAGACAGTAGAAGCGCGCTCATGCTTATATCATGGGGATCTTACATGGAGGG 591
 QY 573 GACCGGAAACATGTTTGATGGCTCAGTCTCGCTGCTTATGGCAACGTCATTTAGCCAC 632
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 QY 633 GCTCACTACCGTCTTGGGGTGTCTCGGTTTCTCAGCACCGGGGACGAGGCTGCAAAAGG 692
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 QY 693 CAACCTATGGGCTCTCGGACCAAGATCCAGGCGCTCGCTGGCTCAGTGAACATCGCCCA 752
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 QY 753 CTTTGGGGGACCGCGAGCGTATCACCATTTTGGTTTCGGGGGAGGGGCTCTCGGT 812
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 QY 993 GAAGCCCTCCCGGAGCTGGTGGACCGAGCGTGCAGCGCTCCCGCTACCACTCGGCTT 1052

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2 PRIOR FILING DATE: 1998-03-11
3 PRIOR APPLICATION NUMBER: 60/077649
4 PRIOR FILING DATE: 1998-03-11
5 PRIOR APPLICATION NUMBER: 60/077791
6 PRIOR FILING DATE: 1998-03-12
7 PRIOR APPLICATION NUMBER: 60/078004
8 PRIOR FILING DATE: 1998-03-13
9 PRIOR APPLICATION NUMBER: 60/078886
10 PRIOR FILING DATE: 1998-03-20
11 PRIOR APPLICATION NUMBER: 60/078936
12 PRIOR FILING DATE: 1998-03-20
13 PRIOR APPLICATION NUMBER: 60/078910
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24 PRIOR FILING DATE: 1998-03-27
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;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 36.4%; Score 912.2; DB 11; Length 3113;
Best Local Similarity 64.7%; Pred. No. 2.5e-206;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGCGAGGAGCGCTTCCGCGTGTGACACGCGCTACGGCGGAGTGC GGCGGTGCGGG 167
DB 112 CACCGAAGACAGATATCCAGTTGTCAACAAATATGCGAAATCCGGGGCTTAAGAAC 171
QY 168 CGAGCTCAACACAGAGATCCTGGGCGCGCTCGTGCAAGTTCTTGGCGTCCCTACGCCAC 227
DB 172 ACCGTTACCCAAATAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCGCTC 231
QY 228 GC CGCGCGCTGGGCGCGCGCTTCAGCGCGCTGAGCGCGCGCGCTCGTGCGCGCGGT 287
DB 232 ACCCGCCACTGGAGAGAGGGGGTTTCAGCGCGCGCGCGCGCGCGCTCGTGCGCGGT 291
QY 288 GCGCAAGCGCCACACCGCTCGCGCGCGCTGCGCGCGCGCGCGCGCGCTGCGCGCGCTGCG 344
DB 292 CCGAAATACTACTCAGTTGCTGCTGTGTCGCCCGCGCGCGCGCGCGCTGCGCGCGCTGCG 351
QY 345 CGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
DB 352 GCATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
QY 405 GAACACAGAGGAGGAGTGCCTGTACCTCAACCTTCTACGTCGCCCGCGCGCGCGCGCGCTGCG 464
DB 412 AGATCAAAATGAGACTGCTTCTTAAACATCTACGTCGCCCGCGCGCGCGCGCGCTGCG 471
QY 465 CACAAAAAAAGCTGAAGAGCGG-----AGCTCAATCCCGCGCGCGCGCGCGCGCGCGCG 515
DB 472 CACAAAGAAAAAGCGAGATGATATAAGAGTATGACCGTGTGTGAGAGCAAGATATTCA 531
QY 516 TGACCTGTG---GGAAGAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
DB 532 TGATCAGAACAGTAAAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
QY 573 GACCGGAAACATGTTGATGGCTCAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
DB 592 CACCGGCAACATGATTGACCGGAGCATTTTGGCAAGCTACGGAACGTCATCGTATCAC 651
QY 633 GCTCAACTACGCTTGGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692
DB 652 CATTAATACCGTCTGGGAATCTAGGGTTTAAAGTACCGGTGACCGGCGAGCAAAAGG 711
QY 693 CAACATGGGCTCTGACACAGATCCAGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
DB 712 CAACATGGGCTCTGATCAGATTCAAGCATGCGGTGGAATGAGGAGATGTGGAGC 771
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QY 933 GGCAGCAAGGTGGCTGTGACCGAGAGGAGTGTGAGCTGTGAGTGTGCTGCGCG 992
DB 952 GGCAGCAAGGTGGCTGTGACCGAGAGGAGTGTGAGCTGTGAGTGTGCTGCGGAA 1011
QY 993 GAAGCGCTCCCGGAGCTGGTGGACGAGGAGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 1052
DB 1012 CAAGAACTACAGAGGCTCATCCAGAGAGGACCATCACCGCGCGCGCGCGCGCGCGCGCGCGCT 1071

QY 1053 TGGCCCGTGTGTGATGGCGACGTGGTCCCGGATGACCTCTGAGATCCTCTAGCAGGG 1112
DB 1072 CGGCGCGGTGATCGAGCGGACGTATCCCGAGACGACCCCGAGATCTGATGAGCAAG 1131
QY 1113 AGAATTCCTCAACTACGACATGCTCATCGGCGTCAACCGAGGAGGGCGCTCAAGTCCGT 1172
DB 1132 CGAGTTCTCAACTACGACATCATGCTGGGCGTCAACCAAGGAGGCGCTGAGTTCTG 1191
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DB 1549 CATGATCGGTCCCGACCGAGCTCTTCAAGTGTAACTTTTCCAGAAACAGCTCATGCTCAG 1608
QY 1593 TGCGGTGTGATGACCTACTGGAACCAACTTCGCGCAAGACTGGGAGACCCCAACAGCGGT 1652
DB 1609 CGCGTGTGATGACCTACTGGAAGCACTTCGCGCAAACTGGTGTATCCAAATCAACAGT 1668
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QY 1833 GCA-----CAGGAGCTCTTCAACACCAAGCTGCGCTGCTCCCTACGCCAGCG 1883
DB 1849 GAACGAGATATTCAGTATGTTTCAACCAAGGTTCTTCCACAGCATGATC 1908
QY 1884 CTGCGCGCTGCTGCG 1943
DB 1909 ATTTCCCTATGGCACCGCGGATCTCCGCGCAAGATATGCGCAACCAACCAACCGCGCG 1968
QY 1944 CTTGCTCCCGAGCG 1982
DB 1969 AATCACTCTGCGCAACCAATCCCAACACTCTAAGGACCTTCAAAACAGAGGCTGAGGA 2028
QY 1983 CTATGACCGCTTCCCGCGGAGCTCACGGGACTTCTCCAGCGAGCTGAGCGTCAACCGTGGC 2042
DB 2029 CACAACTGTCTCTATTGAACCAACAGAGATTATTCACCGAATTAAGTGTACCAATTGC 2088
QY 2043 CGTGGGTGCTGCT 2102
DB 2089 CGTGGGGCGTGGCT 2148

Qy	2103	GGACCGCGCGCAGAGCTGCGGTGCAGCGCGCTTAGCCCACTGGCGGCTCAGGCTCTGG	2162
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Qy	2163	CGTGCCTGTGGGGGCCCCCTGTCTCCCGCGCGGGCGGTGAGTGCACACAGAGAGGA	2222
Db	2209	TATCGCTCATCCAGAACGAAGATCATGTCTCTGCATGAGCAGGTGGAAACGA	2268
Qy	2223	GCTGGTGTCTACTGACGTGAAGCGGGGTGTGGCTGGCGGGAACCTCCGAGGCTCT	2282
Db	2269	TCACGAGTGTGAGTCGTGCGAG-----GACACGACACACT	2304
Qy	2283	GCSCCTTGCTGCCCGCCGACTACACCTGGCCCTGCGCGGGGCGACCGGACAGTGGCC	2342
Db	2305	GAGGCTCACTGCCCGCCAGACTACACCCCTCAAGTGGCGCGGTGCGGACATGACATCCC	2364
Qy	2343	TCCTTTGGCCCCCGGGGCCCTGACCCCTGTGCCCCAGTGGCCTG	2385
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RESULT 15

US-09-981-915A-374
; Sequence 374, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630Pic12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 Query Match 36.4%; Score 912.2; DB 11; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2.5e-206;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;
 QY 108 CGGCGAGGAGCGCTTCCGGTGGTGAACAGCGCTACGGCGAGTGGCGCGTGTGGCGG 167
 Db 112 CAGCAGACAGTATCCAGTTGTCAACACAAATATGGCAAAATCCGGGCTTAAGAC 171
 QY 168 CGAGCTCAACAAACAGATCCCTGGGCCCGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 227
 Db 172 ACCGTTACCAATAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCTC 231
 QY 228 CGCGCCCTGGCGCCCGCTTCCAGCGCTGAGCGCGCTGAGCGCGCGCTGCTGGCGCGCGT 287
 Db 232 ACCCCCACTGGAGAGGCGGTTCAGCCCCAGAACCCCGCTCTCTCTGGATGGCAT 291
 QY 288 CGCAACGCCACCACTCCCTGGCGCCCGCTGCGCCCGCAGAACTGTCACG---GGGCGTGC 344
 Db 292 CGAAATACTACTCAGTTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 351
 QY 345 CGCATCATGCTGCTGT 404
 Db 352 GCATGACATGCTGCCCCATCTGTTTACGCCCAATTTGGATACTTTGTATGACCTATGTTC 411
 QY 405 GAACCAAGCGAGGAGTGCCTGTACTCAACTCACTGTGCCCCACCGAGGACGCTCGCT 464
 Db 412 AGATCAAAATGAGACTGCCCTTACTTAAACATCTACGTGCCCGGAGAGTGGAGCAA 471
 QY 465 CACAAAAAAGCTGACGAGGCGG-----ACGCTCAATCCGCGCAGACACAGATATCCG 515
 Db 472 CACAAAGAAAAACCGAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGATATTC 531
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Search completed: February 19, 2004, 11:54:13
Job time : 824.794 secs

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RESULT 2
US-09-491-356C-6
; Sequence 6, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 4436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: n is not determined
US-09-491-356C-6

Query Match 34.7%; Score 871; DB 4; Length 4436;
Best Local Similarity 67.6%; Pred. No. 8.5e-153;
Matches 1294; Conservative 0; Mismatches 565; Indels 54; Gaps 3;

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 ; Sequence 4, Application US/09491356C
 ; Patent No. 6566061
 ; GENERAL INFORMATION:
 ; APPLICANT: Philibert, Robert A.
 ; APPLICANT: Ginns, Edward I.
 ; APPLICANT: Delisi, Lynn
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
 ; FILE REFERENCE: 9465.6US11
 ; CURRENT APPLICATION NUMBER: US/09/491,356C
 ; CURRENT FILING DATE: 2000-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US99/09365
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: 60/083,465
 ; PRIOR FILING DATE: 1998-04-29
 ; NUMBER OF SEQ ID NOS: 24
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,881
; FILING DATE: June 5, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Blair Hughes
; REGISTRATION NUMBER: 32,901
; REFERENCE/DOCKET NUMBER: 89,852-K
; TELEPHONE: 312/913-0001
; TELEFAX: 312/913-0002
; TELEX: 910/221-5317
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; QY 1181 CTGCAGAGCGGAGCGGTGTGTCTGCCAGC 1212
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; RESULT 10
; US-08-445-050-8
; Sequence 8, Application US/08445050
; Patent No. 5763739
; GENERAL INFORMATION:
; APPLICANT: Blasberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Hernell, Olle
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stroemqvist, Mats
; APPLICANT: Toernell, Jan
; TITLE OF INVENTION: No. 5763739el Polypeptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,050
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,691
; FILING DATE:
; APPLICATION NUMBER: SE 9300686-4
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300722-7
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner Ph.D., Richard J
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2184 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: mammary gland
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 82..2088
; OTHER INFORMATION: /label= Variant_1
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 151..2085
; NAME/KEY: repeat_region
; LOCATION: 1756..2052
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 1756..1788
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; LOCATION: 1855..1887
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; NAME/KEY: repeat_unit
; LOCATION: 1888..1920
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; LOCATION: 1921..1953
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; US-08-445-050-8

Query Match      5.3%; Score 132.4; DB 1; Length 2184;
Best Local Similarity 48.8%; Pred.No. 3.5e-16;
Matches 528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;

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QY 518 ACCTGTATCAGCGCGAGGAGATCGCCACACGCGGAAAGCTCATCGTGTCACTTCAACT 577
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QY 761 GGAACCCGAGGATACCACTTTTGGTTCGGGGGAGGGGCTTCCTGCGTCAACCTTC 820
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QY 698 GGAACCCCAACAATCAGCTCTTCGGGGAGTCTGCTGGAGTGCACGCTCTCTGTC 757
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QY 758 AGACCTCTCTCCCTTACAAAGAGGCGCTCATCCGGGAGCCATCAGCCAGAGCGCGTGG 817
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QY 881 CCATTTCCAGTGTGTCGTCAACTACCGCCGCTCAAGTACACGGGCTGTGTCGAGCCA 940
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938 CCGGAGCCCTGACGCTGGGCTATAAGGTCCGCTGGCAGGCTGGAGTATCCCATCTGCG 997
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1238 TTGTGACAACTGTATGGCTATCCCGGAAGCAAGATGTCTTCGGG-----AGACCA 1291
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1298 CTGTGTGGACTTTGAGACCGATGTCTTCTCTGTGTCGCCACCGAGATTGCCCTAGCCC 1357
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1583 TCATGCTCAGTCCGCTGCTATGACCTACTGACCACTTCCGCAAGCTTGGGGAGCCCA 1642
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1643 AC 1644
1583 AC 1584

RESULT 11
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; Sequence 8, Application US/08204691
; Patent No. 5827683
; GENERAL INFORMATION:
; APPLICANT: Blasekberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Hernell, Olle
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stromqvist, Mats
; APPLICANT: Toernell, Jan
; TITLE OF INVENTION: No. 5827683el Polypeptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas

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CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,691
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: SE 9300686-4
APPLICATION NUMBER: 01-MAR-1993
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300722-7
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-850
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2184 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: 82..2088
OTHER INFORMATION: /label= Variant_T
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 151..2085
FEATURE:
NAME/KEY: repeat region
LOCATION: 1756..2052
FEATURE:
NAME/KEY: repeat unit
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NAME/KEY: repeat unit
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FEATURE:
NAME/KEY: repeat unit
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NAME/KEY: repeat unit
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NAME/KEY: repeat unit
LOCATION: 2020..2052
US-08-204-691-8
Query Match
5.3%; Score 132.4; DB 1; Length 2184;
Best Local Similarity 48.8%; Pred. No. 3 5e-16;
Matches 528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;
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Db |||||
Qy 518 ACCTGTATGACGGCGAGGAGATCCACACACGCGAAACGTCATCGTGGTCACTTCACT 577
Db |||||
Qy 641 ACCGTCTTGGGGTCTCGTCTTCTCAGCACCGCGGACAGGCTGCAAAAGGCAACTATG 700
Db |||||
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Db |||||
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Db |||||
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Qy 1406 AGGTGCAACGCGGACTACCACTCTCCC---GTCTACTTTTACACCTTCTACCACTGCC 1462
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Qy 1358 AGCACAGAGCCAATGCCAAGAGTGCACAGACCTACGCTACCTGTCTTCCCATCTCTC 1417
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 QY 1643 AC 1644
 Db 1583 AC 1584

RESULT 12
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 ; Sequence 31, Application US/09347878C
 ; Patent No. 6376210
 ; GENERAL INFORMATION:
 ; APPLICANT: Yuan, Chong
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
 ; FILE REFERENCE: 25885-1651
 ; CURRENT APPLICATION NUMBER: US/09/347,878C
 ; CURRENT FILING DATE: 1999-07-06
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 31
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 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
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 ; OTHER INFORMATION: Human cholesterol esterase cDNA
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: M85201/GenBank
 ; US-09-347-878-31

Query Match 5.3%; Score 132.4; DB 4; Length 2344;
 Best Local Similarity 48.8%; Pred. No. 3.5e-16;
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 Db 685 AGACCTCTCCCGCTTACAAAGAGGCTCATCCGCGAGCCATCAGCCAGAGCGCGTGG 744
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 Db 805 AGGTGGGTTCCTCTGGGTGATGCGCGCAGGATGCCAGTGTCTGAAGTACTGATC 864
 QY 1001 CCGGGAGCT---GGTGGACAGGAGCTGCAGCTGCCCGCTACCACTCGCCTTTGGG 1057
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QY 1058 CCGTGTGGATGCGGACGTGGTCCCGGATGACCCCTGAGATCCTCATGACGAGGAGAAAT 1117
 Db 925 ACTATGTGGGCTTCGTCCTGTCATTTGATGGAGACTTCATCCCGCTGACCCGATCAACC 984
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RESULT 13
 US-08-445-050-1
 ; Sequence 1, Application US/08445050
 ; Patent No. 5763739
 ; GENERAL INFORMATION:
 ; APPLICANT: Blaeckberg, Lars
 ; APPLICANT: Edlund, Michael
 ; APPLICANT: Hansson, Lennart
 ; APPLICANT: Hernel, Olle
 ; APPLICANT: Lundberg, Lennart
 ; APPLICANT: Stromqvist, Mats
 ; APPLICANT: Toernell, Jan
 ; TITLE OF INVENTION: No. 5763739el Polypeptides
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: White & Case
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States
 ; ZIP: 10036-2787
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/445,050

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; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,691
; FILING DATE:
; APPLICATION NUMBER: SE 9300686-4
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA: SE 9300722-7
; APPLICATION NUMBER: SE 9300722-7
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner Ph.D., Richard J
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: mammary gland
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 82..2319
; OTHER INFORMATION: /product= "bile-salt-stimulated
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; NAME/KEY: exon
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; LOCATION: 2251..2283
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; Query Match 5.3%; Score 132.4; DB 1; Length 2428;
; Best Local Similarity 48.8%; Pred. No. 3.6e-16;
; Matches 528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;
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Qy 641 ACCGTCTTGGGGTGCTCGGTTTCTCAGCACCGGGGACAGGCTGCAGAAAGGCAACTATG 700
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Qy 701 GGCTCCTGACCGATCCAGSCCTGCGTGGCTCAGTGAACATGCCCACTTTGGGG 760
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Qy 878 AGGTGGGTGGCTGTGGGTGATGCCGCCAGGATGGCCAGTGTCTGAAGTTACTGATC 937
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Qy 938 CCCGAGCCCTGACGCTGGCCTATAAGGTGCGCTGGCAGGCCCTGGAGTAGCCCCATGCTGC 997
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RESULT 14

US-08-204-691-1
; Sequence 1, Application US/08204691
; Patent No. 5827683
; GENERAL INFORMATION:
; APPLICANT: Blaeckberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Harnell, Olie
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stroemqvist, Mats
; TITLE OF INVENTION: No. 5827693el Polypeptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,691
; FILING DATE:
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300686-4
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA: SE 9300722-7
; APPLICATION NUMBER: SE 9300722-7
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner Ph.D., Richard J
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2428 base pairs
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: mammary gland
; FEATURE:
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; LOCATION: 82..2319
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; FEATURE:

Db 1583 AC 1584

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Job time : 135.731 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 16:42:38 ; Search time 605.415 Seconds
(without alignments)
1182.718 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2508	100.0	2508	24	Human carboxyleste
2	2508	100.0	4667	24	Human carboxyleste
3	2506.4	99.9	4622	24	Novel human coding
4	2500	99.7	4763	24	Human drug metabol
5	2443.6	97.4	2523	22	Human MBSF4 polype
6	2265.4	90.3	2663	24	Human drug metabol
7	1013	40.4	2865	24	3 isoform protein
8	1010	40.3	4233	21	cDNA sequence of h

9	930.4	37.1	4975	23	AA574457	DNA encoding novel
10	924	36.8	924	21	AA574457	Human ORF ORF498
11	912.2	36.4	3112	21	AA574457	Human PRO701 nucle
12	912.2	36.4	3113	20	AA574457	Human PRO701 nucle
13	912.2	36.4	3113	21	AA574457	Human PRO701 (UNQ3
14	912.2	36.4	3113	25	ABX92581	cDNA encoding huma
15	886.2	35.3	3454	25	ABX92581	CDNA encoding huma
16	886.2	35.3	3751	25	ABX92581	CDNA encoding huma
17	871	34.7	4436	21	AA574457	CDNA sequence of h
18	870.2	34.7	3502	24	ABA97533	Human neurotrophin
19	751.8	30.0	4365	25	ABX92581	CDNA encoding novel
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29	486.8	19.4	856	22	AAH54533	Human cDNA clone (
30	455.8	18.2	1792	22	AA574457	DNA encoding novel
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42	351	14.0	789	22	AA196143	Human neuroblastom
43	301.6	12.0	704	22	AAK91871	Human cDNA 5'-end
44	301.6	12.0	704	22	AAK91871	Human cDNA clone r
45	165.4	6.6	2087	24	AA24096	Human carboxyleste

ALIGNMENTS

RESULT 1
ABA95200
ID ABA95200 standard; cDNA; 2508 BP.
XX ABA95200;
XX ABA95200;
XX 10-JUN-2002 (first entry)
DT Human carboxylesterase family member, 33410 coding sequence.
DE Carboxylesterase; 33410; cytostatic; cardiant; dermatological; human;
KW antidiabetic; antirheumatic; antiarthritic; antiarrhythmic; vasotropic;
KW vulnary; neuroprotective; antiinflammatory; antitumor; antidiabetic;
KW antiallergic; antiviral; hepatotropic; nephrotropic; anti-HIV; gene;
KW aniparkinsonian; tuberculostatic; hypotensive; antithrombotic;
KW neurotropic; antitense therapy; angiogenesis; gene therapy; ss.
XX Homo sapiens.
XX

Key Key Location/Qualifiers
CDS 1..2508
FT /product= "33410 polypeptide"
FT

XX WO200216616-A2.
XX
XX 28-FEB-2002.
XX
XX 21-AUG-2001; 2001WO-US26091.
XX
XX 21-AUG-2000; 2000US-226774P.

XX (MILL-) MILLENNIUM PHARM INC.
 XX Curtis RAJ;
 XX WPI; 2002-257916/30.
 XX P-PSDB; ABB07675.
 XX
 PT New carboxylesterase nucleic acid 33410, useful for the treatment and
 diagnosis of immune, cardiovascular, reproductive and cancerous
 disorders -
 XX
 PS Claim 1; Page 108-110; 123pp; English.
 XX
 CC The invention provides a novel carboxylesterase family member, designated
 CC 33410. Compounds that binds to or modulate the activity or expression of
 CC 33410, are useful for treating or preventing a disorder such as cellular
 CC proliferative or differentiative, neural, cardiovascular, prostatic, skin
 CC brain and skeletal muscular disorders, protein-protein interaction
 CC disorders, signal transduction disorders, immune (e.g. diabetes and
 CC rheumatoid arthritis), reproductive, cardiovascular (e.g. hypertension,
 CC atherosclerosis, coronary artery disease, arrhythmia, ischemic heart
 CC disease and angina pectoris), vascular disorders (e.g. varicose veins,
 CC Wegeners granulomatosis and wound healing) or cancerous disorders,
 CC multiple sclerosis, Crohn's disease, ulcers, asthma, allergy, infection,
 CC kidney disease (glomerulonephritis), idiopathic thrombocytopenic purpura,
 CC hepatitis, tuberculosis, human immunodeficiency virus, Alzheimer's and
 CC Parkinson's. The 33410 polynucleotide and polypeptide are useful for
 CC diagnosis of a predisposition to a disorder, for evaluating the efficacy
 CC of a therapeutic or prophylactic disorder, for chromosome mapping, as
 CC immunogens, for drug screening, for the detection of mutations in the
 CC gene and for tissue typing. The present sequence represents the coding
 CC sequence of the human carboxylesterase family member, 33410.
 XX
 SQ Sequence 2508 BP; 425 A; 906 C; 751 G; 426 T; 0 other;
 Query Match 100.0%; Score 2508; DB 24; Length 2508;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	901	AACCTACAGCGCTCAAGTACACGCGCTCTGSCAGCAAGGTGGGTGTGACCGAG	960
Db	941	AACCTACAGCGCTCAAGTACACGCGCTCTGSCAGCAAGGTGGGTGTGACCGAG	1000
Qy	961	GACAGTCTGAAGCTGTGGAGTGTCTGCGCGGAAGCCCTCCCGGAGCTGTGGACCA	1020

DB	1001	GACAGTCTGAAGCTGTGGAGTGTCTGCGCCGGGAAGCCCTCCCGGAGCTGGTGGACAG	1080
QY	1021	GACGTGCAGCCTGCCCGCTACCAATCGCCTTTTGGGCCCTGTGTGGATGGCGACGTGGTC	1080
DB	1061	GACGTGCAGCCTGCCCGCTACCAATCGCCTTTTGGGCCCTGTGTGGATGGCGACGTGGTC	1120
QY	1081	CCCGATGACCCCTGAGATCTTCATGCAAGCAGGGAGAAATTCCTCAACTACGACATGCTCATC	1140
DB	1121	CCCGATGACCCCTGAGATCTTCATGCAAGCAGGGAGAAATTCCTCAACTACGACATGCTCATC	1180

1141 GCGCTCAACCAAGGAGAGGSCCTCAAGTTCTGFGAGGACTCTGCAGAGAGCGAGCGGT 1200
 1181 GCGCTCAACCAAGGAGAGGSCCTCAAGTTCTGFGAGGACTCTGCAGAGAGCGAGCGGT 1240
 1201 GTGCTCGCAGCGCTTTGACTTCACTGCTCCAACTTTGGAACAACCTGTATGGCTAC 1260
 1241 GTGCTCGCAGCGCTTTGACTTCACTGCTCCAACTTTGGAACAACCTGTATGGCTAC 1300
 1261 CCGAAGGCAAGGATGTGCTTCGGAGACCAATCAAGTTTATGTACACAGCTGGGCGGAC 1320
 1301 CCGAAGGCAAGGATGTGCTTCGGAGACCAATCAAGTTTATGTACACAGCTGGGCGGAC 1360
 1321 CCGGCAATGGGCAATGGCGCGCAAAACCTGCTGGCGCTTTTACTGACCAACAATGG 1380
 1361 CCGGCAATGGGCAATGGCGCGCAAAACCTGCTGGCGCTTTTACTGACCAACAATGG 1420
 1381 GTGGCACCAGCTGTGGCCACTGCCAAGCTGCACGCCGACTACCACTCTCCCGTCTACTTT 1440
 1421 GTGGCACCAGCTGTGGCCACTGCCAAGCTGCACGCCGACTACCACTCTCCCGTCTACTTT 1480
 1441 TACACTTCTACCACTGCCAGCGGAGGCGCGGCTGAGTGGGCGAGATGGGCGGAC 1500
 1481 TACACTTCTACCACTGCCAGCGGAGGCGCGGCTGAGTGGGCGAGATGGGCGGAC 1540
 1501 GGGGATGAAGTCCCTATGTCTTTGGCGTGCCATGGTGGGTGCCACCGACTCTTCCCC 1560
 1541 GGGGATGAAGTCCCTATGTCTTTGGCGTGCCATGGTGGGTGCCACCGACTCTTCCCC 1600
 1561 TGTAACTTCTCAAGATGACGTATGCTCATGTGCGGTGGTCACTGACCTACTGGACCAAC 1620
 1601 TGTAACTTCTCAAGATGACGTATGCTCATGTGCGGTGGTCACTGACCTACTGGACCAAC 1660
 1621 TTGCGCAAGCTGGGAGCCCAACAGCGCGGTGGCGGAGGATACCAAGTTCATCCACAC 1680
 1661 TTGCGCAAGCTGGGAGCCCAACAGCGCGGTGGCGGAGGATACCAAGTTCATCCACAC 1720
 1681 AAGCCCAATCGCTTCGAGGAGGTGTGTGGAGCAAAATTCACACAGGAGGAGACAGTAT 1740
 1721 AAGCCCAATCGCTTCGAGGAGGTGTGTGGAGCAAAATTCACACAGGAGGAGACAGTAT 1780
 1741 CTGCACATAGCTGAAGCCAGCGGTGGTGACAACTACCGGCGCAACAGGTGGCTTC 1800
 1781 CTGCACATAGCTGAAGCCAGCGGTGGTGACAACTACCGGCGCAACAGGTGGCTTC 1840
 1801 TGGCTGGAGCTCGTCCGCCACTGTCAACACCTGCACACGAGCTCTTCAACACACCAACG 1860
 1841 TGGCTGGAGCTCGTCCGCCACTGTCAACACCTGCACACGAGCTCTTCAACACACCAACG 1900
 1861 GCGCTGCTCCCTAGCCACGCGGTGGCGGCTCGTCCCGCTGGCGCCCGCGGCA 1920
 1901 GCGCTGCTCCCTAGCCACGCGGTGGCGGCTCGTCCCGCTGGCGCCCGCGGCA 1960
 1921 GCGCGGCGCGCGCTGCGCAGCTGCTCCGAGCGCGGCGGCGGCGGCGGCGGCGG 1980
 1961 GCGCGGCGCGCGCTGCGCAGCTGCTCCGAGCGCGGCGGCGGCGGCGGCGGCGG 2020
 1981 GCGTATGACCGCTTCCCGGCGGACTCAAGGAGTCTTCAAGGAGCTGAGCGTCAACCGTG 2040
 2021 GCGTATGACCGCTTCCCGGCGGACTCAAGGAGTCTTCAAGGAGCTGAGCGTCAACCGTG 2080
 2041 GCGGTGGGTGCTCCCTCTCTCTCAATCTGCGCTTGGCTGGCTCTACTACAAG 2100
 2081 GCGGTGGGTGCTCCCTCTCTCTCAATCTGCGCTTGGCTGGCTCTACTACAAG 2140
 2101 CCGGACCGGCGGAGAGCTGCGGTGACGAGCGGCTTAGGCCACCTGGCGGCTCAGGCTCT 2160
 2141 CCGGACCGGCGGAGAGCTGCGGTGACGAGCGGCTTAGGCCACCTGGCGGCTCAGGCTCT 2200
 2161 GCGGTGCTGCTGGGGGCGGCTGCTTCCCGCGGCGGCGGCTGAGTGCACACAGAGAG 2220
 2201 GCGGTGCTGCTGGGGGCGGCTGCTTCCCGCGGCGGCGGCTGAGTGCACACAGAGAG 2260

2221 GAGCTGTTCACTGCTGAGCTGAAGCGGGTGTGCGTTCGGGCGGACCTGCGGAGGT 2280
 2261 GAGCTGTTCACTGCTGAGCTGAAGCGGGTGTGCGTTCGGGCGGACCTGCGGAGGT 2320
 2281 CTGCGCCCTGCTGCTGCGGCGGCTGAGCTACCTGCGGCTGCGGCGGACCGGACGATGTG 2340
 2321 CTGCGCCCTGCTGCTGCGGCGGCTGAGCTACCTGCGGCTGCGGCGGACCGGACGATGTG 2380
 2341 CTCTCTTTGGCCCCCGGGCCCTGACCTGCTGCTGCGGCTGCGGCGGACCGGACCGG 2400
 2381 CTCTCTTTGGCCCCCGGGCCCTGAGCTGCTGCTGCGGCTGCGGCGGACCGGACCGG 2440
 2401 CCACCGCCCGCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 2460
 2441 CCACCGCCCGCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCC 2500
 2461 AGCCACAACAACACGCTACCCACCCCACTCCACCTCGGGTATAG 2508
 2501 AGCCACAACAACACGCTACCCACCCCACTCCACCTCGGGTATAG 2548

RESULT 4
 AAD40569
 ID AAD40569 standard; cdna; 4763 BP.
 XX
 AC AAD40569;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Human drug metabolising enzyme (DME-5) cdna.
 XX
 KW Human; drug metabolising enzyme; autoimmune; inflammatory disorder;
 KW acquired immunodeficiency syndrome; AIDS; atherosclerosis; psoriasis;
 KW proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer;
 KW asthma; neurological disorder; Alzheimer's disease; Huntington's disease;
 KW dementia; Parkinson's disease; developmental disorder; anaemia; adenoma;
 KW drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract;
 KW renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer;
 KW anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder;
 KW goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant;
 KW anticonvulsant; nootropic; enzyme; DME-5; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 177..2684
 FT FT /tag= a
 FT /product= "Human DME-5"
 FT sig_peptide 177..218
 FT mat_peptide /tag= b
 FT /tag= c
 FT /product= "Mature human DME-5"
 FT sig_peptide 177..224
 FT /tag= d
 FT mat_peptide 225..2681
 FT /tag= e
 FT /product= "Mature human DME-5"
 XX
 PN WO200246426-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 04-DEC-2001; 2001WO-US47429.
 XX
 PR 08-DEC-2000; 2000US-254308P.
 PR 15-DEC-2000; 2000US-256189P.
 PR 21-DEC-2000; 2000US-25713P.
 PR 19-JAN-2001; 2001US-262706P.
 PR 02-FEB-2001; 2001US-266020P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX

PI	Sanjanwala MM, Yao MG, Au-young J, Baughn MR, Arvizu C, Ring HZ;
PI	Lee EA, Ding L, Hatalia AUA, Tang YT, Yue H, Tribouley CM;
PI	Lu DAN, Lal PG, Warren BA, Yang J, Walia NK, Nguyen DB;
PI	Gandhi AR, Lu Y, Ison CH;
XX	
WT	PID: 2002-519668/55.
DR	P-PSDB; AAZ5020.
XX	
PT	Novel human drug metabolizing polypeptide, useful in diagnosis,
PT	prevention or treatment of autoimmune/inflammatory, cell proliferative,
PT	neurological, developmental, endocrine, metabolic and gastrointestinal
PT	disorders -
XX	
CS	Claim 73; Page 162-164; 169pp; English.
XX	
CC	The invention relates to an isolated human drug metabolising enzyme (DME)
CC	and its nucleotide. DME is useful for diagnosing, treating or preventing
CC	disorders associated with aberrant expression of DME, where the disorders
CC	are selected from autoimmune/inflammatory disorder such as acquired
CC	immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis,
CC	uveitis; a cell proliferative disorder such as arteriosclerosis, as
CC	cirrhosis, hepatitis, and cancer; a neurological disorder such as
CC	Alzheimer's disease, Huntington's disease, dementia, Parkinson's disease;
CC	a developmental disorder such as renal tubular acidosis, epilepsy.
CC	anaemia; an endocrine disorder such as adenoma, thrombosis and
CC	infections; an eye disorder such as conjunctivitis, glaucoma, cataract;
CC	metabolic disorder such as cystic fibrosis, diabetes and goitre; a
CC	gastrointestinal disorder such as anorexia, peptic ulcer; and liver
CC	disorders. DME is useful in a number of drug screening techniques and to
CC	analyse the proteome of a tissue or cell type. The invention is useful
CC	for creating knock-in humanised animals or transgenic animals to model
CC	human diseases, in somatic or germline gene therapy, to generate a
CC	transcript image of a tissue or cell type, for detecting differences in
CC	the chromosomal location due to translocation, inversion, etc. among
CC	normal, carrier or affected individuals, and as hybridisation probes for
CC	mapping naturally occurring genomic sequences. The present sequence is
CC	human DME-5 cDNA.
XX	
SQ	Sequence 4763 BP; 871 A; 1601 C; 1364 G; 927 T; 0 other;
	Query Match 99.7%; Score 2500; DB 24; Length 4763;
	Best Local Similarity 99.8%; Fred. No. 0;
	Matches 2503; Conservative 0; Mismatches 5; Indels 0; Gaps 0
QY	1 ATGTGGCTCCTCGCGTGTTGTCGTGTGGGGCTGGCGGGGCTCAACGCGGGGAGGGGT 60
Db	177 ATGTGGCTCCTGGCTTGTGTCGTGTGGGGCTGGCTGGGCTCAA CGSGAGAGGGGT 236
QY	61 CCCGGCGGGCGGCCCGCGGCGCCCCCGCTGGGCTTGGCGAGCTTGGCGAGAGCGC 120
Db	237 CCCGGCGGGCGGCCCGCGGCGCCCCCGCTGGGCTTGGCGAGCTTGGCGAGAGCGC 296
QY	121 TTCCCGETGGTGAAACAACGCCTACGGGCGAGTGGCGGTGTGGGGCGAGCTCAACAAC 180
Db	297 TTCCCGETGGTGAAACAACGCCTACGGGCGAGTGGCGGTGTGGGGCGAGCTCAACAAC 356
QY	181 GAGATCTGGGCGCGCTGGTGTGAGTTTGTGGCGGTGGTCCCTACGCGCGCCCTTGGGC 240
Db	357 GAGATCTGGGCGCGCTGGTGTGAGTTTGTGGCGGTGGTCCCTACGCGCGCCCTTGGGC 416
QY	241 GCCCGCGCTTCCAGCGCCTTAGSCGCCCGCTCTGTGGCGCCCGCGTGGCGACGCCACC 300
Db	417 GCCCGCGCTTCCAGCGCCTTAGSCGCCCGCTCTGTGGCGCCCGCGTGGCGACGCCACC 476
QY	301 ACCCTGCCCGCCCTTGCOCGAGAACCTGACGGGGCGTGTGGCGCGCATCATGTGCTCCT 360
Db	477 ACCCTGCCCGCCCTTGCOCGAGAACCTGACGGGGCGTGTGGCGCGCATCATGTGCTCCT 536
QY	361 GTGTGGTTACCGCAAACTTGGAGCGCGCCGACACTACGTGAGAACACGAGCGAGGAC 420
Db	537 GTGTGGTTACCGCAAACTTGGAGCGCGCCGACACTACGTGAGAACACGAGCGAGGAC 596
QY	421 TGCGTGTACTTCAACCTCTACGTGCCACCGAGGACGGTCCGCTTCAAAAAAAGCTGAC 480

[illegible]

Db 1677 GGGGATGAACCTGCCCTATGCTTTGGCGTGCCTCCATGGTGGTGCCACCGACCTCTTCCCC 1736
QY 1561 TGTAACTTCTCCAGAGATGACGTCATGCTCAGTCCGCTGCTATGACCTACTGAGCAAC 1620
Db 1737 TGTAACTTCTCCAGAGATGACGTCATGCTCAGTCCGCTGCTATGACCTACTGAGCAAC 1796
QY 1621 TTCCCAAGACTGGGGACCCCAACCAAGCGGCTGCCAGGATACCAAGTTCAACACACC 1680
Db 1797 TTCCCAAGACTGGGGACCCCAACCAAGCGGCTGCCAGGATACCAAGTTCAACACACC 1856
QY 1681 AAGCCCAATCGCTTCAGAGAGTGTGTGGAGAAATTCACAGCAAGAGAGATAT 1740
Db 1857 AAGCCCAATCGCTTCAGAGAGTGTGTGGAGAAATTCACAGCAAGAGAGATAT 1916
QY 1741 CTGCATATAGGCTGAAGCCACGCGCTGCTGACAACTACCGGCCAAAGGTGCTTC 1800
Db 1917 CTGCATATAGGCTGAAGCCACGCGCTGCTGACAACTACCGGCCAAAGGTGCTTC 1976
QY 1801 TGGCTGAGCTGTGCCCCACCTGCAACCTGCAACAGAGCTTTCAACACACCAACG 1860
Db 1977 TGGCTGAGCTGTGCCCCACCTGCAACCTGCAACAGAGCTTTCAACACACCAACG 2036
QY 1861 CGCTGCTCCCTTACGCCACGCGCTGGCGCTCTGTCCTCCCGCTGGCGCCCGGAC 1920
Db 2037 CGCTGCTCCCTTACGCCACGCGCTGGCGCTCTGTCCTCCCGCTGGCGCCCGGAC 2096
QY 1921 CGCGGCCCCCGCTGCCACCTGCTCCCGCTGCTCCCGAGCCCGAGCCCGGCCAAG 1980
Db 2097 CGCGGCCCCCGCTGCCACCTGCTCCCGCTGCTCCCGAGCCCGAGCCCGGCCAAG 2156
QY 1981 GCTATGACGCTTCCCGGCACTACGGGACTACTCCAGAGCTGAGGTACCGTG 2040
Db 2157 GCTATGACGCTTCCCGGCACTACGGGACTACTCCAGAGCTGAGGTACCGTG 2216
QY 2041 GCGTGGGTGCTCCCTCTCTCTCAACATCTTGGCTTTGCTGCTCTTACTACAG 2100
Db 2217 GCGTGGGTGCTCCCTCTCTCTCAACATCTTGGCTTTGCTGCTCTTACTACAG 2276
QY 2101 CGGACCGCGGAGAGCTGCGGTGAGCGGCTTACGCCACCTGGCGGTTCAGGTCT 2160
Db 2277 CGGACCGCGGAGAGCTGCGGTGAGCGGCTTACGCCACCTGGCGGTTCAGGTCT 2336
QY 2161 GCGTGGGTGCTGCGGCGGCTGCTCCCGCGGCGCTGAGCTGCCACGAGAGAG 2220
Db 2337 GCGTGGGTGCTGCGGCGGCTGCTCCCGCGGCGCTGAGCTGCCACGAGAGAG 2396
QY 2221 GAGCTGGTCTACTGAGTGAAGCGGCTGCTGCGGCGGAGCTTCCCGAGGCT 2280
Db 2397 GAGCTGGTCTACTGAGTGAAGCGGCTGCTGCGGCGGAGCTTCCCGAGGCT 2456
QY 2281 CTGGCGCTGCTGCGCGGAGTACACCTGCGCTGCGCGGCGACCGGAGATGTG 2340
Db 2457 CTGGCGCTGCTGCGCGGAGTACACCTGCGCTGCGCGGCGACCGGAGATGTG 2516
QY 2341 CTTCTTTGGCGCGGCGCTGACCTGCTGCGCGAGTGGCGCTGGGCGCACCGGCCACCC 2400
Db 2517 CTTCTTTGGCGCGGCGCTGACCTGCTGCGCGAGTGGCGCTGGGCGCACCGGCCACCC 2576
QY 2401 CCACCGCGCGCTTCTGCTGCTGCTGCGCGCTTCCCGCGCGCTTCCCGCGCGCTTCCCGCGCGCT 2460
Db 2577 CCACCGCGCGCTTCTGCTGCTGCTGCGCGCTTCCCGCGCGCTTCCCGCGCGCTTCCCGCGCGCT 2636
QY 2461 AGCCACAAACACAGCTACCCACCCACCTCCACCTCGGCTATAG 2508
Db 2637 AGCCACAAACACAGCTACCCACCCACCTCCACCTCGGCTATAG 2684

RESULT 5
ID AAF82996
XX AAF82996 standard; cDNA; 2523 BP.
AC AAF82996;
XX

29-JUN-2001 (first entry)
Human MBSP4 polypeptide encoding cDNA (clone 21417374.0.9).
MBSPX; cancer; preclampsia; immune system; neurological; cytostatic;
synecological; antiinflammatory; neuroprotective; inotropic; relaxant;
cardiant; dermatological; gene therapy; human; MBSP4; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 1..2514
/*tag= a
/product= "MBSP4"
XX MO200127277-A2.
XX 19-APR-2001.
PD 13-OCT-2000; 2000MO-US28480.
PF 12-OCT-1999; 99US-0159231.
PR 12-JAN-2000; 2000US-0175670.
PR 12-OCT-2000; 2000US-0159231.
XX (CURA-) CURAGEN CORP.
XX Shimketa RA, Lichenstein H, Boldog FL;
PI WPI; 2001-282030/29.
DR P-PSDB; AAB62400.
Novel human polynucleotide sequences and the membrane bound or secreted polypeptides encoded by these sequences, designated MBSPX -
Claim 9; Page 26-29; 157pp; English.
The invention relates to novel polypeptides, termed MBSPX and polynucleotides encoding the MBSPX polypeptides. The MBSPX polypeptide, nucleic acid and an MBSPX antibody are useful for treating or preventing a pathology associated with the protein especially in humans. The MBSPX nucleic acid can be used to express MBSPX protein (e.g. via a recombinant expression vector in a host cell in gene therapy applications), an to detect MBSPX mRNA in a biological sample or a genetic lesion in a MBSPX gene. Disorders associated with insufficient or excessive production of MBSPX protein include cancer, preclampsia, immune system disorders and inflammation, neurological disorders, cardiovascular disorders; and skin and muscle abnormalities. The anti-MBSPX antibodies can be used to detect and isolate MBSPX proteins and modulate MBSPX activity. The present sequence represents the nucleotide sequence of MBSP4, a human neurologin 2 homologue.
Query Match 97.4%; Score 2443.6; DB 22; Length 2523;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2484; Conservative 0; Mismatches 24; Indels 6; Gaps 2;
QY 1 ATGTGGCTCTGCGCTGTGTCTGTGGGCTGTGGGCGGTCAACGCGGGGAGGGGT 60
Db 1 ATGTGGCTCTGCGCTGTGTCTGTGGGCTGTGGGCGGTCAACGCGGGGAGGGGT 60
QY 61 CCGCGCGGCG 120
Db 61 CCGCGCGGCG 120
QY 121 TTCCCGGTGGTGAACACAGCGCTTACGCGGAGTGCCTGCGCGCGGTGTGCGCGAGTCAACAC 180
Db 121 TTCCCGGTGGTGAACACAGCGCTTACGCGGAGTGCCTGCGCGGTGTGCGCGAGTCAACAC 180
QY 181 GAGATCTCGGCGCGCGCTGTGTGTGCGGTGCTTTGGCGGTGCGCTTACGCGCGCGCTTGGGC 240
Db 181 GAGATCTCGGCGCGCGCTGTGTGTGCGGTGCTTTGGCGGTGCGCTTACGCGCGCGCTTGGGC 240

QY 241 GCCCGCGCTTCAGCGCGCTGAGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 300
Db 241 GCCCGCGCTTCAGCGCGCTGAGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 300
QY 301 ACCCTGCGCGCGCTTCAGCGCGCTGAGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 360
Db 301 ACCCTGCGCGCGCTTCAGCGCGCTGAGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 360
QY 361 GTGTGTTTACCGACCAACTTGGAGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 420
Db 361 GTGTGTTTACCGACCAACTTGGAGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 420
QY 421 TGCGCTGCTACCTCAACCTTACGCTGCGCGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 480
Db 421 TGCGCTGCTACCTCAACCTTACGCTGCGCGCGCGCGCGCTCTGCTGCGCGCGCTGCGCAACGCCACC 480
QY 481 GAGCGACCGCTCAATCCGCGCAGACACAGATATCCGTGACCGCTGGGAGAGAGCGCTGTGATG 540
Db 481 GAGCGACCGCTCAATCCGCGCAGACACAGATATCCGTGACCGCTGGGAGAGAGCGCTGTGATG 540
QY 541 CTGCTTCTCATGCGCGCTCTACATGAGGAGGACCGGAAACATGTTGATGGCTCAGTC 600
Db 541 CTGCTTCTCATGCGCGCTCTACATGAGGAGGACCGGAAACATGTTGATGGCTCAGTC 600
QY 601 CTGCTTCTCATGCGCGCTCTACATGAGGAGGACCGGAAACATGTTGATGGCTCAGTC 660
Db 601 CTGCTTCTCATGCGCGCTCTACATGAGGAGGACCGGAAACATGTTGATGGCTCAGTC 660
QY 661 TTTCTCAGCACCGGAGCAGCGCTGCAAAAGCAACTATGGGCTCTCTGGACAGATCCAG 720
Db 661 TTTCTCAGCACCGGAGCAGCGCTGCAAAAGCAACTATGGGCTCTCTGGACAGATCCAG 720
QY 721 GCCCTCGCTGCTCAGTCAAAACATCGCCACTTGGGGGCGACCGGAGGATACCC 780
Db 721 GCCCTCGCTGCTCAGTCAAAACATCGCCACTTGGGGGCGACCGGAGGATACCC 780
QY 781 ATCTTTGTTTCCGGGCGAGGCGCTCTCTGCTGCAACCTTCTGATCTCTCCACCACTCA 840
Db 781 ATCTTTGTTTCCGGGCGAGGCGCTCTCTGCTGCAACCTTCTGATCTCTCCACCACTCA 840
QY 841 GAGGCTGTTTCCAGAGGCGATCGCCAGAGTGCGACCGCGCAATTCAGCTGCTGTC 900
Db 841 GAGGCTGTTTCCAGAGGCGATCGCCAGAGTGCGACCGCGCAATTCAGCTGCTGTC 900
QY 901 AACTTACCGCGCTCAAGTATACCGCGCTGCTGCGAGCGCAAGCTGCTGTCAGCGAG 960
Db 901 AACTTACCGCGCTCAAGTATACCGCGCTGCTGCGAGCGCAAGCTGCTGTCAGCGAG 960
QY 961 GACAGTGTGAAGCTGTGAGTGTCTGCGCGGAGAGCGCTCTCCAGTCAAGATGCTCATC 1020
Db 961 GACAGTGTGAAGCTGTGAGTGTCTGCGCGGAGAGCGCTCTCCAGTCAAGATGCTCATC 1020
QY 1021 GACGTGACGCTGCGCGCTTACCATCGCTTGGCGCGGCTGCTGAGTGGAGAGTGGTC 1080
Db 1021 GACGTGACGCTGCGCGCTTACCATCGCTTGGCGCGGCTGCTGAGTGGAGAGTGGTC 1080
QY 1081 CCGATGACCTTACGATCTCATGAGCAGGAGAAATTCCTCAACTAGCATGCTCATC 1140
Db 1081 CCGATGACCTTACGATCTCATGAGCAGGAGAAATTCCTCAACTAGCATGCTCATC 1140
QY 1141 GCGCTCAACAGGAGAGGCGCTCAAGTCTGAGGAGACTCTGAGAGAGGAGAGCGGT 1200
Db 1141 GCGCTCAACAGGAGAGGCGCTCAAGTCTGAGGAGACTCTGAGAGAGGAGAGCGGT 1200
QY 1201 GTGTGTCAGCGCGCTTGTACTTCACTGCTTCCAACTTGTGGAGCAACTGTATGGCTAC 1260
Db 1201 GTGTGTCAGCGCGCTTGTACTTCACTGCTTCCAACTTGTGGAGCAACTGTATGGCTAC 1260
QY 1261 CCGGAGGAGAGGATGTGCTCGGAGAGCAATCAAGTTTATGTACAGACTGGGCGGAC 1320
Db 1261 CCGGAGGAGAGGATGTGCTCGGAGAGCAATCAAGTTTATGTACAGACTGGGCGGAC 1320

QY 1321 CGGACAAATGCGGAAATGCGCGGCAAAACCTGCTGCGCGCTTCTTACTGACCAACAATGG 1380
Db 1321 CGGACAAATGCGGAAATGCGCGGCAAAACCTGCTGCGCGCTTCTTACTGACCAACAATGG 1380
QY 1381 GTGACCAAGCTGTGGGCACTGCCAAGCTGCAAGCTGCAAGCTGCTGCGCTTACTTT 1440
Db 1381 GTGACCAAGCTGTGGGCACTGCCAAGCTGCAAGCTGCAAGCTGCTGCGCTTACTTT 1440
QY 1441 TACACCTTCTTACCACTGCTGCGGAGGCGCGGCTGAGTGGGAGATGCGGCGCAC 1500
Db 1441 TACACCTTCTTACCACTGCTGCGGAGGCGCGGCTGAGTGGGAGATGCGGCGCAC 1500
QY 1501 GGGATGAATGCGCGCTTATGCTTTGGGCTGCCAATGCTGGGTCACCGACCTTCTCCC 1560
Db 1501 GGGATGAATGCGCGCTTATGCTTTGGGCTGCCAATGCTGGGTCACCGACCTTCTCCC 1560
QY 1561 TGTAACTTCTTCAAGAAATGAGCTCATGCTCAGTGGCGGTGCTGCTGCTGACCAAC 1620
Db 1561 TGTAACTTCTTCAAGAAATGAGCTCATGCTCAGTGGCGGTGCTGCTGCTGACCAAC 1620
QY 1621 TTGCCAAGACTGGGACCCCAACCGCTGCGGAGGATACCAAGTTTATCCACACC 1680
Db 1621 TTGCCAAGACTGGGACCCCAACCGCTGCGGAGGATACCAAGTTTATCCACACC 1680
QY 1681 AAGCCCAATGCTTCCAGAGGCTGCTGAGCAAAATTCACAGCAGGAGAGAGCTAT 1740
Db 1681 AAGCCCAATGCTTCCAGAGGCTGCTGAGCAAAATTCACAGCAGGAGAGAGCTAT 1740
QY 1741 CTGCACATAGGCTTGAAGCCACCGCTGCTGCAAACTTACCGCGCCCAACAGGTTGCTTC 1800
Db 1741 CTGCACATAGGCTTGAAGCCACCGCTGCTGCAAACTTACCGCGCCCAACAGGTTGCTTC 1800
QY 1801 TGGCTGAGCTGCTGCGGCTGCTGCAAGCTGCTGCAAGCTGCTTTCACCAACACAG 1860
Db 1801 TGGCTGAGCTGCTGCGGCTGCTGCAAGCTGCTGCAAGCTGCTTTCACCAACACAG 1860
QY 1861 CGCTGCTTCTTACGCGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCT 1917
Db 1861 CGCTGCTTCTTACGCGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCT 1920
QY 1918 ACAGCGCGCGCGCGCGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCT 1977
Db 1921 ACAGCGCGCGCGCGCGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCT 1980
QY 1978 AGGCTTATGAGCTTCCCGGCGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCT 2037
Db 1981 AGGCTTATGAGCTTCCCGGCGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCT 2040
QY 2038 GTGCGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2097
Db 2041 GTGCGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
QY 2098 AAGCGGAGCGGCGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCT 2157
Db 2101 AAGCGGAGCGGCGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCT 2160
QY 2158 TCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2217
Db 2161 TCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
QY 2218 GAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
Db 2221 GAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
QY 2278 GCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2337
Db 2281 GCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
QY 2338 GTGCTTCTTGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2397
Db 2341 GTGCTTCTTGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
QY 2398 CCCCCACCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2454

CC	endocrine (e.g. thrombosis, goiter, hyperplasia, amenorrhea and
CC	gynecomastia), eye (e.g. iritis and glaucoma, metabolic (e.g. Addison's
CC	disease, diabetes and obesity), and gastrointestinal disorders (e.g.
CC	anorexia, nausea, abdominal angina, ulcerative colitis, diarrhea and
CC	constipation). The DME polypeptides are useful in drug screening
CC	techniques, and to analyse the proteome of a tissue or cell type. The DME
CC	polynucleotides are useful for creating knock-in humanized animals or
CC	transgenic animals to model human diseases, and in somatic or germline
CC	gene therapy. The present sequence represents a human DME polynucleotide
CC	sequence.
CC	
XX	
Query Match	90.3%; Score 2265.4; DB 24; Length 2663;
Best Local Similarity	99.7%; Pred. No. 0;
Matches 2269; Conservative	0; Mismatches 6; Indels 0; Gaps 0
QY	1 ATGTGGCTCTTGGCGCTGTGTCTGGTGGGCTGTGGCGGGCTCAACGCGGGGAGGGGGT 60
DB	177 ATGTGGCTCTTGGCGCTGTGTCTGGTGGGCTGTGGCGGGCTCAACGGGAGGAGGGGT 236
QY	61 CCCGGCGGCGGCCCGGGGGCGCCCGCGGCTTGGGCTCGGAGCGCTCGGCGAGGAGCG 120
DB	237 CCCGGCGGCGGCCCGGGGGCGCCCGCGGCTTGGGCTCGGAGCGCTCGGCGAGGAGCG 296
QY	121 TTCCCGGTGTGAACACGGGCTACGGCGAGTGCGGGTGTGGCGCGAGGCTCAACAAC 180
DB	297 TTCCCGGTGTGAACACGGGCTACGGCGAGTGCGGGTGTGGCGCGAGGCTCAACAAC 356
QY	181 GAGATCTTGGGCGCGGTGTCAGTCTTGGGGGTGCTCCACGACGCGGCGCTTGGC 240
DB	357 GAGATCTTGGGCGCGGTGTCAGTCTTGGGGGTGCTCCACGACGCGGCGCTTGGC 416
QY	241 GCCCGCGCTTTCACGCGCGCTGAGGGCGCCCGCTCGTGGCGCGGCTGCGCAACGCGAC 300
DB	417 GCCCGCGCTTTCACGCGCGCTGAGGGCGCCCGCTCGTGGCGCGGCTGCGCAACGCGAC 476
QY	301 ACCGTGCGCGCGGCTTGGCGCGAGACTGCGACGGGGCGTGGCGCGATCATGTGCGCT 360
DB	477 ACCGTGCGCGCGGCTTGGCGCGAGACTGCGACGGGGCGCTGGCGCGCATCATGTGCGCT 536
QY	361 GTGTGGTTTCAACGACAACTTTGGAGGGGGCGCGCCACTACGTGCGAAGCCAGAGCGAGAC 420
DB	537 GTGTGGTTTCAACGACAACTTTGGAGGGGGCGCGCCACTACGTGCGAAGCCAGAGCGAGAC 596
QY	421 TGCTGTACTCAACCTCTACGTGCGCACCGAGACGCTTCGCTCACAAAAACGTCAC 480
DB	597 TGCTGTACTCAACCTCTACGTGCGCACCGAGACGCTTCGCTCACAAAAACGTCAC 656
QY	481 GAGGCGACGCTCAATCCGCGCAGACACAGATATCCGTGACCCCTGGGAAGACGCTGTGATG 540
DB	657 GAGGCGACGCTCAATCCGCGCAGACACAGATATCCGTGACCCCTGGGAAGACGCTGTGATG 716
QY	541 CTGTTTCTCATGGCGGCTCTCATATGAGAGGGGACCGGAAACATGTTTCGATGGGCTCAGTC 600
DB	717 CTGTTTCTCATGGCGGCTCTCATATGAGAGGGGACCGGAAACATGTTTCGATGGGCTCAGTC 776
QY	601 CTGGCTCGCTATGCGAACGTCATTGTGAGCAGCGCTCAACTACCGCTTTGGGGTGTCTGGT 660
DB	777 CTGGCTCGCTATGCGAACGTCATTGTGAGCAGCGCTCAACTACCGCTTTGGGGTGTCTGGT 836
QY	661 TTTCTCAGCACCGGGGACGAGGTGCAAAAGCAACTATGGGCTCTCTGGACCAAGATCCAG 720
DB	837 TTTCTCAGCACCGGGGACGAGGTGCAAAAGCAACTATGGGCTCTCTGGACCAAGATCCAG 896
QY	721 GCCCTGGGCTGGCTCAGTGAAGAACATCGGCCCACTTTGGGGGCGACCCCGAGCGATCACC 780
DB	897 GCCCTGGGCTGGCTCAGTGAAGAACATCGGCCCACTTTGGGGGCGACCCCGAGCGATCACC 956
QY	781 ATCTTTGGTTCCGGGCGACGGGCGCTCTGGGTCACCTTCTGATCTCTCCACCATTCAC 840
DB	957 ATCTTTGGTTCCGGGCGACGGGCGCTCTGGGTCACCTTCTGATCTCTCCACCATTCAC 1016

841 CAAGGGCTGTTCCAGAGGGCCATCGCCAGAGTGGCACCCGCCATTTTCCAGCTGGTCTGTC 900
 1017 GAAGGGCTGTTCCAGAGGGCCATCGCCAGAGTGGCACCCGCCATTTTCCAGCTGGTCTGTC 1076
 901 AACTACAGCGCGCTCAAGTACACCGCGTGTGCGAGCCAAAGTGGGCTGTGACCGAGAG 960
 1077 AACTACAGCGCGCTCAAGTACACCGCGTGTGCGAGCCAAAGTGGGCTGTGACCGAGAG 1136
 961 GACAGTCTGAAGCTGTGGAGTGTCTGGCGCGAGAGCCCTCCCGGGAGCTGTGTGACCGAG 1020
 1137 GACAGTCTGAAGCTGTGGAGTGTCTGGCGCGAGAGCCCTCCCGGGAGCTGTGTGACCGAG 1196
 1021 GACGTGAGCGTGCCTTACCAATCGCTTTTGGGCGCGTGTGTGATGGCGACGTGGTC 1080
 1197 GACGTGAGCGTGCCTTACCAATCGCTTTTGGGCGCGTGTGTGATGGCGACGTGGTC 1256
 1081 CCGATGACCTTGATCTCTATGACAGCGAGGAGATTCCTCAACTACGACATGCTCATC 1140
 1257 CCGATGACCTTGATCTCTATGACAGCGAGGAGATTCCTCAACTACGACATGCTCATC 1316
 1141 GCGCTCAACAGGAGAGGGCCCTCAAGTTCGTGGAGGACTCTGCAGAGAGCGAGGACGT 1200
 1317 GGTGTCAACAGGAGAGGGCCCTCAAGTTCGTGGAGGACTCTGCAGAGAGCGAGGACGT 1376
 1201 GTGTCTCCAGCGCTTTGACTTCACTGTCTCCAACTTTGTGTGACAACTGTATGCTATC 1260
 1377 GTGTCTCCAGCGCTTTGACTTCACTGTCTCCAACTTTGTGTGACAACTGTATGCTATC 1436
 1261 CCGGAGGCAAGGATGTCTTCGGAGAGACCATCAAGTTTATGTACACAGACTGGGCGAC 1320
 1437 CCGGAGGCAAGGATGTCTTCGGAGAGACCATCAAGTTTATGTACACAGACTGGGCGAC 1496
 1321 CCGGACAAATGGGAAATGCGCCGCAAAACCTCTGGCGCTCTTTACTGACACCAATGG 1380
 1497 CCGGACAAATGGGAAATGCGCCGCAAAACCTCTGGCGCTCTTTACTGACACCAATGG 1556
 1381 GTGSCACAGCTGTGCACTGCAAGCTGACCGCGACTACAGTCTCCGCTCTACTTT 1440
 1557 GTGSCACAGCTGTGCACTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAG 1616
 1441 TACACCTTTTACCACTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCT 1500
 1617 TACACCTTTTACCACTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCT 1676
 1501 GGGGATGAAGTCCCTTATGTTTGGCGTGCCTATGTTGGTGGTGCACCGACTCTTCC 1560
 1677 GGGGATGAAGTCCCTTATGTTTGGCGTGCCTATGTTGGTGGTGCACCGACTCTTCC 1736
 1561 TGTAACTTCTCCAGAAATGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 1737 TGTAACTTCTCCAGAAATGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796
 1621 TTGCGCAAGACTGGGACCCCAACAGCGGTGCGCGAGGATACCAAGTTTCACTCCACACC 1680
 1797 TTGCGCAAGACTGGGACCCCAACAGCGGTGCGCGAGGATACCAAGTTTCACTCCACACC 1856
 1681 AAGCCCAATCGCTTCAGAGAGTGTGTGGAGGATTCAGCAAGCAAGAGAGAGAGTAT 1740
 1857 AAGCCCAATCGCTTCAGAGAGTGTGTGGAGGATTCAGCAAGCAAGAGAGAGAGTAT 1916
 1741 CTCACATAGGCTGAAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
 1917 CTCACATAGGCTGAAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1976
 1801 TGGCTGAGCTGTGCGCCCACTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAAC 1860
 1977 TGGCTGAGCTGTGCGCCCACTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAAC 2036
 1861 CGCTGCTTCCCTTACCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
 2037 CGCTGCTTCCCTTACCGCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2096
 1921 CGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980

2097 CCCTGGCG 2156
 1981 GCCTATGACCGCTTCCCGGGGACTCAGCGGACTACTCAGCGGACTGAGGCTGACCGGTG 2040
 2157 GCCTATGACCGCTTCCCGGGGACTCAGCGGACTACTCAGCGGACTGAGGCTGACCGGTG 2216
 2041 GCCTGGGTGCTTCCCT 2100
 2217 GCCTGGGTGCTTCCCT 2276
 2101 CCGGACCG 2160
 2277 CCGGACCG 2336
 2161 GCGCT 2220
 2337 GCGCT 2396
 2221 GAGCTGGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2275
 2397 GAGCTGGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2451

RESULT 7
 ABQ61047
 ID ABQ61047 standard; cDNA; 2865 BP.
 XX ABQ61047;
 AC ABQ61047;
 XX DT 26-FEB-2003 (first entry)
 XX DE 3 isoform protein encoding sequence.
 XX KW Neuroprotective; immunomodulator; cancer; chromosome Xq13.1;
 KW cytosolic; anti-inflammatory; gene therapy; nutritional supplement;
 KW wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
 KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
 KW vulnery; gene; ss.
 XX OS Homo sapiens.
 XX PN WO200231111-A2.
 XX PD 18-APR-2002.
 XX PF 11-OCT-2001; 2001WO-US27760.
 XX PR 12-OCT-2000; 2000US-0687527.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX WPI; 2002-426278/45.
 DR N-PSDB; ABP43803.
 XX New polypeptides and their encoded proteins, useful as nutritional
 PT sources or supplements, or in gene therapy, particularly for treating
 PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
 PT inflammation
 XX Claim 1; SEQ ID # 260; 357pp + sequence listing; English.
 PS The invention relates to 446 newly isolated polynucleotide sequences.
 CC The activity of polynucleotides of the invention may be described as,
 CC vulnery, neuroprotective, immunomodulator, cytosolic and
 CC anti-inflammatory. Compositions comprising nucleic acids of the invention
 CC are useful for treating a mammalian subject, or as nutritional sources or
 CC supplements. These are useful in gene therapy, particularly for treating
 CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or

QY 899 TCAACTACGACGCTCAAGTACACGCGCTGCTGCGAGCCAGGCTGCTGACCGAG 958
 DB 1314 TGAATACCAACAGTGAAGTACACAGCCTGCTGCGAGCAAGTGGCTGATGTCG 1373
 QY 959 AGGACGTGCTGAAGCTGTGGAGTGTGCGCCGAGAGCCCTCCCGGAGCTGTGGACC 1018
 DB 1374 TGGACACCGTGGATATGCTGTGGAGCTGTCTTCCGAAAAGAGTGCACAGGAGCTGGTAGAGC 1433
 QY 1019 AGGACGTGCAAGCTGCGCCGCTCAACATCGCCTTTTGGGCCGCTGGTGGATGCGCAGCTGG 1078
 DB 1434 AGGACATCCAGCAGCCGCTCAACAGTGGCTTTGGCCCTGTGATGATGATGATGCA 1493
 QY 1079 TCCCGGATGACCTGAGATCTCATGACAGAGGAGATTCCTCAACTACGACATGCTCA 1138
 DB 1494 TTCCTGATGACCTGAGATCTCATGAGCAGGCGGAGTTCCTCAACTATGACATCATGCG 1553
 QY 1139 TCGCGCTCAACAGGAGAGGCGCTCAAGTTCTGTGAGGAGCTCTGAGAGAGCGAGGAGC 1198
 DB 1554 TAGGTGTCAACAGGCGAGGCTCAAGTTCTGTGAGGAGGCTGTGAGGAGGAGGATG 1613
 QY 1199 GTGTGTCTGCGAGCGCTTTGACCTTCACTGTCTTCCAACTTGTGAGACACTGTATGGCT 1258
 DB 1614 GTGTCTCTGGACCTGACTTTGACATTTCCGTCTCCAAATTTTGTGAGCAATCTGTATGGCT 1673
 QY 1259 ACCGGAAGCAGAGATGTCTTCTGGAGACCACTCAAGTTTATGTATACAGACTGGGCG 1318
 DB 1674 ATCTGAGGGTAGGACACCTGCGAGAGACCACTCAAGTTTATGTATACAGACTGGGCG 1733
 QY 1319 ACCGGGACATGGGAAATGGCGGCAACCTGCTGCGGCTTGTACTGACCACTCACT 1378
 DB 1734 ACCGTGACACCTGAGACCGCGCTTAACACTGTGTGGACTCTTCACTGACCACTCACT 1793
 QY 1379 GGGTGGACCAAGCTGTGGCCACTGCGCAAGTGTGACGCGGAGTACCAAGTCTCCGCTACT 1438
 DB 1794 GGGTGGAGCCTCAGTGTGACAGCGCATCTGATGCGGCTACGGCTGCGCTACTACT 1853
 QY 1439 TTTACACTTCTACCACTGCGGAGCGGAGCGGCGGCTGAGTGGGAGAGTGGGCGC 1498
 DB 1854 TCTACGCTTCTATCATCATCTGCGAGAGCCTCATGAGCGCTGTTGTCAGATGAGCTC 1913
 QY 1499 ACGGGGAGTAACTGCCCTATGCTTTTGGCGTGCCTGAGTGGGTGCGACCGACCTCTTCC 1558
 DB 1914 ATGGGAGTAACTACCTATGTTTGGGGTTCCTATGTTAGGCGCCCACTGACCTTTTCC 1973
 QY 1559 CCTGTACTTCTCAAGAAAGTGTCTGCTGAGTGGGTGCTGAGTGGGTGCTGAGTGGTCA 1618
 DB 1974 CCTGCAACTTCTCAAGAAAGTGTGCTGAGTGGGTGCTGAGTGGGTGCTGAGTGGTCA 2033
 QY 1619 ACTTGGCAGACTGGGAGCCCAACCGAGCGGTGCGGAGGATACCAAGTTCATCCACA 1678
 DB 2034 ACTTGGCAGACTGGGAGTCCCAACCAAGCGGTGCGGAGGATACCAAGTTCATCCACA 2093
 QY 1679 CCAGCCCAATCGCTTGGAGAGGTGTGTGGAGCAATTCACAGCAAGGAGAGCAGT 1738
 DB 2094 CCAAGGCGCAACCGCTTTGAGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2153
 QY 1739 ATCTGCAATAGGCTGGAAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1798
 DB 2154 ACTTTCATCGGCTGAACCAAGGCTCCAGATCATTAACCGGCGCACTAAGTGGCT 2213
 QY 1799 TCTGGTGGAGCTGTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1849
 DB 2214 TTTGGAACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2273
 QY 1850 CCACACCAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1909
 DB 2274 CCACACCAAGTGGCGCTTCCGATACCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2333
 QY 1910 CCGCGGCAACGCGCGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1959
 DB 2334 ATGGCAAGACTGTGAGCAGCAAGCGGCGGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTG 2393
 QY 1960 -----GAGCCCGAGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2010

DB 2394 CCAGGGGTCTTGGAAACGGGAGCCAGGATCCAGGGCCACTCTCTGTGGAGAACCTCGT 2453
 QY 2011 GACTACTCCACGGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2070
 DB 2454 GACTACTCCACCTGAATTAAGTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2513
 QY 2071 ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2130
 DB 2514 GTTCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2573
 QY 2131 CGGCTTAGCCACCTGCGGCTCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2190
 DB 2574 CAGCTAGC-----CCTCAGCGGAGCGCGGCGCGCG 2606
 QY 2191 GCGCGCGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2250
 DB 2607 GAGTTGGGAGCTGCTCAGAGGAGGAGTGGCAGCATTAACAATGGGCGCGCGCGCGCGCG 2666
 QY 2251 GGTGGCGTGGGCGGAGCCTGCGAGGCTGCTGCGCGCTGCTGCGCGCGCGCGCGCGCGCG 2310
 DB 2667 GAGTGTGAGGCGGCTGCTGCGCGCGCTGCTGCGCGCGCTGCTGCGCGCGCGCGCGCGCG 2726
 QY 2311 CTGGCGCTGCGCGGCG 2370
 DB 2727 CTGACCTGCGCGGCTGCTGCG 2786
 QY 2371 CTGCCAGTGGCGCTGG 2386
 DB 2787 ATCCCACTGCTGCTGG 2802

RESULT 9
 AAS74457
 ID AAS74457 standard; cdna; 4975 BP.
 XX AC AAS74457;
 XX DT 13-FEB-2002 (first entry)
 XX DE DNA encoding novel human diagnostic protein #10261.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX OS Homo sapiens.
 XX FN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 XX DR P-PSDB; ABG10270.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 XX PT diagnostics, forensics, gene mapping, identification of mutations
 XX PT responsible for genetic disorders or other traits and to assess
 XX PT biodiversity -
 XX PS Claim 1; SEQ ID NO 10261; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and
 XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

Qy	1721	ACAGCAGGAGAAAGCAGTATCTGCATATAGGCTGAAGCCACGCGTGCGTGCAACTACC	1780
Db	945	ACAGCAGGAGAAAGCAGTATCTGCATATAGGCTGAAGCCACGCGTGCGTGCAACTACC	1004
Qy	1781	GCGCCAACAGGTGGCTTCTGCCTCGAGCTGTGCCCCACCTGCACAACTGCACACGG	1840
Db	1005	GCGCCAACAGGTGGCTTCTGCCTCGAGCTGTGCCCCACCTGCACAACTGCACACGG	1064
Qy	1841	AGCTTTTACCAACAACAAGCGGCTGCCTCTTACGCCACGGGCTGGCGGCTCTGTCCTCC	1900
Db	1065	AGCTTTTACCAACAACAAGCGGCTGCCTCTTACGCCACGGGCTGGCGGCTCTGTCCTCC	1124
Qy	1901	CCGCTGCGGCCCGCGGCACACGCGCGGCCCGCGGCTGCCACCTCTCCCGAGCCCG	1960
Db	1125	CCGCTGCGGCCCGCGGCACAAACGCGCGGCCCGCGGCTGCCACCTCTCCCGAGCCCG	1184
Qy	1961	AGCCGAGCCGCGCCCAAGGCGCTATGACGGTTCTCCCGGAGCTACAGCGGACTACTCCA	2020

Db 1185 AGCCCGAGCCCCCNCCAGGGCCTATGACCGCTTCCCCGGGACTCAGGGACTACTCCA 1244

Accession	Sequence	Length
D8	CGGAGCTGAGCGGTACCGTGGCGGGTGCTCCCTCTCTTCTCAACATCCTGGCCT	1304
1245	CGGAGCTGAGCGGTACCGTGGCGGGTGCTCCCTCTCTTCTCAACATCCTGGCCT	1304
QY	CGGAGCTGAGCGGTACCGTGGCGGGTGCTCCCTCTCTTCTCAACATCCTGGCCT	2083
2021	CGGAGCTGAGCGGTACCGTGGCGGGTGCTCCCTCTCTTCTCAACATCCTGGCCT	2083

Qy	2081	2081	1305	D _b
	TTGTGCCCTCTACTACAAGCGGACCGGGCGGCAGAGCTGCGTGCAGCGCGTTAGCC	TTGTGCCCTCTACTACAAGCGGACCGGGCGGCAGAGCTGCGTGCAGCGCGTTAGCC	TTGTGCCCTCTACTACAAGCGGACCGGGCGGCAGAGCTGCGTGCAGCGCGTTAGCC	TTGTGCCCTCTACTACAAGCGGACCGGGCGGCAGAGCTGCGTGCAGCGCGTTAGCC

ov 2141 CACCTGGCGGGCTCAGGGCTCTGGCGTGGCTGG 2171

[illegible]

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POSIT E 10

AAC74943

XX
ID
AAC/4943. Standard; CDNA; 924 BP.

AC AAC74943 ;

DT 08-FEB-2001 (first entry)

[illegible]

XX

human; open reading frame; ORF; detection; cytosolic; hepatotropic; KW
vulnerary; antipsoriatic; antiparkinsonian; rootronic; neuroprotective; KW

KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;

KW hypotensive; dermatological: immunosuppressive: anti-inflammatory:

KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antiarrhythmic; anticoagulant; anticancer; analgesic; antidiabetic;
KW antihypertensive; antiparasitic; antipsychotic; antidepressant;

KW neurodegenerative disorder; osteoarthritis; graft vs host disease;

KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection.

KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW

thrombosis; contraceptive; ss.
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yy

OS Homo sapiens.

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W0200058473-A2

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PF 31-MAR-2000; 2000WO-US08621.
yy

PR 31-MAR-1999; 99US-0127607.

02-APR-1999; 350S-0127636.
05-APR-1999; 99US-0127728

PR 30-MAR-2000; 2000US-0540763.

PA (CURA-) CURAGEN CORP.

PI Shimketa RA, Leach M;
 XX WPI: 2000-602362/57.
 DR P-PSDB; AAB40734.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 5; Page 969-970; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
 CC osteoprotective; anticonvulsant; antidiabetic; immunosuppressive;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 924 BP; 189 A; 306 C; 261 G; 168 T; 0 other;
 Query Match 36.8%; Score 924; DB 21; Length 924;
 Best Local Similarity 100.0%; Pred. No. 2.2e-147;
 Matches 924; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1003 CGGAGCTGTGGACAGGAGTGGACGCTGCGCGCTTACACATCGCCTTTGGGCGCGTG 1062
 DB 1 CGGAGCTGTGGACAGGAGTGGACGCTGCGCGCTTACACATCGCCTTTGGGCGCGTG 60
 QY 1063 GTGATGCGGACGTGTGCTCCGATGACCTGAGATCTCTATGACGAGGAGGAGTCTCTC 1122
 DB 61 GTGATGCGGACGTGTGCTCCGATGACCTGAGATCTCTATGACGAGGAGGAGTCTCTC 120
 QY 1123 AACTACGACATGCTCATCGGCTCAACGAGGAGAGGCGCTCAAGTTCGTGGAGACTCT 1182
 DB 121 AACTACGACATGCTCATCGGCTCAACGAGGAGAGGCGCTCAAGTTCGTGGAGACTCT 180
 QY 1183 GCAGAGAGGAGGAGGCTGTGCTGCGAGGCGCTTTGACTTCACTCTCTCCAACTTTTG 1242
 DB 181 GCAGAGAGGAGGAGGCTGTGCTGCGAGGCGCTTTGACTTCACTCTCTCCAACTTTTG 240
 QY 1243 GACAACTGTATGCTTACCGGAGAGGCAAGATGTGCTTGGGAGACCATCAAGTTTATG 1302
 DB 241 GACAACTGTATGCTTACCGGAGGCAAGATGTGCTTGGGAGACCATCAAGTTTATG 300
 QY 1303 TACACAGACTGGCGGACCGGACCAATGGGAAATGGCGCAAAACCTGCTGGCGCTC 1362
 DB 301 TACACAGACTGGCGGACCGGACCAATGGGAAATGGCGCAAAACCTGCTGGCGCTC 360
 QY 1363 TTTACTGACCAACCAATGGGTGGACCAAGTGTGGCACTGCCAAGTGTGACGCCGACTAC 1422
 DB 361 TTTACTGACCAACCAATGGGTGGACCAAGTGTGGCACTGCCAAGTGTGACGCCGACTAC 420
 QY 1423 CAGTCTCCGCTCTACTTTTACACCTTCTACACCTTCTACACCTTCTACACCTTCTACAC 1482
 DB 421 CAGTCTCCGCTCTACTTTTACACCTTCTACACCTTCTACACCTTCTACACCTTCTAC 480
 QY 1483 TGGGAGATGGCGGACCGGAGTGAATCGCCTTATGTCTTTGGCGTGCCTATGGTGGT 1542

DB 481 TGGGAGATGGCGGACCGGAGTGAATCGCCTATGTCTTTGGCGTGCCTATGGTGGT 540
 QY 1543 GCCACGACCTCTTCCCTGTAACTTCTCCAAAGATGAGTCACTGCTCAGTGCCTGCTC 1602
 DB 541 GCCACGACCTCTTCCCTGTAACTTCTCCAAAGATGAGTCACTGCTCAGTGCCTGCTC 600
 QY 1603 ATGACCTTACTGGACCAACTTCCCAAGACTGGGGACCCCAACAGCCGCTGCGGAGGAT 1662
 DB 601 ATGACCTTACTGGACCAACTTCCCAAGACTGGGGACCCCAACAGCCGCTGCGGAGGAT 660
 QY 1663 ACCAAGTTCATCCACACCAAGCCCAATCGCTTCGAGGAGTGGTGTGGAGCAAAATTCAC 1722
 DB 661 ACCAAGTTCATCCACACCAAGCCCAATCGCTTCGAGGAGTGGTGTGGAGCAAAATTCAC 720
 QY 1723 AGCAAGGAGAGCAGTATCTGACATAGAGCCCTGAAAGCCACGCGTGGTGACAACTACCG 1782
 DB 721 AGCAAGGAGAGCAGTATCTGACATAGAGCCCTGAAAGCCACGCGTGGTGACAACTACCG 780
 QY 1783 GCCAAAGGTGGCCCTTCTGGGTGGAGCTGCTGCCCTCCACCTGCAACACTGACACGGAG 1842
 DB 781 GCCAAAGGTGGCCCTTCTGGGTGGAGCTGCTGCCCTCCACCTGCAACACTGACACGGAG 840
 QY 1843 CTCTTCCACACCAACGCGCTGCTTCCCTAGCCACGCGTGGCGCTGCTGCTGCTGCTGCT 1902
 DB 841 CTCTTCCACACCAACGCGCTGCTTCCCTAGCCACGCGTGGCGCTGCTGCTGCTGCTGCT 900
 QY 1903 GCTGGGCGCGCGGCGGACACGCGGG 1926
 DB 901 GCTGGGCGCGCGGCGGACACGCGGG 924
 RESULT 11
 AAC58592
 ID AAC58592 standard; cDNA; 3112 BP.
 XX AC AAC58592;
 XX AC AAC58592;
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO701 protein UNQ365 encoding cDNA SEQ ID NO:66.
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatologic; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; neurotropic; neuroprotective;
 KW antianaemic; hepatotropic; virucide; antiproliferative; antiallergic;
 KW osteoarthritis; systemic lupus erythematosus; rheumatoid arthritis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease; ss.
 XX Homo sapiens.
 OS WO200053758-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05841.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99US-0123618.
 PR 12-MAR-1999; 99US-0123957.
 PR 23-MAR-1999; 99US-0125775.
 PR 12-APR-1999; 99US-0128849.
 PR 28-APR-1999; 99WO-US08615.
 PR 04-MAY-1999; 99US-0132445.
 PR 14-MAY-1999; 99US-0132371.
 PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US00217.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 XX

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX

DR WPI: 2000-572271/53.
 DR P-FSD; AAB33427.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
 XX Claim 23; Fig 27; 309pp; English.

CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central,
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.

XX Sequence 3112 BP; 853 A; 867 C; 712 G; 680 T; 0 other;

Query Match 36.4%; Score 912.2; DB 21; Length 3112;

Best Local Similarity 64.7%; Pred. No. 2,3e-145;

Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGCGAGAGCGCTTCCCGTGGTGAACACGCGCTACCGGGGAGTGGCGGTGTGCGGCG 167

Db	112	CAGCCAAAGCAGATATCCAGTTGTCAACACAAATATGCGAAATCCGGGCGCTAAGAAC	171
QY	168	CGAGCTCAACACAGAGATCCCTGGGCCCCGTGCTGAGTTCTTGGGCGTGCCTACGCCAC	227
Db	172	ACCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCTC	231
QY	228	GGCGCCCTTGGGCGCCCGCGCTTCCAGCGCTGAGCGCGCCCGCTCGTGCGCGCGGT	287
Db	232	ACCCCCCACTGGAGAGCGCGTTTACGCCCCAGAACCCCGTCTCTCTGACTGGCAT	291
QY	288	GGCAACGCCACCAACCTCGCCCGCTGCCCGAGAACCTGACG---GGGCGCTGCC	344
Db	292	CGGAATFACTACTAGTTGTGTGTGTCGCCCGACGACCTGGATGAGAGATCCTTACT	351
QY	345	CGCCATCATGTGCTGTGTGTTCACCGAACACTTGGAGCGCGCCCACTACGTGCA	404
Db	352	GCATGACATGTGCCCATCTGTTTACCGCCAAATTTGGATACTTTTGATGACTATGTCA	411
QY	405	GAAACAGAGCGAGACTGCTGTACCTCAACCTCTAGTGCCCGACCGAGGAGCGTCCGCT	464
Db	412	AGATCAAAATGAAGACTGCTTAAACATCTAGTGCCCGACCGAAGATGAGGCCAA	471
QY	465	CACAAAAACGTCGACGAGGCG-----ACGCTCAATCCGCCAGACACAGATATCCG	515
Db	472	CACAAAGAAAAACGAGATGATATAACGAGTAATGACCGTGTGAACGAGATATCA	531
QY	516	TGACCTG---GGAAGAGCTGTGATGCTGTTTCTCATGCGCGCTCTACATGGAGGG	572
Db	532	TGATCAGAACAGTAAGAACCGCTCATGGTCTATATCATGCGGGGATCTTACATGGAGG	591
QY	573	GACCGAAAAATGTTTCGATGGCTCAGTCTTGCTGCTATGGCAACGTCATTTGAGCCAC	632
Db	592	CACCGCAACATGATTGACGCGACATTTGGCAAGCTACGAAACGTCATCGTGATCAC	651
QY	633	GCTCACTACCGTCTTGGGCTGCTGCTTCTCAGCACCGGGGACGAGCTGCAAAAGG	692
Db	652	CATTAACCTACCGTCTGGGAATCTAGGGTTTTAAAGTACCGGTGACCGGCGAGCAAGG	711
QY	693	CAACTATGGGCTCTGACACGAGTCCAGGCGCTGCGCTGCTCAGTCAAAACATCGCCCA	752
Db	712	CAACTATGGGCTCTGATGAGATCAAGCACTGCGGTGATTTGAGGAGATTTGGGAGC	771
QY	753	CTTTGGGGGCGACCCCGAGCGTATCACCATCTTTGGTTCCGGGGGCGAGGGCGCTCTCGT	812
Db	772	CTTTGGGGGCGACCCCAAGAGAGTACCATCTTTGGCTCGGGGCTGGGGCGCTCTGTGT	831
QY	813	CAACTTCTGATCTCTCCCAACATTCAGAGGGCTGTTCCAGAGGCCATCGCCACAG	872
Db	832	CAGCTTTGACCGCTGTCCTACTACTAGAAAGTCTCTTCCAGAGGCCATCATTCAGAG	891
QY	873	TGGCACCGCCATTTCCAGCTGGTCTGTCAACTACCGCGCTCAAGTACACGCGGTGCT	932
Db	892	CGGACCGCGCTGTCAGCTGGGAGTGAATACAGCGCGGCCAGTACATCGGATATT	951
QY	933	GGCAGCCAGGTGGCTGTGACCGAGAGGACAGTGTGAGCTGTGAGTGTGCGCGCG	992
Db	952	GGCAGACAAGGTGGCTGCAACATGCTGGACACCAAGCATGCTAGATGATGCTGCGGAA	1011
QY	993	GAAGCCCTCCCGGAGCTGTGACCGAGGAGTGCAGCGCTGCGCGCTACACATCGCCTT	1052
Db	1012	CAAGAACTACAAGAGCTCATCAGCAGACCATCACCCCGGCCACCTACACATAGCCTT	1071
QY	1053	TGGGCGCGTGGTGGAGTGGGACGTGTGTCGCCGATGACCTTGAGATCCTCATGACGAGG	1112
Db	1072	CGGCGCGGTGATCGACGGGACGTCATCCAGACGACCCCGAGATCCTGATGGAGCAAG	1131
QY	1113	AGATTTCTCACTAGCATGCTCATCGCGCTCAACGAGGAGGAGGCGCTCAAGTTCT	1172
Db	1132	CGAGTTCTCACTAGCATGCTGCGCGCTCAACCAAGGGGAGGCGCTGAAGTTCT	1191
QY	1173	GGAGGACTCTGCAGAGAGGAGGACGCTGTGCTGCCAGCGCTTTGACTTCACTCTCTC	1232

Db	1192	GGACGGCATCGTGGGATAACAGGACGGGTGTGACGCCCAACGACTTTGACTTTCTCGTGTCT	1251
QY	1233	CAACTTTGTGGACAACCTGTATGGCTACCCGGAAGCAAGATGTGTTTCGGGAGACCAT	1292
Db	1252	CAACTTCGTGGACAACCTTTACGGCTACCCGTGAAGGGAAGACACTTTGGGGAGACTAT	1311
QY	1293	CAAGTTTATGTACACAGACTGGGCCGACGGGGAATGGCGAATATGGCCGCGCAAAACCCCT	1352
Db	1312	CAAGTTCATGTACACAGACTGGGCCGATTAAGGAAACCCGGAGACGGGGCGGAAAAACCTT	1371
QY	1353	GCTGCGCTCTTTACTGACCAACCAATGGGTGGCACCACTGTGSCCACTGCAAGCTGCA	1412
Db	1372	GCTGCGCTCTTTACTGACCAACCAATGGGTGGCACCACTGTGSCCACTGCAAGCTGCA	1428
QY	1413	GGCCGACTACCAAGTCTCCGCTTACTTTTACACTTTTACCAACTGCGCAGGCGGAGG	1472
Db	1429	CGCGCAGTACGGCTCCCCCACTACTTCTATGCTTTCTATCATCACTGCCAAAGCGAAAT	1488
QY	1473	CGGCGCTGAGTGGGCGAGATCGGGCGACGGGGATGAATGCCCTATCTCTTTGGCGTGC	1532
Db	1489	GAAAGCCAGCTGGGCGAGATTCGGCCCATGGTGATGAGGTCCCCTATGCTCTTGGCATGCC	1548
QY	1533	CATGTTGGTGGCACCGGACCTCTTCCCGCTGTAACTTCCCAAGAAATGACCTCATGCTCAG	1592
Db	1549	CATGATCGGTCCCAACCGAGCTCTTCAGTTGTAACTTTTCCAAAGAACGACGCTCATGCTCAG	1608
QY	1593	TGCCGTGTCATGACCTACTGCGACCACTTCGCCAAGACTGGGACCCCAACACAGCGGT	1652
Db	1609	CGCGTGTCTATGACCTACTGCGACCACTTCGCCAAGACTGGTATCCAAATCAACCGAT	1668
QY	1653	CGCGAGGATACCAAGTTTCATPCACCAAGCCCAATCGCTTCAGGAGGTGTTGTGGAG	1712
Db	1669	TCCTCAGGATACCAAGTTTCATTCACAAACCAACCCGCTTTGAAGAGTGGCTGGTC	1728
QY	1713	CAAAATCAACAGCAGGAGAGCAGTATCTGCATAGGCCTGAGCCAGCGCTGGTGTA	1772
Db	1729	CAAGTATATCCCAAGACCACTCTATCTGCATATTGGCTTGAACCCAGAGTGAAGA	1788
QY	1773	CAACTACGCGCCAAACAGGTGGCTTCTGGCTGGAGCTCGTGGCCCACTGTCACAACCT	1832
Db	1789	TCACTACGGGCAACGAAGTGGCTTCTGGTTGGAACTCGTTTCTCATTTGCACAACTT	1848
QY	1833	GCA-----CACGGAGCTCTTCACCAACCAACGCGCTCGCTCCCTTACGCCACGG	1883
Db	1849	GAAACGAGATATTCAGTATGTTTCAACCAACAAAGGTTTCCTCCACGACATGCATC	1908
QY	1884	CTGCGCCGCTCGTCCCCCGCTGGCGCCCGGGCACACGCGGCCCGCCGCGCTGCCAC	1943
Db	1909	ATTTCCTATGGCACCGCGGATCTCCGCCAAGATATGSCCAACCAACCAAGCCCGAC	1968
QY	1944	CTGCTCCGAGCCCGAGCCGAGC-----CGGCGCCCAAGGCG	1982
Db	1969	AATCACTCTTCGCAACAATCCCAACACTTAAGGACCTTCACAAACAGGCGCTGAGGA	2028
QY	1983	CTATGACCGGTTCCCGGGGACTCAGGGGACTACTCCAGGAGCTGAGCGTCAACGTCGC	2042
Db	2029	CACAACTGTCTCTATTGAACCAACGAGATATTCCACCGATTAAGTGTCAACATTGC	2088
QY	2043	CGTGGGTGCTTCCTCTCTCTCTCAACTCTGGGCTTTGTGCTCTACTTACAAGCG	2102
Db	2089	CGTGGGGCGTCTGCTCTCTCTCTCAACTTTAGCTTTTGGCGCTGTACTACAAAA	2148
QY	2103	GGACCGCGGCGAGGCTGGGTGCGAGGGGCTTAGCCACCTGGCGGCTCAGGCTCTGG	2162
Db	2149	GGACAGAGCGGCATGAGACTCAGAGGCGCCCATGTCCTCCCAAGAGAAACCCACAAATGA	2208
QY	2163	CGTGTGTGGGGGCCCTGTCTCCCGCGGGGCGGTGAGCTGCCACAGAGAGGA	2222
Db	2209	TATCGCTCAATCCAGAAAGAAAGATCATGTCTCTGCAGATGAAGACGCTGGAACGA	2268
QY	2223	GCTGGGTCTACTGACGTCAGCGGGTGGTGGCTGGGGCGGACCTTCGAGGCTCT	2282
Db	2269	TACAGAGTGTAGTTCCTGCG-----GACACGACACACT	2304

PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083332.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 30-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 07-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 18-MAY-1998; 98US-0085704.
PR 22-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX (GETH) GENENTECH INC.

PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
XX P-PSDB; AA41740.

XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders

XX Claim 2; Fig 150; 530pp; English.

XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders, depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AA43391 to
XX AA43438, and AA41685 to AA41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.

SQL	Sequence	3113 BP; 853 A; 867 C; 712 G; 681 T; 0 other;
	Query Match	36.4%; Score 912.2; DB 20; Length 3113;
	Best Local Similarity	64.7%; Pred. No. 2.3e-145;
	Matches 1503; Conservative	0; Mismatches 748; Indels 72; Gaps 7;
QY	108	CGCGAGGAGCGCTTCCCGGTGGTGAACACCGCCTACGGGCGAGTGCAGGTGTGGCGG 167
DB	112	CAGCCAAAGCAGATATCCAGTTGTCAACACAAATTTATGGCAAAATCCGGGGCTAAGAAC 171
QY	168	CGAGCTCAACACGAGATCCTGGGCGCGCTGTGTCAGTTCTTGGCGCTGCCCTAGCCAC 227
DB	172	ACCGTTACCCATGAGATCTTGGGTCCAGTGGAGAGTACTAGGGGTCCCTCTATGCCTC 231
QY	228	GGCGCCCTGGGCGCGCGCTTCCAGCGCCTGAGGCGCGCGCTGTGGCGCGCGGT 287
DB	232	ACCCCCCACTGGAGAGAGCGGTTTTCAGCCCCCAGAACCCCGCTCTCTTGAGCTGGCAT 291
QY	288	GGGCAACGCCACCCCTGCCGCGCGCTGCCCGAGAACCTTGCAGC---GGGCGCTGCC 344
DB	292	CCGAATATCTACTCAGTTTGTCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351
QY	345	CGCCATCATGTGCTGTGTGCTTACCGCAACTTGGAGCGCGCGCCACCTACGTGCA 404
DB	352	GCATGACATGCTGCCATCTGCTTACCGCAATTTGGATCTTTGATGACCTATGTCA 411
QY	405	GAACGAGGAGGAGTGCCTGTACTCAACTTACGTGCCACCGAGGAGCGTCCGCT 464
DB	412	AGATCAAAATGAAGACTGCTTACTTAAACATCTAGTGCACACGGAAGATGGACAA 471
QY	465	CACAAAACGTCACGAGGCG-----ACGCTCAATCCCGCCAGACACAGATATCG 515
DB	472	CACAAAGAAACGACATGATATACGAGTAATGACCGTGTGAAGACGAATATTTCA 531
QY	516	TGACCTTG---GGAAGAGCGCTGTGATGCTGTTTCTCCATGCGGCGCTCTACATGAGGG 572
DB	532	TGATCAGAAACAGTAAAGACCGCTCATGCTTATATCCATGGGGATCTTACATGAGGG 591
QY	573	GACCGAAACATGTTCCATGGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
DB	592	CACCGCAACATGATGACCGGACGATTTTGGCAAGCTACGGAACCTCATCGTGAATCAC 651
QY	633	GCTCACTACCGTCTTGGGTGCTCGGTTTTCTCAGCACCGGAGCACGAGCTGCAAAAGG 692
DB	652	CATTAACCTACCGCTGGAATCTAGGGTTTTTAAGTACCGTGCACGAGCAGCAGCAAAAGG 711
QY	693	CACTATGGCTCTGACACAGATCCAGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
DB	712	CACTATGGCTCTGCTGATCAGATTCAAGCACTGCGTGTGATTCAGGAGAAATGTGGAGC 771
QY	753	CTTTGGGCGGACCCCGAGCGTATCACCATCTTTTGGTTCCGGGCGAGGCGCTCTCGCT 812
DB	772	CTTTGGGCGGACCCCGAGAGTGAACCTCTTTGGCTCGGCGCTGCGGCGCTCTCGTGT 831
QY	813	CACCTTCTGATCTCTCCACCATTCAGAGGCTGTTCCAGAGGCGCTACGCCACAG 872
DB	832	CAGCTCTTGACCTGTCCCACTACTCAGAAAGTCTCTTCCAGAGGCGCTATTCAGAG 891
QY	873	TGCGACCGCTTTCAGCTGCTGTCTCACTACGAGCGCTCAAGTACACGCGCTGCT 932
DB	892	CGGACCGCGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
QY	933	GGCAGCAAGGTGGCTGTGACCGAGAGGACAGTGTGCTGAAGCTGTGAGTGTCTGGCGCG 992
DB	952	GGCAGCAAGGTGGCTGTGCAACATGCTGGACACCAACCGACATGTTAGATGCTTGGCGAA 1011
QY	993	GAAGCCCTCCGGAGCTGTGACAGGAGCTGTCAGGCTGTCGCGCTACCATCGCTT 1052
DB	1012	CAAGAACTACAGGAGCTCATCAGCAGACCATCACCCCGGCGCTACCATACAGCTT 1071
QY	1053	TGGGCGCGGTGATGGAGTGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1112
DB	1072	CGGCGCGGTGATCGAGCGGAGCTCATCCAGACGACCCCGAGATCTCTGATGGAGCAGG 1131

1113 AGAATTCCTCACTAGCATGCTCATCGCGTCAACAGGAGAGAGCGCTCAAGTTGCT 1172
 1132 CGAGTTCTCTCACTAGCATGCTCGCGTCAACAGGAGAGAGCGCTCAAGTTGCT 1191
 1173 GGAGGACTCTGACAGAGAGAGAGAGCGTGTGCTGCGAGCGCTTTGACTTCACTGTCTC 1232
 1192 GACCGGATCGTGATTAACAGGAGCGTGTGACGCGCAACGACTTTGACTTCTCGGTGC 1251
 1233 CAACTTTGTGACAACTGTATGCTTACCGGAGAGAGAGAGAGTGTCTCGGAGAGCAT 1292
 1252 CAACTTTGTGACAACTTTTACCGCTTACCGTGAAGGAGAGAGACATTTGCGGAGAGCAT 1311
 1293 CAACTTTGTGACAACTTTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1352
 1312 CAACTTTGTGACAACTTTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1371
 1353 GCTGGGCTCTTACTGACCACTGACCACTGACCACTGACCACTGACCACTGACCACTGCA 1412
 1372 GGTGGTCTCTTACTGACCACTGACCACTGACCACTGACCACTGACCACTGACCACTGCA 1428
 1413 CGCGAGTACAGTCTCCGCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 1472
 1429 CGCGAGTACAGTCTCCGCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 1488
 1473 CGCGAGTACAGTCTCCGCTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 1532
 1489 GAAGCCAGTCTGCGGAG 1548
 1533 CATGGTGGTGGCCAGGAGTCTTCCGCTTACTTACTTACTTACTTACTTACTTACTTACT 1592
 1549 CATGATCGTGGCCAGGAGTCTTCCGCTTACTTACTTACTTACTTACTTACTTACTTACT 1608
 1593 TGCGGTGCTCATGACCTTACTGACCACTTCCGAGAGTGGGAGAGAGAGAGAGAGAGAG 1652
 1609 CGCGGTGCTCATGACCTTACTGACCACTTCCGAGAGTGGGAGAGAGAGAGAGAGAGAG 1668
 1653 GCGGAGGATACCAAGTCTATCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1712
 1669 TCCTCAGGATACCAAGTCTATCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1728
 1713 CAAATTCACAG 1772
 1729 CAAATTCACAG 1788
 1773 CAAATTCACAG 1832
 1789 TCCTCAGGATACCAAGTCTATCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1848
 1833 GCA-----CACGAGAGTCTTCCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
 1849 GAAAGAGATATTCAAGTATGTTTCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1908
 1884 CTGGCGGCTCTGTCCT 1943
 1909 ATTTCCTATGGAACCGGAGAGTCTCCGAGAGATATGGCCAAACCAACCAAGAGAGAG 1968
 1944 CTGGCTCTGAG 1982
 1969 AATCACTCTCTGCAACCAATCCCAACCACTCTAAGAGAGAGAGAGAGAGAGAGAGAGAG 2028
 1983 CTATGAGCGGTTCCCGGAGAGTCTACCGGAGTCTACCGGAGTCTACCGGAGTCTACCGG 2042
 2029 CAACTTGTCTCTATTGAAACCAAGAGAGATATTCACCGAATTAAGTGTCTACCGATGTC 2088
 2043 GGTGGGTGCT 2102
 2089 GGTGGGTGCT 2148
 2103 GGACCGGCGAGAGAGTCTCGGTGCAAGGAGAGTCTAGCCAGTCTGCGGAGTCTAGGCTCT 2162
 2149 GGACAGAGAGCGCATGAGACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2208

2163 CGTGCTGCTGGGGGCGCCCTGCTCCCGCGCGCGCGCTGAGCTGCCACACAGAGAGAGGA 2222
 2209 TATCGCTCATCATCAAGAACGAGAGATCATGCTCTCGAGATGAGCAGCTGGACACGA 2268
 2223 GTTGTGTCTACTGACAGCTGAAGCGGGGTGGTGGCGTTCGGGGCGGACCCCTGCGAGGCTCT 2282
 2269 TCACGAGTGTGAGTGCCTGCGAG-----GCACACGACACACT 2304
 2283 GGGCCCTGCTGCTCCCGCGCGCGCTACACCCCTGCGCGCGCGCGCGCGCGCGCGCGCG 2342
 2305 GAGGCTCACTGCTCCCGCGCGCGCTACACCCCTGCGCGCGCGCGCGCGCGCGCGCGCG 2364
 2343 TCTTGTGGCGCGCGCGCGCGCGCTGACCCCTGCTGCGCGCGCGCGCGCGCGCGCGCG 2385
 2365 ACTTATGACGCCAAACACACCATCATCATGATTCACCAACACACTG 2407

RESULT 13

AAC78552
 ID AAC78552 standard; cDNA; 3113 BP.
 XX AAC78552;
 XX AC
 XX XX
 DT 08-FEB-2001 (first entry)
 XX XX
 DE Human PRO701 (UNQ365) nucleotide sequence SEQ ID NO:374.
 XX XX
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 expressed sequence tag; detection; cancer; ss.
 XX OS
 XX Homo sapiens.
 XX WO2000053756-A2.
 XX PD
 XX 14-SEP-2000.
 XX PF
 XX 18-FEB-2000; 2000WO-US04341.
 XX 08-MAR-1999; 99WO-US05028.
 XX 12-MAR-1999; 99US-0123957.
 XX 29-MAR-1999; 99US-0126773.
 XX 21-APR-1999; 99US-0130232.
 XX 28-APR-1999; 99US-0131445.
 XX 14-MAY-1999; 99US-0134287.
 XX 23-JUN-1999; 99US-0141037.
 XX 26-JUL-1999; 99US-0145698.
 XX 29-OCT-1999; 99US-0162506.
 XX 30-NOV-1999; 99WO-US28313.
 XX 02-DEC-1999; 99WO-US28551.
 XX 02-DEC-1999; 99WO-US28565.
 XX 16-DEC-1999; 99WO-US30095.
 XX 30-DEC-1999; 99WO-US31243.
 XX 30-DEC-1999; 99WO-US31274.
 XX 05-JAN-2000; 2000WO-US00219.
 XX 06-JAN-2000; 2000WO-US00277.
 XX 06-JAN-2000; 2000WO-US00376.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
 PI Kijavini IJ, Kuo SS, Napier WA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2000-611443/58.
 DR P-PSDB; AAB44296.
 XX

XX Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 XX
 PS Claim 2; Fig 150; 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 SQ Sequence 3113 BP; 853 A; 867 C; 712 G; 581 T; 0 other;
 Query Match 36.4%; Score 912.2; DB 21; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 2.3e-145;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;
 QY 108 CGGCGAGGAGCGCTTCCCGGTGGTGAACACGGCTACGGCGGAGTGGCGGTGGCGG 167
 DB 112 CAGCCAGCAGATATCCAGTGTGTCACACAAATTTGGCAAAATCCGGGCGCTAAGAAC 171
 QY 168 CGAGCTCAACACAGAGATCTCGGCGCCGCTGTCGACAGTCTTGGGCGTGCCTTACGCCAC 227
 DB 172 ACCGTTACCCAAATGAGATCTTGGGTCCAGTGGAGAGTACTTAGGGGTCCCTATGCCTC 231
 QY 228 GCGCGCCCTGGGCGCCGCGCTTCCAGCGCTGAGGCGCGCGCTCGTGGCGCGGCGT 287
 DB 232 ACCCCCACTGGAGAGAGGGGGTTTTCAGCCCCCAGAAACCCCGTCTCTGGACTGGCAT 291
 QY 288 GCGCAAGCGCACCAACCTGCGCGCCGCTGCGCGCAGAACTTGCACG---GGGCGGTGC 344
 DB 292 CCGAAATACTACTCAGTTTCTGCTGTGTGCGCCCGACACCTGGATGAGAGATCTTACT 351
 QY 345 CGCCATCATGCTGCTGTGTGTGTACACGACACTTGGAGGGCGGCCACCACTACGTGCA 404
 DB 352 GCGATCATGCTGCCCATCTGGTTTACCGCCAAATTTGGATATTTGATGACCTATGTTCA 411
 QY 405 GAACCCAGAGCGAGACTGCTGTACCTCAACCTCTACGTGCGCCACCGAGGAGCGTCCGT 464
 DB 412 AGATCAAAATGAAGACTGCTGCTTACTTAAACATCTACGTGCGCCACGGAAGATGGAGCMA 471
 QY 465 CACAAAAAAGGTGACGAGCG-----ACGCTCAATCCCGCAGACACAGATATCCG 515
 DB 472 CACAAAAAAGAAACGAGATGATATACGAGTAAATGACGCTGTGAAGACGAGATATCA 531
 QY 516 TGACCCCTG---GGAAGAACCTGTGATGCTGTTCTCCATGCGCGCTCTACATGGAGG 572
 DB 532 TGTATGAAACAGTAAGAGCCCGTATGCTCTATATCCATGGGGGATCTTATCATGGAGG 591
 QY 573 GACCGAAACATGTTTGTGATGCTCAGTCTGCTGCTGCTATGCAACGTCATTTGTAGCCAC 632
 DB 592 CACCGCAACATGATGACGCGAGCATTTTGGCAAGCTACGGAACGTCATCGTATCAC 651
 QY 633 GCTCACTACCTCTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692
 DB 652 CATTAATACCTCTGGGAATACTAGGGTTTAAAGTACCGGTGACCGAGGAGCAAAAGG 711
 QY 693 CAACATATGGGCTCCTGGACAGATCCAGCCCTGCGCTGCGTCTGCTGCTGCTGCTGCTG 752
 DB 712 CAACATATGGGCTCCTGGATCAGATTCAGCACTGCGGTGGATTGAGGAGATGCGGAGC 771
 QY 753 CTTTGGGGGCGACCCGAGCGATCAGCATCTTTGGTTCGCGGGGAGGGGCTCTCTGCT 812
 DB 772 CTTTGGCGGGGACCCCAAGAGAGTACCATCTTTGGCTCGGGGGCTGGGGGCTCTGCT 831
 QY 813 CAACCTTCTGATCTCTCCACCATTCAGAGGGGTGTTCCAGAGGCCATCGGCCAGAG 872
 DB 832 CAGCGTGTGACCTGTCCCACTACTCAGAGGTCTCTTCCAGAGGCCATCATTCAGAG 891
 QY 873 TGGCACCGCATTTCCAGTGTGTGTCAACTACAGCGCTCAAGTACACGCGGCTGCT 932

DB 892 CGGCACCGCCCTGTCCAGCTGGGAGTGAACTACCCAGCGCGCAAGTACACTCGATATT 951
 QY 933 GGCACCCAGGTGGGCTGTGACCGAGAGAGACAGTCTGCTGAGTGTGAGTGTCTTGGCGG 992
 DB 952 GGCACACAGGTGGGCTGTGCAACATCTGGACACCAACGACATGTGTAGATGCTCTCGGAA 1011
 QY 993 GAAGCCCTTCCCGGAGCTGGTGGACAGGACGTGCGAGCTGCGCCCTACCACTGCGCTT 1052
 DB 1012 CAAGAACTACAAGGAGCTCATCCAGCAGACCATCAACCCCGCCCTACCACTAGACCTT 1071
 QY 1053 TGGGCCCCGTGGTGTGAGCGAGTGTCTCCGATGACCTGAGATCTCTATGACAGAGG 1112
 DB 1072 CGGGCCGCTGTATCGACGCGGACGTCATCCAGACGACCCCGAGATCTCTGATGGAGCAAG 1131
 QY 1113 AGAAATTCCTCAACTACGACATGCTCATCGGCTCAACACGAGGAGAGGCGCTCAAGTCTG 1172
 DB 1132 CGAGTTCCTCACTAGACATCATGCTGGGCTGTCAACAGGGGAGAGCGCTTGAAGTCTG 1191
 QY 1173 GGAGACTCTTGAGAGAGCGAGCGGTGTGTCTGCCAGCGCTTTGACTTTCACCTGCTC 1232
 DB 1192 GAGCGCATCTGGATTAACGAGGACGCTGTGACGCCCAACGACTTTGACTTCTCGGTGTC 1251
 QY 1233 CAACCTTCTGGACAACTGTATGCTACCCGAGAGGCAAGATGTGCTTCGGGAGACCAT 1292
 DB 1252 CAACCTTCTGGACAACTTTACGGCTACCTTGAAGGAAAGACACTTTGGGGGAGACTAT 1311
 QY 1293 CAAGTTATGTACACAGACTGGGCGGACCGGGAACAATGGGGAATGCGCGCAAAACCT 1352
 DB 1312 CAAGTTATGTACACAGACTGGGCGGATAGGAAACCCCGAGAGCGCGCGGAAACCT 1371
 QY 1353 GCTGGGCTCTTACTGACACCAATGGGTGGACACAGCTGTGGCCACTGTGCCAAGCTGCA 1412
 DB 1372 GGTGGCTCTCTTACTGACCAACAGTGGGTGGGCGCGCGCTGCGCC---GCCGACCTGCA 1428
 QY 1413 CGCGCACTACAGTCTCCCGTCTACTTTTACACCTTACACCACTGCGAGGCGGAGG 1472
 DB 1429 CGCGCAGTACGGCTCCCGACCTTCTATGCTTCTATCACTACCTGCAACAGCGAAT 1488
 QY 1473 CGGCGCTGAGTGGGCGAGATGCGGGCGACGGGATGAACCTGCTTATGCTTTGTCGTCG 1532
 DB 1489 GAAGCCCGAGCTGGGCGAGATTCGGGCCCATGGTGTGAGTGGTCCCTATGCTTCGCGATCCC 1548
 QY 1533 CATGGTGGTGGCCACCGACCTCTTCCCTGTAACTTCTCCAAAGATGACGCTCATGCTCAG 1592
 DB 1549 CATGATCGTCCCGACCGAGCTCTTCACTGTGTAATCTTTCCAGAACGACGCTCATGCTCAG 1608
 QY 1593 TGGCGTGTATGACCTCTGACCACTTTCGCAAGACTTGGGGACCCCAACCGAGCGGT 1652
 DB 1609 CGCGGTGTATGACCTTACTGGACGAACTTGGCCAAATCTGGTGTATCCAAATCAACAGT 1668
 QY 1653 GCGCAGGATACCAAGTTCATCCACACCGAGCCCATCGCTTCGAGAGGTGTGTGGAG 1712
 DB 1669 TCTCAGATACCAAGTTCATCCACAAACCCCAACCCGCTTTGAAGAGTGGCGCTGGTC 1728
 QY 1713 CAATATCAACAGACAGAGAGAGCAGTATCTGACATAGGCTGAAGCCACGCGTGTGCTGA 1772
 DB 1729 CAAGTATAATCCCAAGACCCAGCTCTATCTGCATATTGGCTTTGAACCCAGAGTGAAGA 1788
 QY 1773 CACTACCGGCGCAACAGGTGCGCTTCTGCTGAGTCTGTGCGCCACCTGCAACCT 1832
 DB 1789 TCACTACCGGCGCAACAGAGTGGCTTCTGGTGGAACTGCTTCTCATTTTGCACAACTT 1848
 QY 1833 GCA-----CACGGAGCTCTTCAACACCAACCGCGCTTCCCTACGCCACCGG 1883
 DB 1849 GAACGAGATATTCAGTATGTTTCAACACCAACCAAGGTTCTCCACACAGATGACATC 1908
 QY 1884 CTGGCGCGCTCTGTCGCCCGCTGGGCGCCCGGGGACACGCGCGCGCGCGCGCTGCGCAC 1943
 DB 1909 ATTCTCTATGCAACCGCGGATCTCTCCGCAAGATATGGCCAAACCAACAAACGCGCCAGC 1968
 QY 1944 CTGCGCTCCGAGCGCGCGCGCGAG-----CGGCGCGCGAGGCG 1982
 DB 1969 AATCACTCTCTGCCAACAATCCCAACACTCTAAGGACCTCTCAAAAACAGGCGCTGAGGA 2028

QY 1983 CTATGACCGTCTCCCGGAGCTCAGGGACTACTCAGCGAGCTAGCGTCACTGGC 2042
 Db 2029 CACAACCTGTCTTATTGAAACCAACAGAGATTATTCACCGAATTAAGTGTACCAATTGC 2088
 QY 2043 CGTGGGTGCTCCCTCTCTTCTTCTCAACATCTCTGGCTTTGCTGCTCTTACTACAGCG 2102
 Db 2089 CGTGGGGCTGCTCTCTCTTCTCAACATCTTGTAGCTTTTGGCGCTGTACTACAAA 2148
 QY 2103 GGACCGCGCAGAGCTGGGTGCGAGCGGCTTAGCCACCTGGCGGCTCAGGCTCTGG 2162
 Db 2149 GGACAGAGCGGCATGAGACTCAGAGCGGCCCTCCAGAGAAACACCAAAATGA 2208
 QY 2163 CGTCCCTGTGGGGGCGCCCTGCTCCCGCGCGCGCTGAGCTCCACACGAGAGGA 2222
 Db 2209 TATCGCTCACATCAGAAAGAGATCATGCTCTGAGATGAACAGCTGGAACAGA 2268
 QY 2223 GCTGGTGTACTCAGCTGAGCGGGTGTGGCTCGGGCGGACCCCTGCCAGGCTCT 2282
 Db 2269 TCAGAGTGTAGTCTGCTGAG-----GCACACGACACACT 2304
 QY 2283 GCGCCCTGCTGCCCGCCGACTACACCTGCGCCCTGCGCGCGGACCGGAGTGTGCC 2342
 Db 2305 GAGGCTCAGCTGCCCGCAGACTACACCTCAGCTGCGCGCGGTCCGAGATGATCC 2364
 QY 2343 TCTCTGGCCCCCGGGCGCCCTGACCCCTGCTGCCAGTGGCCTG 2385
 Db 2365 ACTTATGAGCCCAACACCATCACCATGATTCACAAACACACTG 2407

RESULT 14

ABX92581
 ID ABX92581 standard; cDNA; 3113 BP.

XX AC ABX92581;

XX DT 08-MAY-2003 (first entry)
 XX DE cDNA encoding human PRO701 polypeptide.

XX KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
 KW cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 KW genetic disorder; cytosolic; antidiabetic; antiinflammatory;
 KW antithratic; anti-tumour; vulnary; antianaemic; dermatological;
 KW cardiant; gene; ss.

XX OS Homo sapiens.

XX PN US2002169284-A1.

XX PD 14-NOV-2002.

XX PF 16-OCT-2001; 2001US-0978697.

XX PR 07-OCT-1998; 98WO-US21141.
 PR 20-NOV-1998; 98WO-US24855.
 PR 05-JAN-1999; 98WO-US00106.
 PR 08-MAR-1999; 98WO-US05028.
 PR 10-MAR-1999; 98WO-US05190.
 PR 14-MAY-1999; 98WO-US10733.
 PR 02-JUN-1999; 98WO-US12252.
 PR 30-NOV-1999; 98WO-US28313.
 PR 02-DEC-1999; 98WO-US28551.
 PR 02-DEC-1999; 98WO-US28565.
 PR 16-DEC-1999; 98WO-US30095.
 PR 30-DEC-1999; 98WO-US31243.
 PR 05-JAN-2000; 98WO-US31274.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 28-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 22-MAR-2001; 2001WO-US09552.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 17-OCT-1997; 97US-062250P.
 PR 03-NOV-1997; 97US-064249P.
 PR 13-NOV-1997; 97US-065311P.
 PR 21-NOV-1997; 97US-066364P.
 PR 10-MAR-1998; 98US-077450P.
 PR 11-MAR-1998; 98US-077632P.
 PR 11-MAR-1998; 98US-077641P.
 PR 11-MAR-1998; 98US-077649P.
 PR 12-MAR-1998; 98US-077791P.
 PR 13-MAR-1998; 98US-078004P.
 PR 20-MAR-1998; 98US-078866P.
 PR 20-MAR-1998; 98US-078910P.
 PR 20-MAR-1998; 98US-078936P.
 PR 20-MAR-1998; 98US-078939P.
 PR 25-MAR-1998; 98US-079294P.
 PR 26-MAR-1998; 98US-079656P.
 PR 27-MAR-1998; 98US-079663P.
 PR 27-MAR-1998; 98US-079664P.
 PR 27-MAR-1998; 98US-079689P.
 PR 27-MAR-1998; 98US-079728P.
 PR 30-MAR-1998; 98US-079786P.
 PR 30-MAR-1998; 98US-079920P.
 PR 26-MAY-1981; 81US-0267213.
 PR 17-MAR-1998; 98US-0040220.
 PR 26-JUN-1998; 98US-0105413.
 PR 07-OCT-1998; 98US-0168978.
 PR 02-NOV-1998; 98US-0184216.
 PR 06-NOV-1998; 98US-0187368.
 PR 07-DEC-1998; 98US-0202054.
 PR 22-DEC-1998; 98US-0218517.
 PR 05-MAR-1999; 99US-0254465.
 PR 10-MAR-1999; 99US-0256586.
 PR 12-APR-1999; 99US-0284291.
 PR 14-MAY-1999; 99US-0311832.
 PR 14-MAY-1999; 99US-0380137.
 PR 25-AUG-1999; 99US-0380138.
 PR 25-AUG-1999; 99US-0380142.
 PR 08-NOV-2000; 2000US-0709238.
 PR 27-NOV-2000; 2000US-0721749.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-MAR-2001; 2001US-0816744.
 PR 22-MAR-2001; 2001US-0816920.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 30-JUL-2001; 2001US-0918585.

XX PA (GETH) GENENTECH INC.

XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PU, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
DR P-PSDB; ABU61126.
XX
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies
XX
XX Claim 2; Fig 150; 459pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists. The
CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
CC apoptosis or death of the cell. The PRO polypeptides are useful for
CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
CC cardiac insufficiency, nervous system disorders, kidney disorders,
CC bone and cartilage disorders or arthritis, tumours, and wound healing.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
CC generating transgenic animals or knockout animals, and for genetic
CC analysis of individuals with genetic disorders, and in gene therapy.
CC The present sequence encodes a human PRO polypeptide of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdsIDEntry.html.
XX
XX Sequence 3113 BP; 853 A; 867 C; 712 G; 681 T; 0 other;

Query Match 36.4%; Score 912.2; DB 25; Length 3113;
Best Local Similarity 64.7%; Pred. No. 2,3e-145;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 108 CGCGAGGAGCGCTCCCGTGGTGAACACGCGCTACGCGGAGTGCCTGTCGCGCG 167
DB 112 CAGCCCAAGCACAGTATCCAGTGTCTCAACACAAATATGCAAAATCCGGGCGCTAAGAAC 171
QY 168 CGAGCTCAACACAGAGATCCTGGGCGCCGCTGTGAGTCTTCTGGCGTGCCTACGCCAC 227
DB 172 ACCGTTACCAATGAGATCTTGGTCCAGTGAGCAGTACTTAGGGGTCCCTATGCCCTC 231
QY 228 GCCGCCCTGGCGCGCCGCTTCCAGCGCTTACGCGCGCTGAGCGCGCGCTGTGGCGCGCGT 287
DB 232 ACCGCCCACTGAGAGAGAGCGGTTTACGCCCGCCAGAACCCCGCTCTCTGAGTGGCAT 291
QY 288 GCGCAACGACACCGCTGCGCGCGCGCTGCGCGAGAACCTGTGACG---GGCGCTGCC 344
DB 292 CGGAATACTACTCAGTTGTGCTGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 351
QY 345 CGCCATCATGCTGCTGT 404
DB 352 GCATGACATGCTGCCATCTGGTTTACCGCCAAATTTGGATTTGTGATGACTATGTTC 411
QY 405 GACACAGAGCGAGGAGTCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
DB 412 AGATCAAAATGAAGACTCGCTTACTTAAACATCTACGTCGCCACCGAAGATGAGCCAA 471
QY 465 CACAAAAAAGCTGACGAGCGGCG-----ACGCTCAATCCGCGACACAGATATCCG 515
DB 472 CACAAGAAAGACGAGATGATATACAGATATGACCGTGTGAGAGAGAGATATTC 531
QY 516 TGACCCCTG---GGAAGAACGCTGTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 572

DB 532 TGATCAGAACAGTAAGAAGCCCGTCAATGCTATATATCCATGGGATCTTATATGAGGG 591
QY 573 GACCGGAACAGATGTCAGTGTGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632
DB 592 CACCGGCAACATGATGACGCGCAGCATTTTGGCAAGCTACGGAACCGTCACTGCTGATCAC 651
QY 633 GCTCAACTACCGTCTTGGGGTGTCTCGGTTTCTCAGCACCGGGGACCAAGGTCGCAAAAGG 692
DB 652 CATTAACCTACCGTCTGGGAATACAGGTTTAAAGTACCGGTGACCGAGCAGCAAAAGG 711
QY 693 CAACCTATGGGCTCTGACACAGATCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 752
DB 712 CAACCTATGGGCTCTGATTCAGATTCAGGACTCGGCTGATTCAGGAGATGCTGGGAGC 771
QY 753 CTTTGGGGGCGACCCCGAGCGTATCAGCATCTTTGGTTCCGGGCGCAGGGGCTCCTGCTG 812
DB 772 CTTTGGGGGCGACCCCGAGAGATGACATCTTTGGTCTGGGGCTGGGGCTCCTGCTG 831
QY 813 CAACCTTCTGATCTCTCCACCATTCAGAGGCTTTCCAGAGGCTTCAGAGGCTTCAGAGG 872
DB 832 CAGCTGTGTGACCTGTCCCACTACTCAGAGGCTCTCTCCAGAGGCTTCATTCAGAG 891
QY 873 TGGCACCGCATTTCCAGCTGCTGTCACTACCGCGCTCAAGTACAGCGGCTGCT 932
DB 892 CGGACCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
QY 933 GGCAGCCAAAGTGGTGTGACCGAGAGGAGTGTCTGAAGCTGTGAGTGTCTGCGCGCG 992
DB 952 GGCAGACAAAGTGGTGTGACCGAGAGTGTCTGAGACACCGAGCATGTAGATGCTGCGGAA 1011
QY 993 GAAGCCCTCCCGGAGGCTGTGACCGAGAGTGTGAGCTGCGGCTGCGGCTGCGGCTGCGGCT 1052
DB 1012 CAGAACTACAAGAGCTCTCAGAGAGTGTGACCGAGAGTGTGAGCTGCGGCTGCGGCTGCGGCT 1071
QY 1053 TGGGCGCGTGTGATGAGTGTGCGGAGTGTGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1112
DB 1072 CGGCGCGTGTGATGAGTGTGCGGAGTGTGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1131
QY 1113 AGAATTCCTCACTACAGATGCT 1172
DB 1132 CGAGTTCCTCACTACAGATGCT 1191
QY 1173 GAGGAGCTCTGACAGAGCGAGGAGTGTGCT 1232
DB 1192 GAGCGCATCTGTGATGAACGAGAGCGTGTGAGCGCCCAAGCATTTGACTTCTCGGTGTC 1251
QY 1233 CAACCTTGTGGAACAACCTGTATGCT 1292
DB 1252 CAACCTTGTGGAACAACCTGTATGCT 1311
QY 1293 CAAGTTTATGTACACAGCTGCGGCGAGCGGAGCATGCGGAATGCGCGCGCGCAAAACCT 1352
DB 1312 CAAGTTTATGTACACAGCTGCGGCGAGCGGAGCATGCGGAATGCGCGCGCGCAAAACCT 1371
QY 1353 GCTGGCGCTCTTTACTGACCAACATGCGTGTGCGCACCGAGTGTGCGGCTGCTGCGCAAGTGCA 1412
DB 1372 GGTGGCTCTCTTACTGACCAACCTGTATGCT 1428
QY 1413 CGCGGACTACAGCTGCTCCCGTCTACTTTTACACTTCTACACGCTGCGGAGCGGAGCGGAGG 1472
DB 1429 CGCGGAGTACGCTGCTCCCGCTCTCTTCTATGCT 1488
QY 1473 CGGCGCTGATGGGAGAGTGTGCGGCGCACCGGAGTGAACCTGCGCTTATGCTTCTTGGGCTGCG 1532
DB 1489 GAAGCCAGCTGGGAGATTCGCGCCATGCTGATGAGGTCCTGCT 1548
QY 1533 CATGTGGGTGCGACCGGAGCTTCCCTGTAACTTCTCCAAAGATGAGCTCATGCTGAG 1592
DB 1549 CATGATCGGTGCCACCGAGCTTTCAGTTGTAACTTTTCCAAAGACGAGCTCATGCTGAG 1608
QY 1593 TGGCGTGTGCTGATGCTACTGAGCACTTCCCAAGACTTGGGAGCGCCCAACCGAGCGCT 1652

Db 1609 CGCGTGGTCACTACCTACTGGACGAACTTCGCAAAACTGGTGATCCAAATCAACCACT 1669
Qy 1653 GCGCGAGGATACCAAGTTTCATCCACACCAAGCCCAATCGCTTCGAGGAGGTGGTGGAG 1712
Db 1669 TCCTCAGGATACCAAGTTTCATCCACAAACCCCAACCGCTTTGAAGAAGTGGCTGGTC 1728
Qy 1713 CAAATTCACACAGCAAGGAGAGCAGTATCTGCACATAGGCTGGAAGCCACGCGTGGTGA 1772
Db 1729 CAAATTCACCAAGAGCCAGCTCTATCTGATATGGCTTGAACCCAGAGTGAGAGA 1789
Qy 1773 CAACTACCGGCGCAACAAAGTGCGCTTCGCTGGAGCTCGTGGCCCACTGCACAACT 1832
Db 1789 TCACTACCGGCGCAACAAAGTGCGCTTCGCTGGAGCTCGTGGCCCACTGCACAACT 1848
Qy 1833 GCA-----CACGAGCTTCACACACCAAGCGCTTCCTCCCTACGACCGCG 1883
Db 1849 GAACGAGATTCAGATGTTTCAACAACCAAGGTTCTCCACAGACATGACATC 1908
Qy 1884 CTGGCGCTCTGCTCCCGCGCTGGCGCCCGGCGCACACCGCGCGCCCGCGCTGCCAC 1943
Db 1909 ATTCCCTATGGCACCGCGGATCTCCCGCAAGATATGGCCAAACCAACGCGCCAGC 1968
Qy 1944 CTGCTCTCGGAGCCGCGCGCGAGC-----CCGCGCCCAAGGCG 1982
Db 1969 AATCACTCTCGCAACAAATCCCAACACTCTAAGGACCTCAAAACAGGCGCTGAGGA 2028
Qy 1983 CTATGACCGCTTCCCGGCGACTCAAGGAGTACTCCAGGAGTACGCTCACCGTGGC 2042
Db 2029 CACAACTGCTCATTTGAACCAACGAGATTAATCCACGAAATTAAGTGCACCAATGC 2088
Qy 2043 CGTGGTGGCTCCCTCTCTCTCAACATCTGCGCTTTGTCGCTTCTACTACAAGC 2102
Db 2089 CGTGGGCGTGGCTCTCTCTCAACATCTAGCTTTTGGCGGCTGTACTACAAA 2148
Qy 2103 GACCGCGCGGAGAGCTCGGTGAGCGGCTTAGCCACCTGCGGCTCAGGCTCTGG 2162
Db 2149 GACACAGGCGGCTAGACTCAAGGCGCCCGAGTCCCGAGAAACACCAAAATGA 2208
Qy 2163 CGTGCTGGTGGGCGCCCTGCTCCCGCGCGCGCTGAGTGCACACAGAGGAGGA 2222
Db 2209 TATCGCTCACATCCAGAACGAGAGATCATGCTCTGAGATGAGCAGCTGGAACAGA 2268
Qy 2223 GCTGGTGTCACTGACGCTGAGCGGGGTGGTGGCTCGGGCGGACCTGCGGAGGCTCT 2282
Db 2269 TCACGAGTGTAGTCTGCTGCG-----GCACACGACACACT 2304
Qy 2283 GCGCGCTGCTCCCGCGCGACTACACCTGCGCCCTGCGCGCGGACCGGACGATGTGCC 2342
Db 2305 GAGGCTCACTGCGCGCGAGACTACACCTCAGCTGCGCGGTGCGCAGATGACATCCC 2364
Qy 2343 TCTCTTGGCGCGCGGCGCTGACCTGCTGCGCCAGTGGCGCTG 2385
Db 2365 ACTTATGACGCAACACCATCATGATTCACCAACACACTG 2407

RESULT 15
ID ABZ24056
XX AC ABZ24056 standard; DNA; 5454 BP.
XX AC ABZ24056;
XX DT 31-MAR-2003 (first entry)
XX DE CES2 related polynucleotide (GenBank identifier number GI# 6330940).
XX KW CES2; p53; cytostatic; gene therapy; human; angiogenic; cancer;
XX KW carboxylesterase; ds.
XX OS Homo sapiens.
XX PN WO200299041-A2.
XX PD 12-DEC-2002.

XX 03-JUN-2002; 2002WO-US17314.
XX 05-JUN-2001; 2001US-296076P.
PR 10-OCT-2001; 2001US-328605P.
PR 15-FEB-2002; 2002US-357253P.
XX (EXEL-) EXELIXIS INC.
XX Friedman L, Plowman GD, Belvin M, Francis-Lang H;
XX WPI; 2003-156848/15.
XX Identifying a candidate p53 pathway-modulating agent as therapeutic
XX targets for disorders associated with defective p53 function e.g.
XX cancer by contacting an assay system with a test agent where the system
XX provides reference activity -
XX Disclosure; Page 44-47; 60pp; English.
XX The invention relates to identifying a candidate p53 pathway modulating
XX agent. The method involves contacting an assay system comprising purified
XX CES2 polypeptide or nucleic acid, or their functionally active fragment
XX or derivative, with a test agent under conditions where, but for the
XX presence of the test agent, the system provides a reference activity.
XX The methods are useful for identifying modulators of the p53 pathway as
XX therapeutic targets for disorders associated with defective p53 function,
XX such as angiogenic, apoptotic or cell proliferative disorders, e.g.
XX cancer. The modulators are useful as research reagents, diagnostics and
XX therapeutics. Sequences ABZ24051-59 represent CES2 (carboxylesterase)
XX related polynucleotide sequences.
XX Sequence 5454 BP; 1514 A; 1314 C; 1208 G; 1418 T; 0 other;
XX Query Match 35.3%; Score 886.2; DB 25; Length 5454;
XX Best Local Similarity 64.0%; Pred. No. 5.6e-141;
XX Matches 1478; Conservative 0; Mismatches 728; Indels 105; Gaps 5;
Qy 108 CGCGGAGGAGCGCTTCCCGTGGTGAACACGCGCTACGGCGAGTGCAGGCTGGCGG 167
Db 584 CAGCCAGACAGATGATCCAGTTGTCAACAAATATGGCAAAATCCGGGGCGCTAAGAAC 643
Qy 168 CGAGCTCAACACAGAGATCTTGGGCGCCCTGCTGAGTTCTTTGGGCGTCCCTTACGCCAC 227
Db 644 ACCGTTACCGCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGTCCCTATGCTC 703
Qy 228 GCGCGCCCTGGGCGCGCGCTTCCAGCGCTGAGGCGCGCGCTCGTGGCGCGCGCT 287
Db 704 ACCCGCCACTGGAGAGCGGTTTCAGCCCCCAGAACCCCCGCTCTCTCTGAGCTGGCAT 763
Qy 288 GCGCAACGCCACCAACCTGCGCCCGCTGCGCCCGCAGAACCTGCAAG---GGCGCGCTGCC 344
Db 764 CCGAATACTACTCAGTTTGTGCTGTGTGCCCCCAGCACCTGGATGAGATCCTTACT 823
Qy 345 GCGCATCATGCTGCTGTGTGTTTACCGAGAACTTGGAGGGCGCGCGCTACGTGCA 404
Db 824 GCATGACATGCTGCTGCTGTTTACCGCAATTTGGATATCTTTGATGACCTATGTTCA 883
Qy 405 GAACACGAGCGAGGACTGCTGCTGCTCAACCTCTACGTCGCCACCGAGGAGCGTCCGT 464
Db 884 AGATCAATATGAGACTGCTTACTTAAACATCTACGTGCCACGAGATGATTTCA 943
Qy 465 CACAAAACGCTGAGAGGCGACCTCAATCCGCCACACAGATATCCGTGACCTGG 524
Db 944 TGATCAGAACAGT----- 956
Qy 525 GAAGAAGCGCTGATGCTGTTTCTCATGGGGCTCTTACATGGAGGGAGCGGAAACAT 584
Db 957 -AAGAGCCCGTCATGCTATATCCATGGGGATCTTACATGGAGGGACCGGCAACAT 1015
Qy 585 GTTCGATGGCTCAGTCTGCTGCTATGGCAACGCTATTGTAGCCACGCTCAACTACCG 644
Db 1016 GATTGACGCGCAGCATTTTGGCAAGCTACGAAACGCTCATCGTGTATCACTTAATACCG 1075

QY	645	TTCTGGGGTGTCTGGTGTCTTCTCAGCACCGGGAGACAGAGCTGCAAAAGGCAACTATGGGCT	704
Db	1076	TCCTGGGAATACTAGGGTTTTAAAGTACCGGTGACCAAGCAGCAAAAGGCAACTATGGGCT	1135
QY	705	CTTGAGCAGATTCAGAGCCCTGGCTGGCTCAGTGAATAACATGCCCACTTTGGGGCGGA	764
Db	1136	CTTGATCAGATTCAAGCACTCGGTGGATTAGAGAGAAATGGGGAGCCTTTGGCGGGGA	1195
QY	765	CCCCAGCGTATCACCATCTTTGGTTCCGGGGCAGGGCCCTCCCTGCTCAACCTTCTGAT	824
Db	1196	CCCCAAGAGATGACCATCTTTGGCTCGGGGCTGGGGCTCTCTGTGTAGCCTTGTTGAC	1255
QY	825	CTCTCTCCACCATTCAGAAGGGCTGTTCAGAAGGCCATGCCCCAGAGTGGCACCGCCAT	884
Db	1256	CTGTCTCCACTACTCAGAAGGTCTCTTCAGAAGGCCCATCATTCAGAGCGCACCGCCCT	1315
QY	885	TTCCAGCTGGTGTGTCFACTACCAAGCCGCTCAAGTACACGGGCTGTGTCAGCCCAAGGT	944
Db	1316	GTCCAGCTGGGAGTGAATACTACCAAGCCGCGCAAGTACACTCGGATATTGGCAGACAAGGT	1375
QY	945	GGGTGTGACCCGAGAGGACAGTGTGAAGCTGTGGAGTGTCTGCGCGGAAGCCCTCCCG	1004
Db	1376	CGGTCTCAACATGTCTGACACCAACCGGACATGGTAGAATGCTCGGAAACAAGAACTACAA	1435
QY	1005	GAGCTGTGTGACCAAGAGAGCTGACGCTGCCGCTACCAATGCCCTTTGGGCGCCGTGGT	1064
Db	1436	GAGCTCATTCAGCAGACCACTACCCCGGCCACCTACCAATAGCCTTTCGGGCGGTGAT	1495
QY	1065	GGATGGGACGTGGTCCCGCATGACCTGTAGATCCTCATCAGCAGGAGGAATTCCTCAA	1124
Db	1496	CGACGGCAGCTCATCCAGACGACCCCGACATCCTGATGAGCAAGGCGAGTTCCTCAA	1555
QY	1125	CTAGCATGTCTATCGGCTCAACAGGAGAGGGCTCAAGTTCGTGAGAGACTCTGC	1184
Db	1556	CTACGATCATGTCTGGCGGTCAACCAAGGGGAAGGCTTGAAGTTCTGGACGCGCATCGT	1615
QY	1185	AGAGAGCGAGGACGGTGTGTCTGCACGCGCTTGACTTCACCTGTCTCCAACCTTTCTGGA	1244
Db	1616	GGATAACGAGGACGGTGTGACGCCCAACGACTTGTGACTTCTCGTGTCCAACTTCGTGA	1675
QY	1245	CAACCTGTATGGCTACCGGAGGACAGGATGTGTTCTGGGAGACCATCAAGTTTATGTA	1304
Db	1676	CAACCTTTACGGCTACCTTGAAGGGAAGACACTTTTGGGGAGACTATCAAGTTCAATGA	1735
QY	1305	CACAGACTGGGCCGACCGGACAAATGCGCAAAATGCGCCAAACCTCTGTCGGCTCTT	1364
Db	1736	CACAGACTGGGCCGATGAAGGAACCCGAGACGCGCGGAANAACCTTGTGCTCTCTT	1795
QY	1365	TACTGACCAACATGGTGGCAACAGCTGTGGCCACTGCCAAGCTGCACCGCACTACCA	1424
Db	1796	TACTGACCAACAGTGGTGGCGCCCGCGTGGCCACCGCGACCTGCACGCGAGTACGG	1855
QY	1425	GTCTCCCGTCTACTTTTACACTTCTACACCACTGCCAGCGGAGGGCGGCGCTGAGTG	1484
Db	1856	CTCCCCACACTTCTTATGCTCTTATCATCTATCCAAAGGGAATGAAGCCAGCTG	1915
QY	1485	GGCAGATGCGCGCAACGGGATGAATGCCCTATGCTTTGGCGTGCCTCATGTCGGTGC	1544
Db	1916	GGCAGATTCGGCCCATGGTGATGAGGTCCCTATGCTTTCGGCATCCCCATGATCGTCC	1975
QY	1545	CACGACTCTTCCCTGTAACTTCTCAAGATGAGTCACTGCTCAGTGCCTGGTGTAT	1604
Db	1976	CACCGAGCTCTTCAGTTGTAACTTTTCCAGAAACGACGTCATGCTCAGCGCGGTGTAT	2035
QY	1605	GACCTACTGGAACAACTTCCGCCAAGACTGGGACCCCAACAGCGGTGCCAGGATAC	1664
Db	2036	GACCTACTGCGAACCTTCCGCCAABAACCTGGTGATCCAAATCAACAGTTCTCAGGATAC	2095
QY	1665	CAAGTTTCATCCACCAAGCCCAATCGTTCGAGGAGGTGGTGTGGAGCAAAATCAACAG	1724
Db	2096	CAAGTTTCATCAACAACAAACCAACCGCTTGAAGAGTGGCTGTGTCACGATTAATCC	2155

QY	1725	CAAGGAGACGAGTATCTGCACATAGCCCTGAAGCCACGCGTGCATGACAACTACCGCGC	1784
DB	2156	CRAAGACGAGCTTATCTGCATATTCGCTTGAACCCAGAGTGAGAGATCACTTACCGGGC	2215
QY	1785	CAACAAGGTGGCCTTCTGGCTGGAGCTCGTGCAGCTGCGCCACCTGCACAACTGCACAC	1838
DB	2216	AACGAAGTGGCTTCTGGTTGGAATCGTTCTCATTTGCACAACTTGAACGAGATATT	2275
QY	1839	---GGAGCTCTTACACACACACAGCGCTGCTCTCCTACGCCACGCGGTGCGCGCTCG	1895
DB	2276	CCAGTAGTTTCAACAACCAAAAGGTTCCTCACCAGACATGACATCATTTCCCTATGG	2335
QY	1896	TCGCCCCGCTGGCGCCCCGGGCGACACCGCGCCCCCGCGCTGCCACCTGCTCTCCCGA	1955
DB	2336	CACCGGGGATCTCCCGCCGACAGTATGGCCAAACCAACAAAGCCCGAGCAATCACTCTGC	2395
QY	1956	GCCTGAGCCCGAGC-----CCGGCCCCAAGGCCCTATGACCGCTT	1994
DB	2396	CAACAATCCCAAACTCTAAGGACCCCTCACAAAACAGGCGCTTGAGGACACAACCTGCTCT	2455
QY	1995	CCCGGGGACTCACGGGACTTACTCCACGAGCTGAGCGTCAACGTGGCGGTGGGTGCCTC	2054
DB	2456	CATTGAAACCAACGAGATTTCCACCGAATTAAGTGTCAACATTCGCGTGGGGCGCTC	2515
QY	2055	CTCTCTTCTCAACATCCTGGCCTTTCTGCGCTTACTACAAGCGGAGCCGCGGCA	2114
DB	2516	GCTCTCTTCTCAACATCTTAGCTTTTCGGCGGTGTACTACAAAAGGACAAGAGGCG	2575
QY	2115	GGAGCTCGGGTCAGCGGCTTAGCCCACTGGCGGCTCAGGCTTGGGTGCTGTGTGG	2174
DB	2576	CCATGAGACTCAGCGGCGCCAGTCTCCAGAGAAACACCAAAATGATATCGCTCACAT	2635
QY	2175	GGGCCCCCTGCTCCCGCGCGGGCGGTGAGCTGCCACAGAGGAGGAGCTGGTGTCACT	2234
DB	2636	CCAGAACGAAGAGATCATGTCTCTGCAGATGAAGCAGCTGGAAACGATCACAGTGTGA	2695
QY	2235	GCAGCTGAAGCGGGTGTGGCGGTGGGGCGGAGCCCTGCCGAGGCTCTGCGCCCTGCGCTG	2294
DB	2696	GTGCTGTCAG-----GCACACGACACACTGAGGCTCACCTG	2731
QY	2295	CCCGCCGACTACACCTGGCCCTTGCGCGGGCACCGGACGATGTGCTCTCTTCGCGCCC	2354
DB	2732	CCCGCCAGACTACACCTCACGCTGGCGGTCGCCAGATGACATCCCACTTATGACGCC	2791
QY	2355	CGGGGCGCTGACCTGTGCTGCCAGTGGGCTG	2385
DB	2792	AAACACCATCAGCATGATTCAAAACACACTG	2822

Search completed: February 19, 2004, 00:51:38
Job time : 613.415 secs

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OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 16:16:41 ; Search time 8928.48 Seconds
(without alignments)
11491.468 Million cell updates/sec

Title: US-09-934-323-3
Perfect score: 2508
Sequence: 1 atggggccctggcgtgtg.....actcacacacccgggtatag 2508

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank:

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	2508	100.0	2508	6	AX469738	Sequence
2	2508	100.0	4667	6	AX469736	Sequence
3	2506.4	99.9	2793	9	AF376802	Homo sapi
4	2506.4	99.9	4622	6	AX405624	Sequence
5	2500	99.7	4763	6	AX477706	Sequence
6	2443.6	97.4	2523	6	AX179306	Sequence
7	2265.4	90.3	2663	6	AX380442	Sequence
8	2173.4	86.7	3993	10	RNU41662	U41662 Rattus norv
9	1651.8	65.9	3716	9	AB037787	Homo sapi
10	1011.4	40.3	3813	9	AF217411	Homo sapi
11	1006.6	40.1	3868	9	BC051715	Homo sapi
12	919	36.6	3493	10	RNU41663	U41663 Rattus norv
13	887.8	35.4	4115	9	BC034018	Homo sapi
14	886.2	35.3	5454	9	AB033096	Homo sapi
15	886.2	35.3	5454	9	AF376803	Homo sapi
16	884.5	35.3	3751	9	AK055471	Homo sapi
17	875	34.9	113187	2	AC007732	Homo sapi
18	875	34.9	184349	9	AC113189	Homo sapi
19	872.6	34.8	3154	9	AB040913	Homo sapi
20	870.2	34.7	2451	6	AX358051	Sequence
21	870.2	34.7	3502	6	AX358049	Sequence
22	870.2	34.7	5167	9	AF376804	Homo sapi
23	822.8	32.8	4935	9	AB023168	Homo sapi
24	782.8	31.2	146756	2	AC002348	Homo sapi
C 24	778.4	31.0	5631	10	AK122433	Mus muscu
C 25	773.8	30.9	222871	2	AC108094	Homo sapi
C 26	736.6	29.4	4325	10	RNU22952	U22952 Rattus norv
C 27	723.4	28.8	1720	9	AF217412	Homo sapi
C 28	706.8	28.2	185010	2	AC022514	Homo sapi
C 29	706.8	28.2	234182	10	AL603707	Mus muscu
C 30	697.4	27.8	2362	6	BD157856	Primer fo
C 31	697.4	27.8	2362	9	AK022621	Homo sapi
C 32	669	26.7	3245	9	BC032555	Homo sapi
C 33	669	26.7	4960	9	AB028993	Homo sapi
C 34	669	26.7	4960	9	AB028993	Homo sapi
C 35	535.8	21.4	212093	2	AC126237	Canis fam
C 36	523	20.9	223877	2	AC098923	Rattus no
C 37	499.4	19.9	136809	10	AL683892	Mouse DNA
C 38	494.8	19.7	32272	9	AF217413	Homo sapi
C 39	494.8	19.7	201197	9	HS1091N2	Homo sapi
C 40	494.8	19.7	305000	9	HSXDPA	Homo sapi
C 41	493.4	19.7	248178	2	AC093996	Homo sapi
C 42	492.8	19.6	149096	2	AC025083	Rattus no
C 43	492.8	19.6	194715	9	AC078989	Homo sapi
C 44	492.8	19.6	315176	2	AC078956	Homo sapi
C 45	489.6	19.5	146181	9	AC142316	Pan trogl

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
1	AX469738	Sequence 3 from Patent WO0216616.	AX469738	AX469738.1	GI:21901866	Homo sapiens (human)	Homo sapiens	1	Curtis,R.A.	Human carboxylesterase family member and uses thereof	Patent: WO 0216616-A 3 28-FEB-2002;
						Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					

D	b	1320	AAC	TACCAGCGCTCAAGTACACGCGGCTGTGGCAGCCAAAGGTGGGCTGTGACCCGAGAG	1379
Q	y	961	GAC	AGTGCTGAAGCTGTGGAGTGTCTGCGCCGGAAGCCCTCCCGGAGCTGGTGGACGAG	1020
D	b	1380	GACA	GTGCTGAAGCTGTGGAGTGTCTGCGCCGGAAGCCCTCCCGGAGCTGGTGGACGAG	1439
Q	y	1021	GAC	GTGCAGCTGCCCGCTATCACATCGCCTTTGGGCCGCTGGTGGATGGCGAGCGTGGTC	1080
D	b	1440	GAC	GTGCAGCTGCCCGCTACCATCGCCTTTGGGCCGCTGGTGGATGGCGAGCGTGGTC	1499
Q	y	1081	CCC	GATGACCTTGAGATCCTCATGCAGCAGGAGAAATCTCTCAACTACGATCTCTCATC	1140
D	b	1500	CCC	GATGACCTTGAGATCCTCATGCAGCAGGAGAAATCTCTCAACTACGATCTCTCATC	1559
Q	y	1141	GGC	GTCAAACGAGGAGAGGGCTCAAGTTCTGTGGAGGACTCTGCAGAGAGCGGAGCGGT	1200
D	b	1560	GGC	GTCAAACGAGGAGAGGGCTCAAGTTCTGTGGAGGACTCTGCAGAGAGCGGAGCGGT	1619
Q	y	1201	GTG	CTGCGACGCGCTTTGACTTCACATGTCTCCAATCTTTGGACACCTGTATGCTATC	1260
D	b	1620	GTG	CTGCGACGCGCTTTGACTTCACATGTCTCCAATCTTTGGACACCTGTATGCTATC	1679
Q	y	1361	CCG	GAAGGCAAGGATGTGCTTCGGGAGAACATCAAGTTTATGTACACAGACTGGCGGAC	1320
D	b	1680	CCG	GAAGGCAAGGATGTGCTTCGGGAGAACATCAAGTTTATGTACACAGACTGGCGGAC	1739
Q	y	1321	CGG	GACAAATGGCGAAATCGCGCGAACAACCTGCTGGCGCTCTTACTGACACCAATAAG	1380
D	b	1740	CGG	GACAAATGGCGAANAATCGCGCGAANAACCTGCTGGCGCTCTTACTGACACCAATAAG	1799
Q	y	1381	GTG	GCACCAAGCTGTGGCCATGTCACCAAGCTGCACGCGACTACCAAGTCTCCCGCTCTACTTT	1440
D	b	1800	GTG	GCACCAAGCTGTGGCCATGTCACCAAGCTGCACGCGACTACCAAGTCTCCCGCTCTACTTT	1859
Q	y	1441	TAC	ACCTTCTACCACTGCGAGGCGGAGGGCGGCTGAGTGGGAGATGCGGCGAC	1500
D	b	1860	TAC	ACCTTCTACCACTGCGAGGCGGAGGGCGGCTGAGTGGGAGATGCGGCGAC	1919
Q	y	1501	GGG	GAATGAATGCCCTATGTCTTTGGCGTGCCCATGTGGGTGCCACCGACCTCTTCCCC	1560
D	b	1920	GGG	GAATGAATGCCCTATGTCTTTGGCGTGCCCATGTGGGTGCCACCGACCTCTTCCCC	1979
Q	y	1561	TGT	AATCTTCCAGAATGACGTATGCTCAGTGGCGTGGTATGACCTTACTGGAGCAAC	1620
D	b	1980	TGT	AATCTTCCAGAATGACGTATGCTCAGTGGCGTGGTATGACCTTACTGGAGCAAC	2039
Q	y	1621	TTG	CCEAAGACTGGGACCCCAACACGCGGTGCGCAGGATACCAAGTTTATCCACACC	1680
D	b	2040	TTG	CCEAAGACTGGGACCCCAACACGCGGTGCGCAGGATACCAAGTTTATCCACACC	2099
Q	y	1681	AAG	CCCAATTCGCTTCGAGGAGGTGGTGTGGAGCAAAATTCAACAGCAAGGAGAGCAGTAT	1740
D	b	2100	AAG	CCCAATTCGCTTCGAGGAGGTGGTGTGGAGCAAAATTCAACAGCAAGGAGAGCAGTAT	2159
Q	y	1741	CTG	CACATAGGCTGAAGCCACGCGTGGTGCAACTACCGCGCCACCAAGGTGGCTTC	1800
D	b	2160	CTG	CACATAGGCTGAAGCCACGCGTGGTGCAACTACCGCGCCACCAAGGTGGCTTC	2219
Q	y	1801	TG	GCTGGAGCTGTGCCCACTGCAACCTGCAACCGAGCTCTTACCAACCAACGAG	1860
D	b	2220	TG	GCTGGAGCTGTGCCCACTGCAACCTGCAACCGAGCTCTTACCAACCAACGAG	2279
Q	y	1861	CGC	CTGCTTACGACGCGTGGCGCTGCTCCCCCGCTGGCGCCCGCGGCGACA	1920
D	b	2280	CGC	CTGCTTACGACGCGTGGCGCTGCTCCCCCGCTGGCGCCCGCGGCGACA	2339
Q	y	1921	CGC	CGCCCCCGCGCTGTCACCTCTCCGAGCCCGAGCCCGAGCCGCGCCCAAGG	1980
D	b	2340	CGC	CGCCCCCGCGCTGTCACCTCTCCGAGCCCGAGCCCGAGCCGCGCCCAAGG	2399
Q	y	1981	GCT	ATGACGGCTTCCCGGGGACTACGGGACTACTCTCACGGAGCTGAGCGTCAACGTG	2040
D	b	2400	GCT	ATGACGGCTTCCCGGGGACTACGGGACTACTCTCACGGAGCTGAGCGTCAACGTG	2459

QY	2041	GCCTGGGTGCTCCCTCCCTCTTCTCTCAACATCTCTGGCCCTTTGCTGCGCTCTACTACAAG	2100
DB	2460	GCCTGGGTGCTCCCTCCCTCTTCTCTCAACATCTCTGGCCCTTTGCTGCGCTCTACTACAAG	2519
QY	2101	CGGACCCGGCGGAGGAGCTGCGGTGCAGCGCGCTTTAGCCCACTCGCGGCTCAGGCTCT	2160
DB	2520	CGGACCCGGCGGAGGAGCTGCGGTGCAGCGCGCTTTAGCCCACTCGCGGCTCAGGCTCT	2579
QY	2161	GGCGTGCCTGGTGGGGGGCCCCCTGCTCCCGCGCGGGCGGTGAGTGTGCACAGAGGAG	2220
DB	2580	GGCGTGCCTGGTGGGGGGCCCCCTGCTCCCGCGCGGGCGGTGAGTGTGCACAGAGGAG	2639
QY	2221	GAGCTGTGTCTCACTGCAGCTGAAGCGGGGTGGCGGTGCGGGCGGACCTCGCGAGGCT	2280
DB	2640	GAGCTGTGTCTCACTGCAGCTGAAGCGGGGTGGCGGTGCGGGCGGACCTCGCGAGGCT	2699
QY	2281	CTGCGCCCTCCCTGCGCGGGCCGACTACACCTCTGGCCCTCGCGGGCACCGGACGATGTG	2340
DB	2700	CTGCGCCCTCCCTGCGCGGGCCGACTACACCTCTGGCCCTCGCGGGCACCGGACGATGTG	2759
QY	2341	CTCTCTTTGGCCCCCGGGGGCCCTGACCTGCTGCCAGTGGCTGGGGCGACCGCCACC	2400
DB	2760	CTCTCTTTGGCCCCCGGGGGCCCTGACCTGCTGCCAGTGGCTGGGGCGACCGCCACC	2819
QY	2401	CCACCGCCCTCCCTTCATCCCTTTGGGGCGCTTCCCGCCCGCCCTCCACCGCCACC	2460
DB	2820	CCACCGCCCTCCCTTCATCCCTTTGGGGCGCTTCCCGCCCGCCCTCCACCGCCACC	2879
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DB	2880	AGGCACAAACACGCTACCCACCCCACTCCACCTCCGGGTATAG	2927
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ACCESSION	AF376802		
VERSION	AF376802.1	GI:21309946	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Jamain, S., Quach, H., Betancur, C., Rastam, M., Colineaux, C., Gillberg, I.C., Soderstrom, H., Gires, B., Leboyer, M., Gillberg, C., Bourgeron, T., Gillberg, C., Rastam, M., Gillberg, C., Nyden, A., Soderstrom, H., Leboyer, M., Betancur, C., Philippe, A., Gires, B., Colineaux, C., Cohen, D., Chabane, N., Mouron-Simeoni, M.C., Brice, A., Spohnhauer, E., Spurkland, I., Skjeldal, O.H., Coleman, M., Pearl, P.L., Cohen, I.L., Tsiaouris, J., Zappella, M., Menchetti, G., Pompella, A., Aschauer, H., and Van Maldergem, L.		
TITLE	Mutations of the X-linked genes encoding neurologins NLGN3 and NLGN4 are associated with autism		
JOURNAL	Nat. Genet. 34 (1), 27-29 (2003)		
MEDLINE	22608338		
PUBMED	12669065		
REFERENCE			
AUTHORS	Jamain, S., Quach, H., Fellous, M., and Bourgeron, T.		
TITLE	Evolution and expression of the human neurologin family, including two primate specific members on the X and Y chromosomes		
JOURNAL	Unpublished		
REFERENCE			
AUTHORS	Jamain, S., Quach, H., Fellous, M., and Bourgeron, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-MAY-2001) Immunology, Institut Pasteur, 25 rue du		
FEATURES	Docteur Roux, Paris 75015, France		
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BASE COUNT 464 a 1001 c 843 g 485 t
ORIGIN

Query Match 99.9%; Score 2506.4; DB 9; Length 2793;
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QY	181	GAGATCTGGGCGGCTGTGAGTCTTGGGCTGCTCAACGGCGGCGGCTGGGCT	240
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QY	301	ACCCTGCGCGGCTTCCAGCGGCTGAGGCGGCGGCTGTGGCGGAGTGGCGGAG	360
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QY	421	TGCTGTACTCAACTTACGCTGAGGCGGCGGCTGAGTGGCGGAGTGGCGGAG	480
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QY	481	GAGGCGAGCTCAATCCGCGACACACAGATATCCGTGACCTTGGGAGAAAGCTGTGATG	540
DB	554	GAGGCGAGCTCAATCCGCGACACACAGATATCCGTGACCTTGGGAGAAAGCTGTGATG	613
QY	541	CTGTCTTCTCATGGGCTTCTTACATGAGGAGGAGCGGAAACATGTTTCGATGGCTCAGTC	600
DB	614	CTGTCTTCTCATGGGCTTCTTACATGAGGAGGAGCGGAAACATGTTTCGATGGCTCAGTC	673
QY	601	CTGTGCTGCTATGGCAACGTCTATGAGCGGCTCAACTACCGTCTTGGGGTGTCTGGT	660

Db	674	CTGGCTGCTATGGCAACGTCAATTGTAGCCAGCTCAACTACCGTCTTGGGGTGTCTGGT	733
QY	661	TTTCTCAGCACCGGGACACAGCTGCAAAAGGCAACTATATGGCTCTCTGGACACAGATCCAG	720
Db	734	TTTCTCAGCACCGGGACACAGCTGCAAAAGGCAACTATATGGCTCTCTGGACACAGATCCAG	793
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QY	781	ATCTTTGTTCGGGGGACGGGCTCTCTGCTCAACCTTCTGATCTCTCTCCCAACCATTC	840
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QY	1021	GACGTGAGCTGCGGCTTACCACATCGCTTTGGGCGGCTGTGGTGGAGTGGGAGCGTGGT	1080
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QY	1081	CCCAGTACCTGAGATCTCTCATGACAGCGAGAAATTCCTCAACTACGACATGCTCATC	1140
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QY	1201	GTGTCTCCAGCGCTTGTGACTTCACTGTCTCAACTTTGTGGACACCTGTATGGCTAC	1260
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QY	1261	CCGAGAGCAAGATGTCTTCCGGAGACCATCAAGTTTATGTACAGACTGTGGCGGAC	1320
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QY	1381	GTGGCACAGCTGTGGCCACTGTCAGAGCTGACGCGGACTTACCAGTCTTCCCGTCTACTTT	1440
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QY	1441	TACACTTCTTACCACTGCGCAGGCGGAGGGCGGCTGAGTGGGAGAGTGGGCGGAC	1500
Db	1514	TACACTTCTTACCACTGCGCAGGCGGAGGGCGGCTGAGTGGGAGAGTGGGCGGAC	1573
QY	1501	GGGATGAACCTGCGCTATGTCTTTGGCTGCGCATGCTGGTGGTCCACCGACCTTCCCC	1560
Db	1574	GGGATGAACCTGCGCTATGTCTTTGGCTGCGCATGCTGGTGGTCCACCGACCTTCCCC	1633
QY	1561	TGTAACCTTCTCAAGAAATGACGTCTCAGTCCGCTGTATGACCTTCTGAGCAAC	1620
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QY	1621	TTCCGCAAGACTGGGACCCCAACACCGGCTGCGCAGGATACCAAGTTCATCCACAC	1680
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QY	781	ATCTTTGGTTCCGGGGCAGGGGCTCTGTCGCTCAACCTTCTGATGTCCTCCACCATTC A	840
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ORGANISM					
REFERENCE					
AUTHORS					
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JOURNAL					
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LOCUS Sequence 30 from Patent WO2004612.			
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ACCESSION AX380442			
VERSION AX380442.1 GI:19575351			
KEYWORDS Homo sapiens (human)			
SOURCE Homo sapiens			
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS			
Baughn,M.R., Bruns,C.M., Das,D., Ding,L., Elliott,V.S.,			
Gandhi,A.R., Rafalia,A.J., Kearney,L., Khan,F.A., Lai,P., Lee,E.A.,			
Lu,D.A., Lu,Y., Nguyen,D.B., Patterson,C., Ramkumar,J., Ring,H.Z.,			
Sanjanwala,M.S., Tang,Y.T., Thornton,M. and Tribouley,C.M.			
Drug metabolizing enzymes			
TITLE			
JOURNAL			
Patent: WO 0204612-A 30 17-JAN-2002;			
Incyte Genomics, Inc. (US)			
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QY	61	CCCGCGGGCGGGCGCCCGGGGGGCGCCCGGCTCGGCGCTCGGCGAGCGAGCGC	120
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RESULT 9
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 VERSION AB037787.1 GI:7243112
 KEYWORDS
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (sites)
 Nagase,T., Kikuno,R., Ishikawa,K.I., Hirose,M. and Ohara,O.
 Prediction of the coding sequences of unidentified human genes.
 XVI. The complete sequences of 150 new cDNA clones from brain which
 code for large proteins in vitro
 DNA Res. 7 (1), 65-73 (2000)
 JOURNAL 20181126
 MEDLINE 10718198
 PUBMED
 2 (bases 1 to 3716)
 Chara,O., Nagase,T. and Kikuno,R.
 Direct Submission
 Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
 Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
 222-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
 URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
 Fax:+81-438-52-3914)
 FEATURES
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 ORIGIN

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RESULT 10

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 VERSION AF217411.1 GI:7960130
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 3813)
 AUTHORS Philibert,R.A., Winfield,S.L., Sandhu,H.K., Martin,B.M. and
 Ginns,E.I.
 TITLE The structure and expression of the human neurotrophin-3 gene
 JOURNAL Gene 246 (1-2), 303-310 (2000)
 MEDLINE 20231756
 PUBMED 10767552
 REFERENCE 2 (bases 1 to 3813)
 AUTHORS Philibert,R.A., Winfield,S.L. and Sandhu,H.K.
 TITLE Direct Submission
 JOURNAL Submitted (17-DEC-1999) Psychiatry, University of Iowa, 500 Newton,
 Iowa City, IA 52242, USA

FEATURES

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DB	1143	CAGAGGACTTTTCCAGAGGCCATATCCAAAGTGGCTGTGCTCTGTCAGCTGGGCTG	1202

QY	899	TCAACTACAGCCGCTCAAGTACACGGCGCTGTGGCAGCCAGGTGGCTGTGACCGAG	958
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RESULT 13
BC034018

LOCUS
DEFINITION
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ACCESSION
BC034018

VERSION
BC034018.1

KEYWORDS
GI:21706446

SOURCE
MGC.

ORGANISM
Homo sapiens (human)

REFERENCE
Homo sapiens

AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farnet, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Donald, M.F., Casavant, T.L., Schect, F.E., Brownstein, M.J., Usdin, T.B., Loquellano, N.A., Peters, G.J., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., McEwan, P.J., Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.C., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PMID
22388257

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AUTHORS
Strausberg, R.

TITLE
Direct Submission

JOURNAL
Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-3590, USA

REMARK
NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Center Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: (Dickson, Mark) mcdspaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

FEATURES
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USA

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.

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SGGNSNLPHGHSITRV"
BASE COUNT 1139 a 1082 c 926 g 968 t
ORIGIN
Query Match 35.4%; Score 887.8; DB 9; Length 4115;
Best Local Similarity 64.0%; Pred. No. 4.9e-109;
Matches 1479; Conservative 0; Mismatches 727; Indels 105; Gaps 5;
QY 108 CGCGAGAGGCGCTTCCCGTGGTGAACACAGCCCTACGGCGAGTGGCGGTGCGGCG 167
DB 550 CAGCCAGACAGTATCAGTTGTCAACACAAATATATGGCAAAATCGGGCCCTAGAAC 609
QY 168 CGAGCTCAACACAGATCTCGGCGCCCGTGTGTCAGTCTTGTGGCGTGCCTACGCCAC 227
DB 610 ACCGTACCCAAATGAGATCTTGGGTGCAGTGGAGCAGTACTTGGGGTCCCTATGCTC 669
QY 228 GCCGCCCTGGCGCCCGCGCTTCCAGCCGCTGAGCGCCCGCCCTCGTGGCGCCGCGT 287
DB 670 ACCCCACACAGAGAGGCGGTTCAGCCCCAGAACCCCGCTCTCTGACTGGCAT 729
QY 288 GCGCAAGCCACACCTTGGCGCCCGCTGCGCCGCGAGAACCTGACG ---GGCGCTGCC 344
DB 730 CCGAAATACTACTCAGTTTGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789
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DB 790 GCATGACATGCTGCCCATCTGTTTACCGCAATTTGGATCTTTGATGACCTATGTTCA 849
QY 405 GAACGAGGAGGAGTGTGCTGCTACCTCAACCTCTACGTGCCACCGAGGACGCTCCGCT 464
DB 850 AGATCAAAATGAAGACTGCTGCTTACTTAAACATCTACGTGCCACGAGGAGATATCA 909
QY 465 CACAAAACGTCGACGAGGAGCGCTCAATCGCCAGACAGATATCGGTGACCCCTGG 524
DB 910 TGATCAGACAGT-----922
QY 525 GAAGAAGCTGTGATGCTGTTTCTCATGCGGCTCTCATGAGGGGACCGGAAACAT 584
DB 923 -AAGAAGCCCGTCATGCTATATCATGCGGATCTTACATGGAGGACCGCGCAACAT 981
QY 585 GTTCGATGGCTCAGTCTGCTGCTGCTATGGCAAGCTCATGTAGCCACGCTCAATACG 644
DB 982 GATTGAGGAGCAGATTTGGCAAGCTACGGAACGTCATTGTGATCACCATTAACTACCG 1041
QY 645 TCTTGGGGTCTCGGTTTTCTCAGCACCGGGACAGGCTGCAAAAGGCAACTATGGGCT 704

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DB 1042 TCTGGGAATACTAGGGTTTTTAAGTACCGGTGACCGAGCGCAAAAAGCAACTATGGGCT 1101
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DB 1102 CTTGGATCAGATTCAGCACTGCGGTGGATTGAGAGAGATGTGGAGGCTTTTGGCGGGGA 1161
QY 765 CCGCGAGCTATCACCATCTTTGGTTCCGGGGGAGGGGCTCTCTGCGTCAACCTTCTGAT 824
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QY 885 TTCAGCTGTCTGTCAACTACAGCGCTCAAGTACACGCGCTCTGGCAGCCCAAGGT 944
DB 1282 GTCAGCTGGGAGTGAATCACTCCAGCGGCAAGTACACTCGGATATTCGACACAAGGT 1341
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DB 1402 GGAGCTCATCCAGCAGACCATCACTCCGCGCACCTACCACTAGCCTTCGGGCGGTGAT 1461
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DB 2002 GACTTCTGGACCAACTTCGCGAAACTGGTGTATCCAAATCAACAGTTCTCTCAGGATAC 2061
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 1076 TCTGGGAAATACAGGGTTTAAAGTACCGGTACAGGCGAGCAAAAGGCACTATGGCT 1135
 705 CTGAGACAGATCCAGGCGCTCGCTGGCTCAGTGAAGAACATCGCCACATTTGGGGCGGA 764
 1136 CTTGGATCAGATTCAAGCATCGGTGGATTGAGGAGAAATGAGGAGCTTTGGCGGGGA 1195
 765 CCCGAGCGGTATCACCATCTTTGGTTCCGGGACAGGGGCTCTCGCTCAACCTTCTGAT 824
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 2276 CAGATGTTTCAACACACACGAGGTTCTTCCACAGATGACATCATTTCCATATGG 2335
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 1956 GCGCGGCGCGGAGC-----CGGCGGCGGCGCTATGACCGCTT 1994
 2396 CACAGTCTCCAAACACTCTAAGGACCTTCAAAACAGGCGCTGAGGACACAACTGCTCT 2455
 1995 CCGCGGAGCTCAACGAGTACTCAAGGAGTGAAGTCAAGTGGCGCTGGGCTGCTC 2054
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 2355 CCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2385
 2792 AAACACCATCATCATGATTCCAAACACACTG 2822

RESULT 15

AF376803
 LOCUS Homo sapiens neuroligin X mRNA, complete cds.
 DEFINITION AF376803
 ACCESSION AF376803.1
 VERSION Gi:21309948
 KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 5454)
 Jamain, S., Quach, H., Betancur, C., Rastam, M., Colineaux, C., Gillberg, I.C., Soderstrom, H., Giros, B., Leboyer, M., Gillberg, C., Bourgeron, T., Gillberg, C., Rastam, M., Gillberg, C., Nyden, A., Soderstrom, H., Leboyer, M., Betancur, C., Phillippe, A., Giros, B., Colineaux, C., Cohen, D., Chabane, N., Mouren-Simeoni, M.C., Brice, A., Sponheim, S., Spurkland, I., Skjeldal, O.H., Coleman, M., Beal, P.L., Cohen, I.L., Tsoukias, J., Zappella, M., Menchetti, G., Pompella, A., Aschauer, H. and Van Maldergem, L.
 Mutations of the X-linked genes encoding neuroligins NLGN3 and NLGN4 are associated with autism

	D	b			944	TGATCAGAACAGT-----	956
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	Q	y			585	GTTTCGATGGCTCAGTCTTGCTGCCTATGGCAAGCTCATTTGATGACCACGGCTCAAATAACG	644
	D	b			1016	GATTGACGGCAGCAATTTTGGCAAGACTACGAAACGTCATCGTAGATACCAATTACTACTACG	1075
	Q	y			645	TCITGGGGTGCTCGGTTTTCTCAGCACCGGGACACAGGCTGCAAAAGCGCAACTATGSGCT	704
	D	b			1076	TCCTGGGAATACTAGGGTTTTTAAGTACCAGTGACCGAGCAGAAAGCAACTATNGGCT	1135
	Q	y			705	CCTGGACCATCAGACCGCCCTGGCTGGCTCAGTGA AAA CATCCGCACTTTTGGGGCGGA	764
	D	b			1136	CCTGGATCAGATTCAAGCACTGGCGGTGGATTGAGAGGAAATGCTGGAGCCCTTTGGCGGGGA	1195
	Q	y			765	CCCCGACGCTATCACCACTTTTGGTTCCGGGGCAGGGGCTCCTCGGTCAACCTTTCTGAT	824
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	D	b			1376	CGGCTGCAACATGCTGSAACACACGACATGTTAGAA TGCTTCGCGAA CAGNACTACAA	1435
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	D	b			1436	GGAGCTCATCCAGACACCACTCACCCGCGCCACTTACCACATAGCCTTGGGCGCGTGT	1495
	Q	y			1065	GGATGGCGAGTGGTCCCAGATGACCCTCAGATCTCTATGACAGGAGGAAATTCCTCAA	1124
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	Q	y			1125	CTACGACATGCTCATCGGCGTCAAC CAGGAGAGGGCCTCAAAGTTGTTGAGGAC TCTGC	1184
	D	b			1556	CTACGACATCATGCTGGGCGTCAAC CAAGGGGA AGSCCTGAAGTTCTGGA CGGCATCGT	1615
	Q	y			1185	AGAGACGAGGAGCGTGTCTCTGCAGCGCTTTGACTTCATCTGTCTCAACTTTGTGGA	1244
	D	b			1616	GGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAAGTTCTGTGA	1675
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	D	b			1676	CAACCTTTACGGCTACCTCTGAAGGGAAGACACTTTGGGGNAGACTATCAAGTTCATGTA	1735
	Q	y			1305	CACAGACTGGGCGGACCGGGA CAATGGCGA AATGCGCGAAAAACCTGTCTGGCGCTCTT	1364
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	Q	y			1545	CACGACCTCTTCCCCTGTA ACTTCTCCAAGAAATGACGTCTATGTCTCA GTGCGGTGTCAT	1604

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 Db 2156 CAAGACCAAGCTCTATCTGCATATGGCTTGAACCCAGAGTGAGATCACTACCGGCG 2215
 Qy 1785 CAACAAGTGGCTTCTGGCTGGAGCTGTCGCCACCTGACCAACCTGACAC----- 1838
 Db 2216 AAGCAAGTGGCTTCTGGCTGGAGCTGTCGCCACCTGACCAACCTGACCAACCTGACCA 2275
 Qy 1839 ---GGAGCTTTCACACCAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1895
 Db 2276 CCAGTATGTTTCAACAACCAACAGGTTCCTCCACAGACATGACATCATTTCCCTATGG 2335
 Qy 1896 TCCGCCGCTGGCGCCCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1955
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 Db 2396 CAACAATCCCAACACTCTAAGAGCCCTCACAACAGGGCTGAGGACACAACTGTCT 2455
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Search completed: February 19, 2004, 00:22:40
 Job time : 8937.48 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 16:16:41 / Search time 16614.5 Seconds
(without alignments)
11491.468 Million cell updates/sec

Title: US-09-934-323-1

Perfect score: 4667

Sequence: 1 ggcacgaggaacttggtctt.....ttgcctcttgactgccttc 4667

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenBank:

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.ats.*
12: gb.by.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
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25: em.pl.*
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32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.man.*
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41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4332.4	92.8	4763	6	AX477706 Sequence
3	4246.6	91.0	4622	6	AX405624 Sequence
4	3363	72.1	3716	6	AB037787 Homo sapi
5	2780.4	59.5	2793	9	AF376802
6	2581.6	55.4	3993	10	RU041662
7	2587.8	55.4	184349	9	AC113189
8	2586.2	55.4	113187	2	AC007732
9	2508	53.7	2508	6	AX469738
10	2452.6	52.6	2523	6	AX179306
11	2383.4	51.1	2663	6	AX380442
12	2350	50.4	146756	2	AC002348
13	1704.8	36.5	22871	2	AC108094
14	1172.2	25.1	185010	2	AC022514
15	1171.4	25.1	234182	10	AL603707
16	1012.6	21.7	3813	9	AF217411
17	1007.8	21.6	3868	9	BC051715
18	942.4	20.2	223877	2	AC098923
19	919	19.7	3493	10	RU041663
20	907.4	19.4	212093	2	AC126237
21	887.8	19.0	4115	9	BC034018
22	886.2	19.0	5454	9	AB033086
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0216616.
ACCESSION AX469736
VERSION AX469736.1 GI:21901864
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Curtis, R.A.
TITLE Human carboxylesterase family member and uses thereof
JOURNAL Patent: WO 0216616 A 1 28-FEB-2002

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REFERENCE  1
AUTHORS    Sanjanwala, M.M., Yao, M.G., Au-Young, J., Baughn, M.R., Arvizu, C.,
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ORGANISM	Homio sapiens		
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AUTHORS	Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F., Xue, A.J., Yang, Y., Wehrman, T. and Brmanac, R.T.		
TITLE	Novel nucleic acids and polypeptides		
JOURNAL	Patent: WO 0222660-A 39 21-MAR-2002; HYSEQ, INC. (US)		
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Best Local Similarity	99.8%;	Pred. No. 0;	
Matches 4282; Conservative	0;	Mismatches 4;	Indels 3; Gaps 3;
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AB037787
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (sites)
 Nagase, F., Kikuno, R., Ishikawa, K.I., Hirose, M. and Ohara, O.
 Prediction of the coding sequences of unidentified human genes.
 XVI. The complete sequences of 150 new cDNA clones from brain which
 code for large proteins in vitro
 DNA Res. 7 (1), 65-73 (2000)
 20181126
 MEDLINE
 10718198
 PUBMED
 2 (bases 1 to 3716)
 Chara, O., Nagase, F. and Kikuno, R.
 Direct Submission
 Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
 Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp)
 URL: http://www.kazusa.or.jp/huge/, Tel: +81-438-52-3913,
 Fax: +81-438-52-3914

FEATURES

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BASE COUNT

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RESULT 5
AF376802

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VERSION	AF376802.1	GI:21309946			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

REFERENCE	1 (bases 1 to 2793)
AUTHORS	Jamain,S., Quach,H., Betancur,C., Rastam,M., Colineaux,C., Gillberg,C., I.C., Soderstrom,H., Giros,B., Leboyer,M., Gillberg,C., Bourgeron,T., Gillberg,C., Rastam,M., Gillberg,C., Nyden,A., Soderstrom,H., Leboyer,M., Betancur,C., Philippe,A., Giros,B., Colineaux,C., Cohen,D., Chabane,N., Mouten-Simoni,M.C., Brice,A., Spohnheim,E., Spurkland,J., Skjeldal,O.H., Coleman,M., Pearl,P.L., Cohen,I.L., Tsouris,J., Zappella,M., Menchetti,G., Pompella,A., Aschauer,H. and Van Maldergem,L.
TITLE	Mutations of the X-linked gene encoding neurologins NLGN3 and NLGN4 are associated with autism
JOURNAL	Nat. Genet. 34 (1), 27-29 (2003)
MEDLINE	22608338
PUBMED	12669055
REFERENCE	2 (bases 1 to 2793)
AUTHORS	Jamain,S., Quach,H., Fellous,M. and Bourgeron,T.
TITLE	Evolution and expression of the human neurologin family, including two primate specific members on the x and y chromosomes
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 2793)
AUTHORS	Jamain,S., Quach,H., Fellous,M. and Bourgeron,T.
TITLE	Direct Submission
JOURNAL	Submitted (04-May-2001) Immunology, Institut Pasteur, 25 rue du Docteur Roux, Paris 75015, France
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QY	1967	CGACCTCTTCCCTGTAACTCTTCCAAGAATGACGTATGCTCAGTGCCGTGGTTCATGAC	2026
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AUTHORS	1. (bases 1 to 3993)		
TITLE	Ichchenko, K., Nguyen, T. and Sudhof, T. C. Structures, alternative splicing, and neuroligin binding of multiple neuroligins		
JOURNAL	J. Biol. Chem. 271 (5), 2676-2682 (1996)		
MEDLINE	96162010		
PUBMED	8576240		
AUTHORS	2. (bases 1 to 3993)		
TITLE	Ichchenko, K., Nguyen, T. and Sudhof, T. C. Direct Submission		
JOURNAL	Submitted (01-DEC-1995) Konstantin Ichchenko, Molecular Genetics, UTSWMC@Dallas, 5323 Harry Hines Blvd., Dallas, TX 75235, USA		
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 113187)
 Birren,B., Nusbaum,C. and Lander,E.
 Homo sapiens chromosome 17, clone RP5-1030A12
 Unpublished
 2 (bases 1 to 113187)
 Birren,B., Linton,J., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
 Castile,A., Cerny,J., Collangelo,M., Collins,S., Collymore,A.,
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 Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
 Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
 Direct Submission

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Submitted (05-JUN-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 113187)
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
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 Comarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
 Cooke,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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 Direct Submission

TITLE
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 COMMENT

Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome
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 On Sep 12, 2002 this sequence version replaced GI:21700697.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIGR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L528
 Center clone name: 1030_A_12

* NOTE: This is a 'working draft' sequence. It currently
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 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 39427: contig of 39427 bp in length
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RESULT 9
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LOCUS
DEFINITION
Sequence 3 from Patent WO0216616.
ACCESSION
AX469738
VERSION
AX469738.1
KEYWORDS
GI:21901866
SOURCE
Homo sapiens (human);
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Curtis, R.A.
AUTHORS
Human carboxylesterase family member and uses thereof
TITLE
Patent: WO 0216616-A 3 28-FEB-2002;
JOURNAL
Millennium Pharmaceuticals, Inc. (US)
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BASE COUNT
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ORIGIN

Query Match 53.7%; Score 2508; DB 6; Length 2508;
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DEFINITION Sequence 7 from Patent WO0127277.
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VERSION   AX179306.1 GI:14598977
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS   Shinkets, R.A., Lichenstein, H. and Boldog, F.I.
TITLE     Proteins and polynucleotides encoded thereby
JOURNAL   Patent: WO 012727-A 7 19-APR-2001;
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RESULT 11
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ACCESSION AX380442
VERSION AX380442.1 GI:19575351
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
AUTHORS Baughn M.R., Bruns, C.M., Das, D., Ding, L., Elliott, V.S.,
Gandhi, A.R., Rafalia, A.J., Kearney, L., Khan, F.A., Lai, P., Lee, E.A.,
Lu, D.A., Lu, Y., Nguyen, D.B., Patterson, C., Ramkumar, J., Ring, H.Z.,
Sanjanwala, M.S., Tang, Y.T., Thornton, M. and Tribouley, C.M.
TITLE Drug metabolizing enzymes
JOURNAL Patent: WO 0204612-A 30 17-JAN-2002;
Incyte Genomics, Inc. (US)
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location/Qualifiers
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QY 1558 TCGGGGTCAACCGAGGAGAGGGGCTCAAGTTCGTGGAGGACTCTGCGAGAGCGAGGAGC 1617

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Db	1315	TCGTTGTACACGAGGAGGAGGCTCAAGTTCTGGAGGACTCTGACGAGCGAGGACG	1374
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Db	1375	GTGTGTCTGCGAGCGCTTTGACTTCACTGTCTCCAACTTTTGGACAACTGTATGGCT	1434
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Db	1435	ACCGGGAAGCAAGGATGCTTCGGAGACCATCAAGTTATGTATACACAGACTGGCGG	1494
Qy	1738	ACCGGACAAATGCGAAATGCGCGCAAAACCTGCTGGCGCTCTTTACTGACCAACCAAT	1797
Db	1495	ACCGGACAAATGCGAAATGCGCGCAAAACCTGCTGGCGCTCTTTACTGACCAACCAAT	1554
Qy	1798	GGTGGCACACGCTGGGCACTGCGCAAGCTGACGCCGACTACAGTCTTCCCGTCTACT	1857
Db	1555	GGTGGCACACGCTGGGCACTGCGCAAGCTGACGCCGACTACAGTCTTCCCGTCTACT	1614
Qy	1858	TTTACACCTTTTACCACCACTGCCAGGCGGAGGCGGCGCTGAGTGGCAGATGGCGGC	1917
Db	1615	TTTACACCTTTTACCACCACTGCCAGGCGGAGGCGGCGCTGAGTGGCAGATGGCGGC	1674
Qy	1918	ACGGGATGAATGCGCTATGCTTTGGGTGCCATGCGTGGTGGTGGTGGTGGTGGTGGT	1977
Db	1675	ACGGGATGAATGCGCTATGCTTTGGGTGCCATGCGTGGTGGTGGTGGTGGTGGTGGT	1734
Qy	1978	CTGTAACTTTTCCAAAGATGACGTCATGCTCAGTGGCGGTGCTGATGACCTACTGGA	2037
Db	1735	CTGTAACTTTTCCAAAGATGACGTCATGCTCAGTGGCGGTGCTGATGACCTACTGGA	1794
Qy	2038	ATTTCGCAAGACTGGGACCCCAACACCGCGTSCCGAGGATACCAAGTTTCATCCACA	2097
Db	1795	ATTTCGCAAGACTGGGACCCCAACACCGCGTSCCGAGGATACCAAGTTTCATCCACA	1854
Qy	2098	CCAAAGCCCAATCGCTTCAGAGGAGTGTGTGAGCAAAATTCACAGCAGAGAGAGAGT	2157
Db	1855	CCAAAGCCCAATCGCTTCAGAGGAGTGTGTGAGCAAAATTCACAGCAGAGAGAGAGT	1914
Qy	2158	ATCTGCATAGGCTGAAGCAGCAGCGTGTGTGACAACTACCGCGCCCAACAGGTGCGCT	2217
Db	1915	ATCTGCATAGGCTGAAGCAGCAGCGTGTGTGACAACTACCGCGCCCAACAGGTGCGCT	1974
Qy	2218	TCTGCTGAGCTGTGCGCCCACTGACACCTGTCGACGAGCTTTTCCACCAACCA	2277
Db	1975	TCTGCTGAGCTGTGCGCCCACTGACACCTGTCGACGAGCTTTTCCACCAACCA	2034
Qy	2278	CGCGCTGCTTCCCTACGCCACGCGCTGGCGGCTGTCTCCCGCGTGGCGCCCGGCA	2337
Db	2035	CGCGCTGCTTCCCTACGCCACGCGCTGGCGGCTGTCTCCCGCGTGGCGCCCGGCA	2094
Qy	2338	CACGCGGCGCCCGCGCTGCGCACTCTGCTCCGAGCCGAGCCGAGCCCGGCGCAA	2397
Db	2095	CACGCGGCGCCCGCGCTGCGCACTCTGCTCCGAGCCGAGCCGAGCCCGGCGCAA	2154
Qy	2398	GGGCTTATGACCGCTTCCCGGGGACTCACGGGACTTCTCCAGAGCTGAGGTACCG	2457
Db	2155	GGGCTTATGACCGCTTCCCGGGGACTCACGGGACTTCTCCAGAGCTGAGGTACCG	2214
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Qy	2578	CTGCGTCTCTGTTGGGGGCGCCCTGCTCCCGCGCGCGCGCTGAGCTGCCACCAAGAG	2637
Db	2335	CTGCGTCTCTGTTGGGGGCGCCCTGCTCCCGCGCGCGCGCTGAGCTGCCACCAAGAG	2394
Qy	2638	AGGAGCTGCTTCTACTGACCTGAGCGGGTGGTGGCTGCGGGCGGACCTTGGCG	2694

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LOCUS	AC002348		
DEFINITION	Homo sapiens chromosome 17 clone 363G12 map 17, *** SEQUENCING IN		
PROGRESS ***	11 unordered pieces.		
ACCESSION	AC002348		
VERSION	AC002348.1		
KEYWORDS	HTG: HTGS PHASE1		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 146756)		
AUTHORS	Birren, B., Fasnman, K., McKernan, K., Munro, C., Nussbaum, C., Richardson, P., and Lander, E.		
TITLE	Homo sapiens chromosome 17, clone 363G12		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 146756)		
AUTHORS	Hawkins, T.L., Reeve, M.P., Christoffersen, A., Birren, B.W., Fasnman, K.H., Lander, E.S., McKernan, K., Munro, C., Richardson, P., Barna, N., Chang, A., Cooke, P., Daly, M.J., Devon, K., Dewar, K., Porreest, C., Gage, D., Geraigery, K., Guitau, G., Hagos, B., Huang, J., Jacobot, L., Lane, M., Lee, K., Mackenzie, J., Marquis, N., McDermott, J., Mollia, M., Moloney, N., Morrow, J., Nachman, A., Naylor, J., O'Connor, T., Olotu, A., Peterson, K., Rollins, G., Spencer, J., Stillwell, J., Stone, C., Strickland, C., Sydney, K., Tang, L., Traish, A., Wilmer, F., Zentsava, I. and Zody, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-JUL-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
COMMENT	On Dec 11, 1997 this sequence version replaced gi:2661149. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.		
	All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html.		
	* NOTE: This is a 'working draft' sequence. It currently		
	* consists of 11 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
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	* 2413: contig of 2413 bp in length		
	* 2414 gap of unknown length		
	* 4445: contig of 2032 bp in length		
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	* 9225: contig of 4780 bp in length		
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	* 27338 gap of unknown length		
	* 59287: contig of 31950 bp in length		
	* 59288 gap of unknown length		
	* 100645: contig of 41358 bp in length		
	* 100646 gap of unknown length		
	* 103698: contig of 3053 bp in length		
	* 103699 gap of unknown length		
	* 109010: contig of 5312 bp in length		
	* 109011 gap of unknown length		
	* 113388: contig of 4378 bp in length		
	* 113389 gap of unknown length		
	* 131151: contig of 17763 bp in length		
	* 131152 146756: contig of 15605 bp in length.		
FEATURES	Location/Qualifiers		
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	/organism="Homo sapiens"		

QY	2948	CCT--CCCGCGCCCTCCTCGCCCGGCGCACTCCGAAAGCGAGGAGAGACTTTGGCAACTG	3006
Db	42430	CTTCCCCCGNCCCTCCTCGCCCGGCGCACTCCGAAAGCGAGGAGAGACTTTGGCAACTG	42371
QY	3007	GCTTTTCTCCTGTGGAGTCG-----TCACAGCCCAATCCAGCAGCGCTAAGGTG	3054
Db	42370	GCTTTTCTCCTGTGGANNNNNGNTNNNNCGTNCACAGCCCAATCCAGCAGCGCTAAGGTG	42311
QY	3055	GACATGGGATTCCTCTCC-TGCGATGGTGTCTTTTCCACGACAGAAAGCCCGAGTCTCTT	3113
Db	42310	GACATGGGATTCCTCCNTGCGATGGTGTCTTTCCACGACAGAGAG-CCAGTCTCTT	42252
QY	3114	CTCTGGATCTGGGCGCTTTGAAACAATCGGGGCGTTTTTCTCCCCCAATGGGA-CACCA	3172
Db	42251	CTCTGGATCTGGGCGCTTTGAAACAATCGGGGCGTTTTTCTCCCCCAATGGGANCAACA	42192
QY	3173	GTCCTCGGTGTGTGGAAATGTGGTATTTTCCGCGGTGGAGGTGTCTTCTCACACGGGG	3232
Db	42191	GTCCTCGGTGTGTGGAAATGTGGTATTTTCCGCGGTGGAGGTGTCTTCTCACACGGGG	42132
QY	3233	TGTGTTTTCCATGTGCAGGGTGAAGTTTTTTTTTGGCAACCTGACACATGTTGGCCCC	3292
Db	42131	TGTGTTTTCCATGTGCAGGGTGAAGTTTTTTTTTGGCAACCTGACACATGTTGGCCCC	42072
QY	3293	CTCAAGAAATTTCTGTGGGATTTGTACCCACAGATCTGTTCCTCCCAATCCTTCTCCCA	3352
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QY	3353	CCTCTCCGCTCTCCCTCCCTCCCTGG-----AGACCTCGAAGTGTGTGTT	3398
Db	42011	CCTCTCCGCTCTCCCTCCCTCCCTGGNNNNNAGNACNNNNNNCCTGGAAGTGTGTGTT	41952
QY	3399	CACATACGTGACCTTGGCACACAGACACACAGAGGATGGAGCTTGGGAACACGAGGA	3458
Db	41951	CACATACGTGACCTTGGCACACAGACACACAGAGGATGGAGCTTGGGAACACGAGGA	41892
QY	3459	AATCACAGCCCTCGCCCTCCTTGCCTTGCCTTACCCCGGGGAAGCATGTGTT-CCCCC	3517
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QY	3518	CGAGCCCCCTTGGCACACAGTCAAGACAGTCTGCGGGGAGGCCCTCACCTTC	3577
Db	41831	CGAGCCCCCTTGGCACACAGTCAAGACAGTCTGCGGGGAGGCCCTCACCTTC	41772
QY	3578	CAGAGAGGACAGACAGATTTCTGCTGGGGAGGAGAGTCCACGATCCTGATGCT	3637
Db	41771	CAGAGAGGACAGACAGATTTCTGCTGGGGAGGAGAGTCCACGATCCTGATGCT	41712
QY	3638	GCCTGGAAGCTTATTTTCGTGGCCAGGACGATTTCTCTGAGTGGAAACAGGTTCTTG	3697
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QY	3698	CATGTGGATGTGTGTTTCCACAGGACAGCGCCCTCTCTTCCAGACATTTCCCTCGCTC	3757
Db	41651	CATGTGGATGTGTGTTTCCACAGGACAGCGCCCTCTCTTCCAGACATTTCCCTCGCTC	41592
QY	3758	CCCC-AGGCCTCAGGCCACGACCCAGTTCTCTCTCATGCGAGGTGAGACAGACTTC	3816
Db	41591	CCCCNAGGCCTCAGGCCACGACCCAGTTCTCTCTCATGCGAGGTGAGACAGACTTC	41532
QY	3817	TAGTTGGCAGAGCTGAGAGGGTGAACAAACCCGAGGAGGCGCGGCCCTTGCTCCCG	3876
Db	41531	TAGTTGGCAGAGCTGAGAGGGTGAACAAACCCGAGGAGGCGCGGCCCTTGCTCCCG	41472
QY	3877	AGTTGGGGGAGGGGGTGTGGCAACGTGCCCCCGCAGAGGCCACGCAATGTTTGACCAA	3936
Db	41471	AGTTGGGGGAGGGGGTGTGGCAACGTGCCCCCGCAGAGGCCACGCAATGTTTGACCAA	41412
QY	3937	GCCC-TCATGTGTGTCGAGACAGCCTTTTCCCGAGCCTCAGACATGTCATCCGT	3995
Db	41411	GCCCNCTCATGTGTGTCGAGACAGCCTTTTCCCGAGCCTCAGACATGTCATCCGT	41352
QY	3996	GCC-AAACTGGGTAGGTGGATTTTGAGCGGAAAGCTCCCAAAATGTGCCAAGAAATTTCC	4054

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Db 41351 GCCNAACTGGTAGGTGATTGAGGGGAAAGACTCCCAAAATGTGCGAGAAATTTCCC 41292
QY 4055 AGTCCAGGAGGAGGAGGGAACCTAAGGGCAAGCAGGATACAGGGCGAGGATGTGCA 4114
Db 41291 AGTCCAGGAGGAGGAGGGAACCTAAGGGCAAGCAGGATACAGGGCGAGGATGTGCA 41232
QY 4115 GGTGAGGGGCTCCCGCTGTGCCCC-TTCTCTCTACCAATGTCTCCCCACCCCTGCTCA 4173
Db 41231 GGTGAGGGGCTCCCGCTGTGCCCCTTCTCTCTACCAATGTCTCCCCACCCCTGCTCA 41172
QY 4174 GTTCTCGTTCCCTTCATCTCGTCCCTCTTTGAAGCTGTCCCAATCTCAGTGTGAG 4233
Db 41171 GTTCTCGTTCCCTTCATCTCGTCCCTCTTTGAAGCTGTCCCAATCTCAGTGTGAG 41112
QY 4234 ACCAGCCTTCTCTCTCATCTGACCAACCTCTCTGACCGAGCCCTCTCTGTCTGAAAG 4293
Db 41111 ACCAGCCTTCTCTCTCAGTACCAACCTCTCTGACCGAGCCCTCTCTGTCTGAAAG 41052
QY 4294 AAAGGACCTTGAATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4353
Db 41051 AAAGGAGCCTTGAATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 40992
QY 4354 GAGAAATGAGGTGAGCGGTGTCTGGGAAACAGATGAGGGGGGAGTGGGACAGGGGCTTGGG 4413
Db 40991 GAGAAATGAGGTGAGCGGTGTCTGGGAAACAGATGAGGGGGGAGTGGGACAGGGGCTTGGG 40932
QY 4414 CAGACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4473
Db 40931 CAGACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 40872
QY 4474 GGGCAATTTGGGAAAGAAATGATGTCTGGAAGGCTTAAGGGGACACAGTGGGACAGGGGAG 4533
Db 40871 GGGCAATTTGGGAAAGAAATGATGTCTGGAAGGCTTAAGGGGACACAGTGGGACAGGGGAG 40812
QY 4534 AGTCTCATCTGCTGCAATTTTGGGGTGTGTAGTGCACCAATCTGAGGAGGAGGAGGAGG 4593
Db 40811 AGTCTCATCTGCTGCAATTTTGGGGTGTGTAGTGCACCAATCTGAGGAGGAGGAGGAGG 40752
QY 4594 GCTGTCTTCCACTGACACCAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4652
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QY 4653 TCTTGACTGTCCCT 4666
Db 40691 TCTTGACTGTCCCT 40678

RESULT 13
AC108094/c 222871 bp DNA linear HTG 25-JAN-2002
LOCUS Homo sapiens chromosome 16 clone CTD-2547L19, WORKING DRAFT
DEFINITION
SEQUENCE, 25 unordered pieces.
ACCESSION AC108094
VERSION AC108094.1 GI:18369940
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 222871)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 222871)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

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FEATURES
source

Project Information
Center Project Name: 808312
Center clone name: CITB-El_2547L19

Summary Statistics
Consensus quality: 201820 bases at least Q40
Consensus quality: 211667 bases at least Q30
Consensus quality: 213645 bases at least Q20
Estimated insert size: 221000; agarose-fp estimation
Quality coverage: 6.36 in Q20 bases; agarose-fp estimation
Quality coverage: 6.37 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 11298 11297: contig of 1504 bp in length
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* 12888 16802: contig of 3915 bp in length
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* 20642 20741: gap of unknown length
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Location/Qualifiers
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/organism="Homo sapiens"

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Ransley, J., Gill, R., Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kovar, C., Liu, J., Liu, M., Louised, H., Lozano, R.J., Martin, R., Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Perez, L., Nelson, A., Nguyen, R., Nguyen, N., Ogun, N., Parish, B., Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., Worley, K. and Gibbs, R.

TITLE

Direct Submission

REFERENCE

Unpublished

2 (bases 1 to 185010)

AUTHORS

Worley, K.C.

TITLE

Direct Submission

Submitted (05-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this sequence version replaced gi:11079353.

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: MAAS
Center clone name: RP23-257C7
----- Summary Statistics
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye; 81% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 165161 bases at least Q40
Consensus quality: 183003 bases at least Q30
Consensus quality: 189902 bases at least Q20
Estimated insert size: 187232; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 68138 68237: gap of unknown length
* 68238 78523: contig of 10286 bp in length
* 78524 87604: gap of unknown length
* 87605 87704: gap of unknown length
* 87705 94722: contig of 7018 bp in length
* 94723 94822: gap of unknown length
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* 158886	158885:	gap of unknown length
* 158886	162886:	contig of 3901 bp in length
* 162887	162986:	gap of unknown length
* 162987	165635:	contig of 2649 bp in length
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* 172812	172911:	gap of unknown length
* 172912	175653:	contig of 2742 bp in length
* 175654	175753:	gap of unknown length
* 175754	177766:	contig of 2013 bp in length
* 177767	177866:	gap of unknown length
* 177867	180157:	contig of 2291 bp in length
* 180158	180257:	gap of unknown length
* 180258	182295:	contig of 2038 bp in length
* 182296	182395:	gap of unknown length
* 182396	185010:	contig of 2615 bp in length.

FEATURES
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1..185010
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-257C7"

BASE COUNT 46226 a 44836 c 45415 g 45499 t 3034 others

ORIGIN

Query Match 25.1%; Score 1172.2; DB 2; Length 185010;
Best Local Similarity 72.4%; Pred. No. 7.1e-155;
Matches 1971; Conservative 0; Mismatches 558; Indels 194; Gaps 27;

QY	2053	GGGACCCCAACAGCGCGTGGCGAGGATACCAAGTTATCCACACCAAGCCCAATCGCT	2112
Db	63598	GTGACCCCAACAGCGCTGTGCCACAGGACCAAGTTATCCACACCAAGCCCAATCGCT	63599
QY	2113	TGAGAGGTGTGTGGAGCAAAATTCACAGCAAGAGAGAGTATCTGCACATAGGCC	2172
Db	63538	TTGAAGAGGTAGTGTGGAGCAAGTTCAACAGCAAGAGAGAGTATCTGCACATAGGCC	63479
QY	2173	TGAAGCCACGCTGTGGTGCACAACTACCGCGCCCAAGTGGCTTCTGGCTGGAGCTCG	2232
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QY	2233	TGCCCCAAGTGTGCACAACTGTGCACAGGAGCTTTCACACCAAGCGGCTTGCCTCCCT	2292
Db	63418	TGCCCCAAGTGTGCACAACTGTGCACAGGAGCTTTCACACCAAGCGGCTTGCCTCCCT	63359
QY	2293	AGCCACCGCTGTGGCGCTGTGCTCCCGCGG---CTGGCGCGCGGGGACACGCCGCC	2349
Db	63358	ATGCCACCGCTGTGGCGCTGTGCTCCCGCGG---CTGGCGCGCGGGGACACGCCGCC	63299
QY	2350	CGCCGCTGTGCCACCTTCCCTCCCGAGCGCGGAGCGCGGCTTATGACC	2409

1	4657	100.0	4667	10	US-09-934-323-1	Sequence 1, Appl
2	2508	53.7	2508	10	US-09-934-323-3	Sequence 3, Appl
3	2383.4	51.1	2663	13	US-10-274-694-30	Sequence 30, Appl
4	1618.2	34.7	1966	11	US-09-764-891-7886	Sequence 7886, App
5	1092	23.4	1446	11	US-09-809-391-139	Sequence 139, App
6	1092	23.4	1446	13	US-09-882-171-439	Sequence 139, App
7	912.2	19.5	3113	10	US-09-978-295A-374	Sequence 374, App
8	912.2	19.5	3113	10	US-09-978-697-374	Sequence 374, App
9	912.2	19.5	3113	10	US-09-978-192A-374	Sequence 374, App
10	912.2	19.5	3113	10	US-09-978-832A-374	Sequence 374, App
11	912.2	19.5	3113	11	US-09-978-189-374	Sequence 374, App
12	912.2	19.5	3113	11	US-09-978-608A-374	Sequence 374, App
13	912.2	19.5	3113	11	US-09-978-585A-374	Sequence 374, App
14	912.2	19.5	3113	11	US-09-978-191A-374	Sequence 374, App
15	912.2	19.5	3113	11	US-09-978-403A-374	Sequence 374, App

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 Db 2461 CCGTGGGTGCTCCCTCTCTCTCTCAACATCTGGCTTTGCTGCTTCTACTACAAGC 2520
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 Db 2581 GCGTGCCTGCTGGGGGCGCCCTGCTCCCGCGGCGGCTGAGCTGCCACAGAGAGG 2640
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Db 3421 CCAGACACAGAGTGGAGCTGGAGAGCGAGGAAATCAAGCCCCCTCGCCCTG 3480
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 Db 4081 AGGCGAAGCAGGATACAGGCGGAGGATGTCAGTGGAGGCGGCTCCCGCTTGTGCCCC 4140
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 Qy 4621 GAATCCCTGGTCTTGAGTCCCAAGAACTTTGCTCTTTGACTGTCCTC 4667
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RESULT 2

US-09-934-323-3
 ; Sequence 3, Application US/09934323
 ; Patent No. US20020150910A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Rory A. J.
 ; TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
 ; FILE OF INVENTION: FAMILY MEMBER AND USES THEREOF
 ; FILE REFERENCE: 10448-081001
 ; CURRENT APPLICATION NUMBER: US/09/934,323
 ; PRIOR FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: US 60/226,774
 ; PRIOR FILING DATE: 2000-08-21
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 2508
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-934-323-3

Query Match 53.7%; Score 2508; DB 10; Length 2508;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Qy 480 CCCGGCGGCG 539
 Db 61 CCCGGCGGCG 120
 Qy 540 TTCGGGTGTGAACAGCGCTACGGCGAGTGGCGCGGTGTGGCGCGAGCTCAACAAC 599
 Db 121 TTCGGGTGTGAACAGCGCTACGGCGAGTGGCGCGGTGTGGCGCGAGCTCAACAAC 180
 Qy 600 GAGATCTGGGCG 659
 Db 181 GAGATCTGGGCG 240
 Qy 660 GCGCGCGCTTCAGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
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 Qy 720 ACCCTGCGCGCGCGCTGCGCGAGACCTGCGCGGCGGTGGCGCGATCATGTGCT 779
 Db 301 ACCCTGCGCGCGCGCTGCGCGAGACCTGCGCGGCGGTGGCGCGATCATGTGCT 360
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 Db 361 GTGTGGTTACCGAACAATTGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
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 Qy 900 GAGCGAGCGTCAATCGCGCAGACACAGATATCCGTGACCGCTGGGAGAGCGTGTGATG 959
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[illegible][illegible]

RESULT 3

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Qy 778 CTGTGTGTTCACGCAACCTTGTGAGGCGCGCCGCAACCTAGTGTGAGAACGAGCGAGG 837
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Qy 2158 ATCTGCATATAGCCCTGAAAGCCACGCTGCTGCTGACAACTTACCGCCCAACAGGCTG 2217
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Db 2215 TGGCGTGGGTGCTCTCCCTCTCTTCTCAATCTGCGCTTTGCTGCCCTCTACTACA 2274
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RESULT 4

US-09-764-891-7886
; Sequence 7886, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

```

; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7886
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7886

Query Match      34.7%; Score 1618.2; DB 11; Length 1969;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1642; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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QY 3081 TGTCTTTCCACAGAGAGAGCCCGAGTCTCTCTCTGATCTGGGCTTTGAACTG 3140
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QY 3141 GGGGGCGTTTCTCCCGCCCAATGGGACACCAAGTCTTCGGTGTGGAAATGGTATTTT 3200
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QY 3261 TTTTGTTCACACCTGGACACATGTGTCCTCAAGAAATTTCTGTGGGGAATTTGAC 3320
Db 240 TTTTGTTCACACCTGGACACATGTGTCCTCAAGAAATTTCTGTGGGGAATTTGAC 299

QY 3321 CCAGAAATCTGTTCGCCATCCCTTCGACCTCTCCCTCCCTCCCTCCCTGGAGA 3380
Db 300 CCAGAAATCTGTTCGCCATCCCTTCGACCTCTCCCTCCCTCCCTCCCTGGAGA 359

QY 3381 CCCTGGAAGTGTGTTCACATACAGTACACCTTGGCCACACAGACACAGAGATGAG 3440
Db 360 CCCTGGAAGTGTGTTCACATACAGTACACCTTGGCCACACAGACACAGAGATGAG 419

QY 3441 CTTGGGAGAGCAGAGAGAAATACAGCCCTTGGCCCTCCCTCCCTCCCTCCCTCC 3500
Db 420 CTTGGGAGAGCAGAGAGAAATACAGCCCTTGGCCCTCCCTCCCTCCCTCCCTCC 479

QY 3501 GCGAAGCATTTCCCGCCGACGCCCCCTTGGCAAGTCAAGTCAAGCAAGTCAAGTCA 3560
Db 480 GCGAAGCATTTCCCGCCGACGCCCCCTTGGCAAGTCAAGTCAAGTCAAGTCAAGTCA 539

QY 3561 GGGAGGCCCTCAGTTCACAGAGAGACAGACAGATTTCTGCTGGGGAGGGAGAGT 3620
Db 540 GGGAGGCCCTCAGTTCACAGAGAGACAGACAGATTTCTGCTGGGGAGGGAGAGT 599

QY 3621 CCAGCATCTGATGTGCTGGAAGCTTATTTCCGTCGAGGAGGCAATTTCTGTA 3680
Db 600 CCAGCATCTGATGTGCTGGAAGCTTATTTCCGTCGAGGAGGCAATTTCTGTA 659

QY 3681 GTGAAACAGGTCTTTCATGTGGATGTGTGTTCCCGAGGAGAGCGCCCTCTCTCC 3740
Db 660 GTGAAACAGGTCTTTCATGTGGATGTGTGTTCCCGAGGAGAGCGCCCTCTCTCC 719

QY 3741 CAGCACTTCCCTCCCTCCCGAGGCTCAGGCGCCAGCACCAGTTCCTCCCTCAGTSCA 3800
Db 720 CAGCACTTCCCTCCCTCCCGAGGCTCAGGCGCCAGCACCAGTTCCTCCCTCAGTSCA 779

QY 3801 GGTGAGCAGACTTCTAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 3860
Db 780 GGTGAGCAGACTTCTAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 839

QY 3861 CCGGCCCTTCTCCCGAGTGTGGGGAGGGGTGTGGCAACGTCGCCCGCCCGCAGAGGCCA 3920

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840 CCGGCCCTTCTCCCGAGTGTGGGGAGGGGTGTGGCAACGTCGCCCGCCCGCAGAGGCCA 899
3921 CCGATGTTTGACCAAGAGCCCTCATTTGCTGTCGAGGACAGCCCTTTTCCCGAGGCTCAGA 3980
900 CCGATGTTTGACCAAGAGCCCTCATTTGCTGTCGAGGACAGCCCTTTTCCCGAGGCTCAGA 959
3981 GCATTGCTCATCCGTGCGCAAACTGGGTAGTGTGATTTGAGCGGAAAGACTCCCAAAATGT 4040
960 GCATTGCTCATCCGTGCGCAAACTGGGTAGTGTGATTTGAGCGGAAAGACTCCCAAAATGT 1019
4041 GCCAAGATTTCCAGTCCCGAGGACGGGACGGAATAAGGCAAGCAGGATACAGGG 4100
1020 GCCAAGATTTCCCGTCCCGAGGACGGGACGGAATAAGGCAAGCAGGATACAGGG 1079
4101 CGAGGATGTGCGAGGTGAGGGGCTCCCGCTGTCGCGCTTCTCTCTCCCTCACCATCTCTCCC 4160
1080 CGAGGATGTGCGAGGTGAGGGGCTCCCGCTGTCGCGCTTCTCTCTCCCTCACCATCTCTCCC 1139
4161 CCAGCTGCTCAGTCTCCCTTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4220
1140 CCAGCTGCTCAGTCTCCCTTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1199
4221 ATCTCAGTGTGAGACAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4280
1200 ATCTCAGTGTGAGACAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1259
4281 CTTTCTCTGAAAGAGAGCCCTTGAATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTCA 4340
1260 CTTTCTCTGAAAGAGAGCCCTTGAATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTCA 1319
4341 CCGGACAGGTTTGGGAGAAATGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 4400
1320 CCGGACAGGTTTGGGAGAAATGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 1379
4401 GACAGGCTTGGGAGAGACACAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTCC 4460
1380 GACAGGCTTGGGAGAGACACAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTCC 1439
4461 GGGGCTTGGGCTTGGGCAATTTGGGAAAGAAATGATGTCTGGAAGGGCTTAAAGGACACAG 4520
1440 GGGGCTTGGGCTTGGGCAATTTGGGAAAGAAATGATGTCTGGAAGGGCTTAAAGGACACAG 1499
4521 TGGAGAGGGGAGGAGTCTCATCTGCTGGGCAATTTGGGAGGAGGAGGAGGAGGAGGAGGAG 4580
1500 TGGAGAGGGGAGGAGTCTCATCTGCTGGGCAATTTGGGAGGAGGAGGAGGAGGAGGAGGAG 1559
4581 TAGGGGCTGGGAGTGTCTCTTCCACTGACCCAAATCCAGAAATCCCTGCTGTGAGT-C 4639
1560 TAGGGGCTGGGAGTGTCTCTTCCACTGACCCAAATCCAGAAATCCCTGCTGTGAGTCC 1619
4640 CCAGAACCTTGGCTCTTCACTGTCCCT 4666
1620 CCAGAACCTTGGCTCTTCACTGTCCCT 1646

RESULT 5
US-09-391-139
; Sequence 139, Application US/09/809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Homo sapiens

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FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-809-391-139

Query Match      23.4%; Score 1092; DB 11; Length 1446;
Best Local Similarity 99.0%; Pred. No. 1.1e-257;
Matches 1133; Conservative 6; Mismatches 1; Indels 4; Gaps 4;

QY 3524 CCCCCTTGGCAGAGTCAGATGAAGACAGCTCTCCGCGGGAGGCCCTCACCTTCCAGAGA 3583
DB 3 CCCCCTTGGCAGAGTCAGATGAAGACAGCTCTCCGCGGGAGGCCCTCACTTCCAGAGA 62

QY 3584 GGACAGACACAGATTTCTCTCTCGGGGAGGAGAGTCCACGATCTCTGATGCTCCCTGG 3643
DB 63 GGACAGACACAGATTTCTCTCTCGGGGAGGAGAGTCCACGATCTCTGATGCTCCCTGG 122

QY 3644 AAGCTTATTTTCCCGTGGCCAGACAGCATTTCTCTGAGTGGAAACAGGTTCTTGCATGTG 3703
DB 123 AAGCTTATTTTCCCGTGGCCAGACAGCATTTCTCTGAGTGGAAACAGGTTCTTGCATGTG 182

QY 3704 GATGTGTGTTTCCCGAGCAGACAGGCCCTCTCTTCCAGACATCTTCCCTGCTCCGCCAG 3763
DB 183 GATGTGTGTTTCCCGAGCAGACAGGCCCTCTCTTCCAGACATCTTCCCTGCTCCGCCAG 242

QY 3764 GCCTCAGGCCAGCACCCAGTCTCTCTCACATGGCAGGTGAGCAGACAGACTTCTAGTTGG 3823
DB 243 GCCTCAGG-CCAGCACCCAGTCTCTCTCACATGGCAGGTGAGCAGACAGACTTCTAGTTGG 301

QY 3824 CAGGAGCTGAGGAGGTGAAACAAACCCCGAGGAGGCCCGCCCTGTCTCCGAGTTGGG 3883
DB 302 CAGGAGCTGAGGAGGTGAAACAAACCCCGAGGAGGCCCGCCCTGTCTCCGAGTTGGG 361

QY 3884 GGGAGGGGGTGTGCAACGTGCCCCCGCAGAGGCCACGATGTTTGACAAAGCCCTCA 3943
DB 362 GGGAGGGGGTGTGCAACGTGCCCCCGCAGAGGCCACGATGTTTGACAAAGCCCTCA 421

QY 3944 TTGTGTCGAGACAGCTTTTCCCGAGGCTCAGAGCATTTGCTCATCTCCGTGCGAAACT 4003
DB 422 TTGTGTCGAGACAGCTTTTCCCGAGGCTCAGAGCATTTGCTCATCTCCGTGCGAAACT 481

QY 4004 GGGTAGTGTGATTTAGCGAAAGACTCCCAAAATGTGCAAGAAATTTCCAGTCCCGAGG 4063
DB 482 GGGTAGTGTGATTTAGCGAAAGACTCCCAAAATGTGCAAGAAATTTCCCGTCCCGAGG 541

QY 4064 CAGGCGAGGAGAACTAAGGCGAAGCAGGATACAGGCGAGGAGTGTGCGAGTGAGGGG 4123
DB 542 CAGGCGAGGAGAACTAAGGCGAAGCAGGATACAGGCGAGGAGTGTGCGAGTGAGGGG 601

QY 4124 GCTCCGCGCTGTGCGCCCTTCTCTCACCATGTCTCCCGCAGCTGCTCAGTTCTCCGTT 4183
DB 602 GCTCCGCGCTGTGCGCCCTTCTCTCACCATGTCTCCCGCAGCTGCTCAGTTCTCCGTT 661

QY 4184 CCGCTTCATCTCCGTCGCCCTCTTTGAAGTGTCCCATCTCAGTGTGAGCAGCCCTTC 4243
DB 662 CCGCTTCATCTCCGTCGCCCTCTTTGAAGTGTCCCATCTCAGTGTGAGCAGCCCTTC 721

QY 4244 TCCTCATCTGACACACCTCTCTGAGCGCGCCCTCTCTGCTGCTGAAAGAAAGAGGCT 4303
DB 722 TCCTCATCTGACACACCTCTCTGAGCGCGCCCTCTCTGCTGCTGAAAGAAAGAGGCT 780

QY 4304 TGAATGTGAGGAGGAGCAGTGGGGAAGAAAGTCTCACCGGACAGGTTGGGAGAAATGAGG 4363
DB 781 TGAATGTGAGGAGGAGCAGTGGGGAAGAAAGTCTCACCGGACAGGTTGGGAGAAATGAGG 840

QY 4364 TCAGCGTGTCTGGGGAACAGATGAGGAGGAGTGGGGAAGAGGCTTGGGAGACACCCAG 4423
DB 841 TCAGCGTGTCTGGGGAACAGATGAGGAGGAGTGGGGAAGAGGCTTGGGAGACACCCAG 900

QY 4424 CAGGAATAATTTGAATGTGTGAGGTGACTCCCCGAGGCGCTTGGGCTTGGGCAATTTGG 4483
DB 901 CAGGAATAATTTGAATGTGTGAGGTGACTCCCCGAGG-GGCCTTGGGCTTGGGCAATTTGG 959

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RESULT 6
US-09-882-171-119
; Sequence 139, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
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; PRIOR APPLICATION NUMBER: 60/038,621
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140 PRIOR APPLICATION NUMBER: 60/056,908
141 PRIOR FILING DATE: 1997-08-22
142 PRIOR APPLICATION NUMBER: 60/048,964
143 PRIOR FILING DATE: 1997-06-06
144 PRIOR APPLICATION NUMBER: 60/057,650
145 PRIOR FILING DATE: 1997-09-05
146 PRIOR APPLICATION NUMBER: 60/056,884
147 PRIOR FILING DATE: 1997-08-22
148 PRIOR APPLICATION NUMBER: 60/057,669

; PRIOR FILING DATE: 1997-09-05

Query Match 23.4%; Score 1092; DB 13; Length 1446;
 Best Local Similarity 99.0%; Pred. No. 1.1e-257;
 Matches 1133; Conservative 6; Mismatches 1; Indels 4; Gaps 4;

QY	3524	CCCCCTTGGCACAAGTCAGATGAAGACAGTCCTGCGGGAGGAGCCCTCACCTCCACAGAGA	3583
DB	3	CCCCCTTGGCACAAGTCAGATGAAGACAGTCCTGCGGGAGGAGCCCTCACCTCCACAGAGA	62
QY	3584	GGACACACAGATTTCTGCTGGGGAGGAGAGTCCACGCATCTCTGATGCTGCCTGG	3643
DB	63	GGACACACAGATTTCTGCTGGGGAGGAGAGTCCACGCATCTCTGATGCTGCCTGG	122
QY	3644	AAGCTTATTTTCCGCTGGCCAGGACGATTTCTCTGAGTGAACAGGTTCTTGGCATGTG	3703
DB	123	AAGCTTATTTTCCGCTGGCCAGGATGATTTCTCTGAGTGAACAGGTTCTTGGCATGTG	182
QY	3704	GATGTGTGTTTCCCAAGGAGGAGGCGCCCTCTCTTCCAGCACTTCCCTGCGTCCGCCAG	3763
DB	183	GATGTGTGTTTCCCAAGGAGGAGGCGCCCTCTCTTCCAGCACTTCCCTGCGTCCGCCAG	242
QY	3764	GCTCAGGCCCCAGCACCCAGTTCTTCCCTCACATGCGAGTGACACACTTCTAGTTGG	3823
DB	243	GCTCAGG-CCAGCACCCAGTTCTTCCCTCACATGCGAGTGACACACTTCTAGTTGG	301
QY	3824	CAGGAGCTGAGGAGGTGAACAAACCCCGAGGAGGCGCCCTTGTCTCCGAGTTGGG	3883
DB	302	CAGGAGCTGAGGAGGTGAACAAACCCCGAGGAGGCGCCCTTGTCTCCGAGTTGGG	361
QY	3884	GGGAGGGGTGGCAACGCTGCCCCCGCCAGGAGGCGACGATGTTGACAAAGCCCTCA	3943
DB	362	GGGAGGGGTGGCAACGCTGCCCCCGCCAGGAGGCGACGATGTTGACAAAGCCCTCA	421
QY	3944	TTGTGCTCCGAGCAGAGCTTTTCCCAAGGCTCAGAGCATTTGCTCATCCGTGCCAACT	4003
DB	422	TTGTGCTCCGAGCAGAGCTTTTCCCAAGGCTCAGAGCATTTGCTCATCCGTGCCAACT	481
QY	4004	GGGTAGTGGATTGAGCGGAAAGACTCCCAAAATGTCGCAAGAAATTTCCAGTCCCAGG	4063
DB	482	GGGTAGTGGATTGAGCGGAAAGACTCCCAAAATGTCGCAAGAAATTTCCAGTCCCAGG	541
QY	4064	CAGGCGAGGGGAAACTAAGGGGACAGGATACAGGGGAGGAGGATGGCAGGTGAGGGG	4123
DB	542	CAGGCGAGGGGAAACTAAGGGGACAGGATACAGGGGAGGAGGATGGCAGGTGAGGGG	601
QY	4124	GCTCCCGCTGTGCGCTTCTCCTACCATGTCCTCCCAAGGCTGCTGCTGCTGCTGCTGCT	4183
DB	602	GCTCCCGCTGTGCGCTTCTCCTACCATGTCCTCCCAAGGCTGCTGCTGCTGCTGCTGCT	661
QY	4184	CCCTTTCATCTCCGTCCTCTTTGAGCTGTCCTCCATCTCAGTGTACAGCCGCTTC	4243
DB	662	CCCTTTCATCTCCGTCCTCTTTGAGCTGTCCTCCATCTCAGTGTACAGCCGCTTC	721
QY	4244	TCCTCATCTGACCCCTCTCTGACCGACGCCCCCTCTTCTGCTGCTGCTGCTGCTGCTGCT	4303
DB	722	TCCTCATCTGACCCCTCTCTGACCGACGCCCCCTCTTCTGCTGCTGCTGCTGCTGCTGCT	780
QY	4304	TGAATGTTGGAGGAGGAGTGGGAGGAGGAGTCTACCGACAGGTTGGGAGATGAGG	4363
DB	781	TGAATGTTGGAGGAGGAGTGGGAGGAGGAGTCTACCGACAGGTTGGGAGATGAGG	840
QY	4364	TCAGCGTGTCTGGGAAACAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	4423
DB	841	TCAGCGTGTCTGGGAAACAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	900
QY	4424	CAGGATTAATTTGAATGTGTGAGTGAATCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGG	4483
DB	901	CAGGATTAATTTGAATGTGTGAGTGAATCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGG	959
QY	4484	GAAGAAGATGATGCTGGAAGGCTTAAGGACACAGTGAAGGAGGAGGAGGAGGAGGAGGAGG	4543
DB	960	GAAGAAGATGATGCTGGAAGGCTTAAGGACACAGTGAAGGAGGAGGAGGAGGAGGAGGAGG	1019

RESULT 7
 US-09-978-295A-374
 ; Sequence 374, Application US/09978295A
 ; Patent No. US2002015606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC11
 ; CURRENT APPLICATION NUMBER: US/09/978,295A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
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QY	4544	TGCTGGCATTTTGTGGGGTGTAGTGCCAAACTTGAATAGGGCTGGGTGCTGCTTCC	4603
DB	1020	TGCTGGCATTTTGTGGGGTGTAGTGCCAAACTTGAATAGGGCTGGGTGCTGCTTCC	1079
QY	4604	ACTGACACCCCAATCCAGAAATCCCTGGTCTTGTAGT-CCCAGAACTTGTCCCTTGTAGTGT	4662
DB	1080	ACTGACACCCCAATCCAGAAATCCCTGGTCTTGTAGT-CCCAGAACTTGTCCCTTGTAGTGT	1139
QY	4663	CCCT 4666	
DB	1140	CCCT 1143	

1	PRIOR APPLICATION NUMBER: 60/078888
2	PRIOR FILING DATE: 1998-03-20
3	PRIOR APPLICATION NUMBER: 60/078936
4	PRIOR FILING DATE: 1998-03-20
5	PRIOR APPLICATION NUMBER: 60/078910
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7	PRIOR APPLICATION NUMBER: 60/078939
8	PRIOR FILING DATE: 1998-03-20
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71	PRIOR APPLICATION NUMBER: 60/082804
72	PRIOR FILING DATE: 1998-04-22
73	PRIOR APPLICATION NUMBER: 60/082700

Query Match 19.5%; Score 912.2; DB 10; Length 3113;
Best Local Similarity 64.7%; Pred. No. 1.4e-213;

Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY 527 CGCGGAGGACCGTTCCTCCGCTGTGTAACACAGCGCTACCGGCGAGTCGGGCTGTGCGCG 586
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Db 172 ACCGTTACCAATAGATCTTGGTCCAGTGGAGCAATTAAGGGTCCCTATGCCCTC 231
QY 647 GCGGCGCTGGGCGCGCGCTTCAGCGGCTGAGGCGCGCGCTGCTGCTGCGCGCGCT 706
Db 232 ACCGCCCACTGGAGAGAGCGGTTTCAGCGCCAGAACCCCGCTCCTCTGACTGGCAT 291
QY 707 GCGCAACGCGCACCACTCGCGCGCTGCGCGCTGCGCGAGACCTGCAAG---GGGCGCTGCC 763
Db 292 CGGAATACTACTCAGTTTGTCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 351
QY 764 CGGCATCTGCTGCTGTGTGTGTACCGCAACTTGGAGGCGCGCGCGCGCGCGCGCGCG 823
Db 352 GCATGACATCTGCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 411
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Db 412 AGATCAAAATGAGACTGCTTCTTAAACATCTACGTCGCGCGCGCGCGCGCGCGCGCG 471
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Db 532 TGATCAGAACATAGAGAGCGCGTGTGCTGTATATCTTCCATGCGCGCGCGCGCGCGCG 591
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Db 1489 GAAGCGCGAGTGGGCGAGTTCGGCGCGATGGTGTGAGTTCCTTATGCTTCTGCGCATCC 1548
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QY 2402 CTATGACCGCTTCCCGGAGCTCAAGGAGTACTTCAAGGAGTGTGCTGCTGCTGCTGCT 2461
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QY 2702 GCGCCCTGCTGCGCGCCGACCTACACCCCTGCGCGCGGACCGGACGATGTGCC 2761
DB 2305 GAGGCTCACCTGCGCGCGGACACTACACCCCTCAAGCTGCGCGGTCGCCACGATGACATCCC 2364
QY 2762 TCTCTTGCGCCCGCGCGGCGCTGACCCCTGCTGCGCCAGTGGCGCTG 2804
DB 2365 ACTTATGACGCCCAACACCATCAACCATGATTCAAAACACTG 2407

RESULT 8

US-09-978-697-374

; Sequence 374, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Auscin L.

; APPLICANT: Hillan, Kenneth J

; APPLICANT: Kijavrin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C27

; CURRENT APPLICATION NUMBER: US/09/978,697

; PRIOR FILING DATE: 2001-10-16

; PRIOR FILING DATE: 2001-07-30

; PRIOR FILING DATE: 1997-10-17

; PRIOR FILING DATE: 1997-11-03

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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 19.5%; Score 912.2; DB 10; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 1.4e-213;
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QY	587	CGAGCTCAACACAGAGATCTGGGCGCGCGTCTGGAGTCTTGGGGGTGCGCTACGCCAC	646
DB	172	ACGGTTACCAATGAGATCTTGGTCAAGTGGAGCAGTACTTAGGGGTCCCTTATGCCTC	231
QY	647	GGCGCCCTGGGCGCGCGCTTCCAGCGCGCTGAGGCGCGCGCTCTGTGGCGCGCGCT	706
DB	232	ACCGCCCATCTGGAGAGAGCGGTTTACGCCCGCAGAACCCCGCTCTCTGGAGTGGCAT	291
QY	707	GGCGAAGCGCCACACCTGCGCGCGCGCTGCGCGAGAACCTTCACG---	763
DB	292	CGGAATATCTACGTTTGTCTGTGTGCGCGCGCGCTGATGAGAGATCCCTTACT	351
QY	764	CGCCATCATCTGCTGCTGTGTGTTCACCGACAACTTGGAGGGCGCGCGCACCTTACGTGA	823
DB	352	GCATGACATGTGCCCATCTGGTTTACCGCAATTTGGATACCTTTGATGACCTATGTTCA	411
QY	824	GRACGAGAGGAGGACTGCTGATCTTAACTCTAGTGGCGCGCGAGGAGCGTCCGT	883
DB	412	AGATCAAAATGAAGACTGCTTACTTAAACATCTACGTGCCCGCGCGAGATGGAGCCAA	471
QY	884	CACAAAAAAGCTGACGAGCGG-----ACGCTCAATCCCGCAGACACAGATATCCG	934
DB	472	CACAAAGAAAAAGCGCAGATGATATACAGATTAATACCGTGGTGAAGACAGATATTC	531
QY	935	TGACCCGTG---GGAAGAGCCTGTGATGTGTCTTCCATGGCGCGCTCTACATGAGGG	991
DB	532	TGATCAGAAACAGTAAGAGCGCGTCTGCTCTATATCCATGGGGGATCTTACATGAGGG	591
QY	992	GACCGGAAACATGTTTCGATGGGCTCAGTCTCGCTGCTGCTGATGCAACGCTCATTTGAGCCAC	1051
DB	592	CACCGGCAACATGATTGACGGCAGCATTTTGGCAAGTACGGAACGCTCATCTGATCAC	651
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DB	652	CATTAACCTACCGTCTGGGAATACTAGGGTTTTTAAAGTACCGGTGACCGAGCAAAAGG	711
QY	1112	CAACTATGGGCTCCCTGGACAGATCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1171
DB	712	CAACTATGGGCTCCCTGGATCAGATTCAGATTCAGGCTGCGGTGAGGAGATGTTGGAGC	771
QY	1172	CTTTGGGGCGACCCCGAGCGCTATCCCATCTTTGGTTCCGGGGCAGGGGCTCTCGGT	1231
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DB	832	CAGCCTGTTGACCTGTCTCCACTACTCAGAGGGTCTCTTCCAGAGGCGCATCATTCAGAG	891
QY	1292	TGGCACCCCATTTTCAGCTGCTGTCTCACTACAGCGCTCAAGTACACGCGGCTCT	1351
DB	892	CGGCACCGCCCTGTCTCAGCTGGGAGTGAACCTACAGCGCGCGCATCTCGGATATT	951
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QY	1412	GAAAGCCCTTCCCGGAGCTGTGGACCGAGGAGTGTGAGCTGCGCGCTACCATCGGCTT	1471
DB	1012	CAAGAACTTACAGGAGCTCATCAGAGGAGCATCACCGCGCGCATCATCCATAGGCTT	1071
QY	1472	TGGGCGCGTGTGATGGCGAGCTGTGCTCCCGATGACCTGTGAGATCTCTATGACGAGGG	1531
DB	1072	CGGGCGCGTGTGATGACGCGCGAGTCTATCCAGAGACCGCGCGAGTCTGTGAGGAGG	1131
QY	1532	AGAAATTCCTCAACTACGACATGCTCATCGGCGTCAACCGAGGAGGCGCTCAGTTGCT	1591
DB	1132	CGAGTCTCTCACTACGACATCATGCTGGGGGTCAACCAAGGGAGGCGCTGAGATTCTGT	1191

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QY	2702	CGCGCCCTGCTTGCCTCCCGCGGATTTACACCTTGGCCCTGCGCGGACACGGACGATGTGCC	2761	
Db	2305	GAGGCTCACCTGCTCCCGCCAGACTACACCTCTACGCTGCGCGGTCGCGCAGATGACATCCC	2364	
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; Patent No. US20020177553A1				
GENERAL INFORMATION:				
; APPLICANT: Ashkenazi, Avi				
; APPLICANT: Baker Kevin P.				
; APPLICANT: Botstein, David				
; APPLICANT: Desnoyers, Luc				
; APPLICANT: Eaton, Dan				
; APPLICANT: Ferrara, Napoleon				
; APPLICANT: Filvaroff, Ellen				
; APPLICANT: Fong, Sherman				
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; APPLICANT: Gerber, Hanspeter				
; APPLICANT: Gerritsen, Mary E.				
; APPLICANT: Goddard, Audrey				
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; APPLICANT: Kljavin, Ivar J.				
; APPLICANT: Kuo, Sophia S.				
; APPLICANT: Napier, Mary A.				
; APPLICANT: Pan, James;				
; APPLICANT: Paoli, Nicholas F.				
; APPLICANT: Roy, Margaret Ann				
; APPLICANT: Shelton, David L.				
; APPLICANT: Stewart, Timothy A.				
; APPLICANT: Tumas, Daniel				
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; APPLICANT: Wood, William I.				
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic				
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; CURRENT FILING DATE: 2001-10-15				
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21 PRIOR APPLICATION NUMBER: 60/079920
22 PRIOR FILING DATE: 1998-03-30
23 PRIOR APPLICATION NUMBER: 60/079923
24 PRIOR FILING DATE: 1998-03-30
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73 PRIOR APPLICATION NUMBER: 60/082797

74 PRIOR FILING DATE: 1998-04-22
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76 PRIOR FILING DATE: 1998-04-23
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88 PRIOR FILING DATE: 1998-04-29
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91 PRIOR APPLICATION NUMBER: 60/083554
92 PRIOR FILING DATE: 1998-04-29
93 PRIOR APPLICATION NUMBER: 60/083558
94 PRIOR FILING DATE: 1998-04-29
95 PRIOR APPLICATION NUMBER: 60/083559
96 PRIOR FILING DATE: 1998-04-29
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101 PRIOR APPLICATION NUMBER: 60/084366
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134 PRIOR FILING DATE: 1998-05-15
135 PRIOR APPLICATION NUMBER: 60/085573
136 PRIOR FILING DATE: 1998-05-15
137 PRIOR APPLICATION NUMBER: 60/085704
138 PRIOR FILING DATE: 1998-05-15
139 PRIOR APPLICATION NUMBER: 60/085697

Query Match 19.5%; Score 912.2; DB 10; Length 3113;
Best Local Similarity 64.7%; Pred. NO. 1.4e-213;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

Db 2269 TCACGAGTGTGAGTGTGAG-----GCACACGACACT 2304
QY 2702 GCACCTGCTGCTGCCCGCCGACATACACCTTGGCCCTGCGCCGCGGACACGAGATGTGCC 2761
Db 2305 GAGGCTCACCTGCTGCCCGCCGACATACACCTTGGCCCTGCGCCGCGGATGATGATGCC 2364
QY 2762 TCTCTTGGCCCGCGCGGCGCTGACCTGTGCTGCCAGTGCCTG 2804
Db 2365 ACTTATGACGCCCAACACCATCACCATGATTCACACACACTG 2407

RESULT 10
US-09-999-832A-374
; Sequence 374, Application US/0999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Fertara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 19.5%; Score 912.2; DB 10; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 1.4e-213;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;
 QY 527 CGCGAGGAGCGCTTCCCGTGTGTGAACACGGCTACGGCGAGTGCAGGCTGTGCGCG 586

Db	112	CAGCAGACAGTATCCAGTTCTCAACAAATATGCGGCTTACAGAC 171
Qy	587	CGAGTCACACAGAGATCTGGGCCCCGCTGTCAGTTCTTGGGCGTCCCTACGCCAC 646
Db	172	ACCGTTACCAATGAGATCTTGGGTCAGTGGAGCAGTACTTAGGGGTCCTTATGCTTC 231
Qy	647	GCAGCCCTTGGGCGCCCCGCTTTCAGAGCCCTGAGGGCCCCGCTCTGTCGGCGCGCT 706
Db	232	ACCCCTCACTGGAGAGAGCGGTTTTCAGCCCCCAGAACCCCTCTCTCTGAGCTGGCAT 291
Qy	707	GGCAACGCCACACCCCTGCGCCCCGCTGCGCGCAGAACTTGCAGC-----GGGCGTGGC 763
Db	292	CCGAATATCTACTCAGTTTGTCTGTGTCGCCCCAGCACCTGATGAGAGATCTCTTACT 351
Qy	764	CGCCATCATCTGCTGCTGTGTGTTTCAACGACAACTTGGAGGGCGCGCCACCTTACGTGCA 823
Db	352	GCATGACATCTGCTGCCCATCTGTTTACGCCCAATTTGGATACTTTTGTATGACCTATGTTCA 411
Qy	824	GAACAGAGGAGGAGTCTGCTGTACCTCAACCTTACGTGCGCCACCGAGGACGTCCTGCT 883
Db	412	AGATCAAAATGAAGACTGCGCTTTTACTTAAACATCTACTGTCGCCACCGAAGATGGAGCCAA 471
Qy	884	CACAAAAAAGCTGACGAGGCG-----ACGCTCAATCCGCCACAGACACAGATATCGC 934
Db	472	CACAAAGAAAACGACAGATGATATACGAGTATGACCTGCTGAGACGAAGATATCA 531
Qy	935	TGACCTG---GGAAGAAGCTGTGATGCTGTTTCTCCATGCGCGCTCTCATGAGGG 991
Db	532	TGATCAAGACAGTAAGAAGCCCGTCATGCTTATATCCATGGGGGATCTTACATGAGGG 591
Qy	992	GACCGAAACATGTTGATGGGTTCAGTCTGCTGCTTATGCAACGTCATTTAGTGTAGCCAC 1051
Db	592	CACCGCAACATGATGACGGCAGCATTTTGGAGCTACGGAACGTCATCTGATCAC 651
Qy	1052	GCTCACTACCTCTTGGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1111
Db	652	CATTAATCTACCTGCTGCGGAATATAGGGTTTAAAGTACCGGTGACCGGACGCAAAAGG 711
Qy	1112	CAACTATGGCTCTCGGACAGATCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171
Db	712	CAACTATGGCTCTCGGACAGATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 771
Qy	1172	CTTTGGGGGAGCGCGGAGCGTATCACCATCTTTGGTTCGGGGGAGGGGCTCTCTGCTGCT 1231
Db	772	CTTTGGCGGGGAGCGCGGAGCGTATCACCATCTTTGGTTCGGGGGAGGGGCTCTCTGCTGCT 831
Qy	1232	CAACTCTTCTGATCTCTCCACCATTCAGAGGGCTGTTCCAGAGGGCATCGCCACAG 1291
Db	832	CAGCTTGTGACCTCTCTCCACCATTCAGAGGGCTGTTCCAGAGGGCATTCATTCAGAG 891
Qy	1292	TGGCACCGCCATTTTCAGCTGTGTCTCACTACAGCGGCTCAAGTACAGCGGCTGCT 1351
Db	892	CGGACCGGCTCTCCAGCTGGGAGTGAACCTTACAGCGCGGCTCAAGTACAGCGGATATT 951
Qy	1352	GGCAGCAAGGTGGGCTGTGACCGAGAGAGAGTCTCAAGCTGTGGAGTCTCTGCGCGC 1411
Db	952	GGCAGCAAGGTGGGCTGTGACCGAGAGAGAGTCTCAAGCTGTGGAGTCTCTGCGCGC 1011
Qy	1412	GAAGCCCTTCCCGGAGCTGTGGACAGAGAGTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGT 1471
Db	1012	CAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCCGGCGCCCTTACCATAGCCTT 1071
Qy	1472	TGGGCGCGTGTGGATGGGAGCTGCTCCGATGACCTGAGATCTCTCATGACGAGGG 1531
Db	1072	CGGCGCGTGTGGATGGGAGCTGCTCCGATGACCTGAGATCTCTCATGACGAGGG 1131
Qy	1532	AGATTTCTCAACTACGATGCTCATCGGCTCAACCGAGGAGAGGGCTCTCAAGTTCGT 1591
Db	1132	CGAGTTCTCTCAACTACGATGCTCATCGGCTCAACCGAGGAGAGGGCTCTCAAGTTCGT 1191
Qy	1592	GGAGGACTCTGAGAGAGCGGAGCGTGTGCTGCCAGCGCTTTTGTGCTTCACTTGTCTC 1651

QY	2702	GGCGCTGTGCTGGCCGGCCGACATACACCTGGCCCTGGCCGGGACCGGACGATGTGCC	2706
DB	2305	GAGGCTCACCTGGCCGGCCAGACTACACCTCTACGCTGGCCGGGTGCCGAGATGACATCCC	2364
QY	2762	TCCTTTGGCCCCGGGGGCCCCCTGACCCCTGTCTGCCAGTGGCCTG	2804
DB	2365	ACTTATGACGCCAAACACCATCACCATGATTCAAACACACTG	2407

RESULT 11

US-09-978-189-374

Sequence 374, Application US/09978189

Publication No. US20030004102A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrarara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

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APPLICANT: Gerber, Hanspeter

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APPLICANT: Pan, James;

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APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630PLC7

CURRENT APPLICATION NUMBER: US/09/978,189

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918595

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

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;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
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;; PRIOR APPLICATION NUMBER: 60/083545
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;; PRIOR APPLICATION NUMBER: 60/084637
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;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 19.5%; Score 912.2; DB 11; Length 3113;
Best Local Similarity 64.7%; Pred. No. 1.4e-213;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

Qy

527 CGCGGAGGAGCGCTCCCGGTGACACACGCGCTACGCGGAGTGCGGCTGTCGCGC 586

Db 112 CAGCAAGCAGATCCAGTTGTCAACACAAATTAATGGCAAAATCCGGGGCTTAAGAAC 171
 Qy 587 CGAGCTCAACACAGAGATCTGGGCCCCGTCGTCAGTTCTTGGGCGTCCCTACGCCAC 646
 Db 172 ACCGTTACCCAAATAGATCTGGGTCAGTGAGCAGTACTTAGGGGTCCCTATGCTC 231
 Qy 647 GCCGCCCTGGGGCCCCGCTTCAGCGCTGAGCGCCGCTGTCGTCGCGGGGT 706
 Db 232 ACCCCCACTGGAGAGAGGGGTTTCAGCCCCAGAACCCCGTCTCTCTGACTGGCAT 291
 Qy 707 GCGCAAGCCACACACCTCGCGGCCGCTGCGCGAGAACCTGCAAG---GGGCGCTGCC 763
 Db 292 CGAAATACTACTAGTTTCTGCTGTGTGTCGCCCCAGCACCTGGATGAGAGATCTTACT 351
 Qy 764 CGCCATCTGCTGCTGTGCTGCTGTCACACACTTGGAGGGCGCGCACCTACGTGCA 823
 Db 352 GCATGACATGCTGCCCATCTGTTTACCGCCAAATTTGGATCTTTGATGACTATGTTCA 411
 Qy 824 GAACGAGCGAGGACTGCTCTGTAACCTCAACCTCTACGTGCCCCACCGAGGACGCTCCGCT 883
 Db 412 AGATCAAAATGAAGACTGCTCTTACTTAAACATCTACGTGCCACCGAAGATGGAGCAA 471
 Qy 884 CACAAAAAAGCTGACGAGGGG-----ACGCTCAATCGCGCAGACACAGATATCCG 934
 Db 472 CACAAAGAAAACGAGATGATATAACGAGTAAATGACCGTGTGAAGACGAAGATATTCA 531
 Qy 935 TGACCTCG---GGAAAGACCTGTGATGCTGTTTCTCCATGCGGCTCCTACATGGAGGG 991
 Db 532 TGATCAGAACATAAGAGCCGTCATGCTATATCCATGGGGATCTTACATGGAGGG 591
 Qy 992 GACCGGAACATGTTGATGGCTAGTCTGCTGCTGCTATGGCAACGTCATGTAGCOAC 1051
 Db 592 CACCGGCAACATGATGACGAGCAATTTTGGCAAGCTACGGAACGTCATCGTATCAC 651
 Qy 1052 GCTCAACTACCGTCTGGGGTGTCTCGGTTTCTCAGCACCGGGACCGAGGTCGAAAGG 1111
 Db 652 CATTAATACCGTCTGGGAATACAGGCTTTTAAGTACCGGTGACCGAGCAGCAAAAGG 711
 Qy 1112 CAACTATGGGCTCTGGACAGATCCAGGCTGCGCTGAGTCAAGTGAAGAACATCGCCCA 1171
 Db 712 CAACTATGGGCTCTGGATCAGATTCAGACATCGGTGATTCAGGAGATGTGGAGC 771
 Qy 1172 CTTTGGGGCGACCCGAGCGCTATCACCATCTTTGGTTTCGGGGCAGGGCTCTCGCT 1231
 Db 772 CTTTGGGGGACCCCAAGAGTACCATCTTTGGCTCGGGGCTGGGGCTCTCTGT 831
 Qy 1232 CAACTCTCTGATCTCTCCACCAATCAGAGGCTGTTCAGAGGCTGTTCAGAGGCTATCGCCAG 1291
 Db 832 CAGCTGTGTGACCTGTCCCACTACTCAGAGGCTCTTCCAGAGGCTCTTCCAGAGGCTATTCAGAG 891
 Qy 1292 TGGCACCGCCATTTCCAGCTGCTGTCACTACCGCGCTCAAGTACAGCGGCTGCT 1351
 Db 892 CGGCACCGCTCTCCAGCTGGGAGTGAATACAGCGCGCCCAAGTACACTCGGATATT 951
 Qy 1352 GGCAGCCAAAGTGGGCTGTGACCGAGGAGCAGTGTCTGAAGCTGTGGAGTGTCTGCGCCG 1411
 Db 952 GGCAGCAAGTGGGCTGCAACATGCTGGACACCAACGCAATGTTAGATGCTCTGGGA 1011
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 Qy 1472 TGGGCCGCTGTGTGATGGCAGCTGTGTCGCGATGACCTTGAGATCTCATGACAGAGG 1531
 Db 1072 CGGGCCGCTGATCGACGGGAGCTCATCCAGACGACCCCGATCTGTATGAGCAAGG 1131
 Qy 1532 AGAATTCCTCACTACAGCATGCTATCGGCTCAACCGAGGAGGCGCTCAAGTTCTG 1591
 Db 1132 CGAGTTCTCACTACAGCATGCTATGCTGGGCTCAACCAAGGGGAAAGGCTGAAGTTCTG 1191
 Qy 1592 GGAGGACTCTGACAGAGCGAGGAGCTGTGCTGCGAGCGCTTTGACTTCACTGCTC 1651
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Qy 1652 CAATTTGTGCAACCTGTATGCTACCCGAGGCAAGGATGTGCTTTCGGAGACCAT 1711
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 Qy 1712 CAATTTATGTACAGACTGGGCGGACCGGCAATATGGGAAATGCGCGCAAAACCTT 1771
 Db 1312 CAATTTATGTACAGACTGGGCGGATAGGAAACCCCGAGACGCGGCGGAAACCTT 1371
 Qy 1772 GCTGGCGCTCTTTACTGACCAATGGGTGGCAGAGTGTGCGCACTGCGCAAGTGA 1831
 Db 1372 GGTGGCTCTTTACTGACCAACGAGTGGGTGGGCCCCCGCGCTGGCC---GCCACCTGA 1428
 Qy 1832 CGCGCACTACAGTCTCCGCTTACTTTTACACTTCTACCACTTACCACTGCGCAGCGGAGG 1891
 Db 1429 CGCGCACTACAGTCTCCGCTTACTTTATGCTTCTATCATCTGCGCAAGCGAAAT 1488
 Qy 1892 CGCGCTGAGTGGGAGATGCGGCGACGGGAGTGAATGCCCCATATGCTTTGGCGTGC 1951
 Db 1489 GAAGCCAGTGGGAGATTCGSCCATGATGAGGTCCCTATGCTTTCGCGATCCC 1548
 Qy 1952 CATGGTGGTGGCCAGCTCTTCCCTGTAACTTCTCCAAAGATGAGTCTATGCTCAG 2011
 Db 1549 CATGATCGGTCCCAACGAGCTCTTCACTTGAATTTTCCAAAGACGAGTCACTCAG 1508
 Qy 2012 TGCCTGCTCATGACCTACTGACCAACTTGGCAAGACTGGGAGCCCAACAGCGGT 2071
 Db 1609 CGCGTGGTCACTGACTGAGCAACTTCGCAAACTGGTGAATCCAATCAACAGT 1668
 Qy 2072 GCGCAGGATACCAAGTTTCACTCACCAAGCGCAATCGTTTCGAGGAGTGTGTGGAG 2131
 Db 1669 TCCTCAGGATACCAAGTTTCACTCACCAAAACCAACCGCTTGAAGAGTGGCTGTGTC 1728
 Qy 2132 CAAATTCACAGGAGGAGAGAGTATCTGCATAGAGCTGAAAGCCAGCGTGGTGA 2191
 Db 1729 CAAATTAATTCCAAGACCAAGCTCTATCTGATATTTGGCTTGAACCCAGAGTGAAGA 1788
 Qy 2192 CAACTACCGCGCAACCAAGTGGCTTCTGGCTGAGCTCGTGGCCCACTGCAACCT 2251
 Db 1789 TCATACCGGGCAACGAAAGTGGCTTCTGGTTGAATCTGTTCTCTATTTGCAACTT 1848
 Qy 2252 GCA-----CAGGAGCTTTCACCAACAGCGCGCTCTCTCTAGCCACGCG 2302
 Db 1849 GAACGAGATATTCCAGTATGTTTCAACCAACCAAAAGGTTCTCCACAGACATGACATC 1908
 Qy 2303 CTGGCGCTCTCTCCCGCTGGCGCCCGGCGCACACCGCGCCCGCGCTGCGAC 2362
 Db 1909 ATTTCCCTATGCAACCGCGATCTCCCGCAAGATATGGCCCAACCAACGCGCCAGC 1968
 Qy 2363 CTGCTCTCCGAGCCCGAGCCCGAGC-----CGGCCCCAAGGCG 2401
 Db 1969 AATCACTCTGCCAAATTCCAAACTCTAAGGACCTCAAAACAGGGCTTGAGGA 2028
 Qy 2402 CTATGACCGCTTCCCGGGGACTCAGGAGTACTTCCAGAGCTGAGCTCAGCTGGC 2461
 Db 2029 CAAACTGTCTCTATTGAACCAACAGAGATTTATCCACCGAATTAAGTGTCACTATGC 2088
 Qy 2462 CGTGGTGCCTCTCTCTCTCAACATCTGCGCTTTTCTGCTGCTCTACTTACAAGCG 2521
 Db 2089 CGTGGGCGCTGCTCTCTCTCTCAACATCTTAGCTTTTTCGGGGCTGTACTACAAA 2148
 Qy 2522 GACCGGGCAGAGCTGCGGTGAGGCGCTTAGCCCACTGCGGCTCAGGCTCTGG 2581
 Db 2149 GCAAGAGGGCGCATGAGACTCAAGGCGCCAGTCCCGAGAGAAACCAACAAATGA 2208
 Qy 2582 CGTGCCTGGTGGGGCGCCCTGCTCCCGCGCGCGGCGCTGAGCTGCGCACAGAGGAGGA 2641
 Db 2209 TATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGAGATGAAGAGCTGGACAGGA 2268
 Qy 2642 GCTGGTGTACTGAGCTGAAGCGGGGTGGTGGGCTCGGGCGGAGCCCTGCGAGGCTCT 2701
 Db 2269 TCACGAGTGTAGTCTGCTGCAG-----GCACACGACACACT 2304

Qy	2702	GC	GCCTTGCCTGC	CGCGCCGAGTAC	CCCTGGCCCTGC	CGCGGACACCGAGCATGTGC	2761
Db	2305	GAGCT	CACCTGCGCGG	CAGTACACCTT	CACCTGCGCGGTGCGCATGACATCCC		2364
Qy	2762	TC	CTTGGCCCCCGG	CGCCCTGACCCCTGCTGCCACAGTGGCTG		2804	
Db	2365	AC	TATGACGCCAAAC	ACCATCACCATGATTC	CAACACACTG		2407

RESULT 12

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US-09-978-608A-374
; Sequence 374, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 374
; LENGTH: 3113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-374

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Query Match 19.5%; Score 912.2; DB 11; Length 3113;
Best Local Similarity 64.7%;
Pred. No. 1.4e-213;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

527	CGCGAGGAGCGCTTCCGGTGTGGAACA	CGGCGTACGGGCGAGTGC	CGCGTGTGCGGC	586
112	CAGCGAAGCAGTATCCAGTTGTCAACA	CAAAATATGGCAAAATCGGGGCC	TAGAAC	171
587	CGAGCTCAACAACAGAGATCTGGCCCCG	TGTGTCAGTTCCTTGGCGGTGCC	TACGCCAC	646
172	ACGCTTACCCATAGAGATCTTGGTCCAG	TGGAGCAGTACTTAGGGTCC	CCCTATGCCTC	231
647	GCGCCTCTGGGCGCCCGCGCTTTCAC	SCGCGCTTGAGCGCCCGCTCTGTGGCC	CGCGGT	706
232	ACCCCCACTGGAGAGGCGGTTTCAG	CCCCCAGAACCCCTCTCTGTGACTGGCAT		291
707	GGCGAACCGCCACCACTGTGCGCGCG	CTGCGCGAGACCTGCACG---	GGCGGTGC	763
292	CCGAAATACTACTCAGTTTCTGCTGTG	TGCCCCGACCTGGATGAGAGATCTCT	TACT	351

1832 CGCGACTACAGTCTCCCGTCTACTTTTACACCTTCTACCACTGCGCGCGGAGG 1891
 1429 CGCGAGTACGCTCCCGACCTACTTCTATGCTTCTATCATCTGCGCAAGGAAT 1488
 1892 CGGCTGAGTGGGAGATGCGGCGACGCGGATGAACCTGCTTGTGCGTGC 1951
 1489 GAAGCCAGCTGGGAGATTCGGCCCATGGTATGAGTCCCTATGCTTCGGCATCC 1548
 1952 CATGTGGGTGCGCACCGACTCTTCCCTGTAACTTCCAGATGAGTCACTGCTCAG 2011
 1549 CATGATCGTCCCGAGCTCTTCTGTTGTAATTTCCAGAACGAGCTGCTCAG 1608
 2012 TGGGTGCTGATGACTTCTGACCACTTCCCAAGACTGGGACCCCAACCGCGGT 2071
 1609 CGCGGTGCTCATGACTTCTGACCACTTCCCAAGACTGGGACCCCAACCGGT 1668
 2072 GCGCAGGATACCAAGTCTATCCACCAAGCCCAATGCTTGGAGGAGTGGTGAG 2131
 1669 TCTCAGGATACCAAGTCTATCCACCAAGCCCAATGCTTGGAGGAGTGGTGAG 1728
 2132 CAAATTCACAGCAAGGAGAGAGTATCTGCATAGGCTGAAAGCCAGCGCTGCTGA 2191
 1729 CAAATTCACAGCAAGGAGAGTATCTGCATAGGCTGAAAGCCAGCGCTGCTGA 1788
 2192 CAATACCGCGCCACAGAGTGGCTTCTGCTGAGTCTGTCGCTGCTGCTGCTGCT 2251
 1789 TCACTACCGCGCCACAGAGTGGCTTCTGCTGAGTCTGTCGCTGCTGCTGCTGCT 1848
 2252 GCA-----CAGGAGCTTCAACCAAGGAGAGTATCTGCATAGGCTGAAAGCCAGCGCTGCTGA 2302
 1849 GAAAGAGATATTCAGTATGTTTCAACCAAGGAGTATCTGCATAGGCTGAAAGCCAGCGCTGCTGA 1908
 2303 CTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2362
 1909 ATTTCCTATGACACCGCGGATCTCCCGCAAGATATGCGCAACCAACCGCGGAGC 1968
 2363 CTGCTCTCCGAGCGCGGAGCGGAGC-----CGGCGCGAGCGG 2401
 1969 AATCACTCTGCGCAACATCCCAACTCTAAGGACCTTCAAAAACAGGCGCTGAGGA 2028
 2402 CTATGACCGCTTCCCGGGAATCAAGGAGTCTTCAAGGAGTCTGAGCGCTGAGCGGCTGAG 2461
 2029 CACAATCTCTCTTCAATGAAACCAAGAGATTAATTCAGCGAATTAAGTGTCACTTGC 2088
 2462 CGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2521
 2089 CGTGGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2148
 2522 GGAACCGCGGAGGAGTCTGCGGTGAGCGGCTTACGCGGCTTACGCGGCTTACGCGGCTTACG 2581
 2149 GGAACAGAGGCGCATGAGACTACAGGCGCGGCTTACGCGGCTTACGCGGCTTACGCGGCTTACG 2208
 2582 CGTGGCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2641
 2209 TATCGCTCATATCAGAACGAGAGATCATGCTCTGCTGAGATGAGCGAGTGAACACGA 2268
 2642 GCTGGTGTCACTGAGTGAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2701
 2269 TCAGAGTGTGAGTCTGAG-----GCACACACACACT 2304
 2702 CGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2761
 2305 GAGGCTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2364
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 2365 ACTTATGACCGCAACACCATCATCATGATTCACCAACACACTG 2407

RESULT 13

US-09-978-585A-374
 ; Sequence 374, Application US/0978585A
 ; Publication No. US20030049633A1

GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deanoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Giddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Wickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C15
 ; CURRENT APPLICATION NUMBER: US/09/978,585A
 ; CURRENT FILING DATE: 2001-10-16
 ; NUMBER OF SEQ ID NOS: 624
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 374
 ; LENGTH: 3113
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-978-585A-374

Query Match 19.5%; Score 912.2; DB 11; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 1.4e-213;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;
 QY 527 CGCGCAGAGAGCGCTTCCCGTGGTGAACACGCGCTACGCGGAGTGGCGGTGGCGG 586
 Db 112 CAGCCAGCAGAGTATCCAGTTGTCAACAATATGCGCAATTCGGGCGCTAAGAAC 171
 QY 587 CGAGCTCAACACAGAGATCTTGGGCGGCGTCTGTCAGTCTTGGGCGTGGCGTACGCCAC 646
 Db 172 ACCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTATGCTC 231
 QY 647 GCGGCGGCTGGGCGGCGGCGGCTTCCAGCGGCTGAGGCGGCGGCGGCGGCGGCGG 706
 Db 232 ACCCGGCGGCTGGAGAGCGGCTTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 291
 QY 707 GCGCAACCGCACCCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 763
 Db 292 CGCAATATCTACTCAGTTTGTGCTGTGTCGCCCGCCAGCACTGTGATGAGAGATCTTACT 351
 QY 764 GCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 823
 Db 352 CGATGACATGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
 QY 824 GAAACAGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883
 Db 412 AGATCAATATGAGACTGCTTACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 471
 QY 884 CACAAAAAAGCTGACGAGCG-----ACGCTCAATCCCGCCAGACAGATATCCG 934
 Db 472 CACAAAGAAAAACGAGATGATATACGAGTAATGACCGGTGGTGAAGACGAGATATTC 531

QY 935 TGACCCCTG---GGAAGAGCCTGTGATGCTGTTCTCCATGCGGCTCCTCATGAGGG 991
DB 532 TGATCAGAAACAGTAAGAGCCCGCTCATGGTCTATATCCATGGGGATCTTATGAGGG 591
QY 992 GACCGGAAACATGTTGGATGGCTCAGTCTGCTGCTATGCAAGCTCATTGTAGCCAC 1051
DB 592 CACCGGAAACATGATTGACGGGAGCATTTTGGCAAGCTACGGAAACGTCATCGTATCAC 651
QY 1052 GCTCAACTACCGTCTGGGGTGTCTGGTCTTCTCAGCACCGGGGACAGGCTGCAAAAGG 1111
DB 652 CATTTAACTACCGTCTGGGATATAGGGTTTAAAGTACCGGTGACCGAGGAGGAAAGG 711
QY 1112 CAACATAGGGCTCTGAGACAGATCCAGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 1171
DB 712 CAACATAGGGCTCTGAGATCAGATTCAGGACTGCGGTGGATTTGAGGAGAAATGTTGGAGC 771
QY 1172 CTTTGGGGGCGACCCCGAGCGTATCACCATTCTTTGGTCTCGGGGAGGGGCTCTCTGCT 1231
DB 772 CTTTGGGGGCGACCCCGAGAGAGTGACCATCTTTGGCTCGGGGCTGCGGGCTCTCTGCT 831
QY 1232 CAACCTTCTGATCTCTCCACCATTCAGAGGGCTGTTCCAGAGGCGCATGCCCGAGAG 1291
DB 832 CAGCCTGTTGACCTCTCTCCACTACTCAGAGGCTCTCTTCCAGAGGCGCATCAITCAGAG 891
QY 1292 TGGCACCGCCATTTCCAGCTGCTCTGCTCAACTACAGCGCTCAAGTACAGCGGCTGCT 1351
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QY 1352 GGCAGCCAGGCTGGCTGTCAGCAGAGAGCTGCTGAAAGCTGTTGAGTGTCTGCGCG 1411
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QY 1472 TGGGCGGCTGGTGGAGAGCTGCTGCTCCCGATGACCTGATGCTCATGACAGAGG 1531
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DB 1132 CGAGTTCTCTCACTACGACATCATGCTGGGCTCAACGAGGAGGCTGAGTTGCT 1191
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QY 1772 GCTGGGCTCTTTACTGACCAACCAATGGGCTGACCAAGCTGCTGCTGCTGCTGCTGCTGCT 1831
DB 1372 GCTGGGCTCTTTACTGACCAACCAATGGGCTGACCAAGCTGCTGCTGCTGCTGCTGCTGCT 1428
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DB 1428 CGCGGAGTACGCTCTCCGCTCTACTTTTACACTTCTTACCACTGCTGCTGCTGCTGCTGCT 1488
QY 1892 CGGCGCTGAGTGGGAGAGTGGGCGAGCGGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1951
DB 1489 GAAGCCAGCTGGGCGAGATTCGCGCCATGCTGATGAGGTCCTGCTGCTGCTGCTGCTGCTGCT 1548
QY 1952 CATGGTGGGTCGACCGAGCTCTTCCCTGTAACCTTCTTCCAGAAATGAGCTCATGCTGAG 2011
DB 1549 CATGATCGGTCGACCGAGCTCTTCACTGTAACCTTCTTCCAGAAATGAGCTCATGCTGAG 1608
QY 2012 TGCGGTGCTCATGACTACTGGACCAACTCTGCGCAAGACTGCGGAGACCCCAACGAGCGGT 2071

DB 1609 CGCGTGGTCTGACCTACTGACGAACTTCCGCAAACTGGTATCCAAATCAACCACT 1668
QY 2072 GCGCAGGATACCAAGTTTCACTCCACCAAGCCCAATCGCTTGGAGAGGTTGGTGGAG 2131
DB 1669 TCTCAGGATACCAAGTTTCACTCCACCAAAACCCCAACCGCTTGAAGAGTGGCTGGTC 1728
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DB 1729 CAAATTCACACAGCAGAGGAGCAGTATCTGCATATGCTGCTGCTGCTGCTGCTGCTGCTG 1788
QY 2192 CAAATTCACACAGCAGAGGAGCAGTATCTGCATATGCTGCTGCTGCTGCTGCTGCTGCTG 2251
DB 1789 TCACTACCGGGCAACGAAAGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1848
QY 2252 GCA-----CACGAGCTCTTCCACCAACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2302
DB 1849 GAACGAGATATTCCAGTATGTTTCAACCAACCAAGGTTCTCCACCAAGATGACATC 1908
QY 2303 CTGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2362
DB 1909 ATTTCCTATGACACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1968
QY 2363 CTTGCTCTCCGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2401
DB 1969 AATCACTCTCTGCGCAACATCCCAACACTCTTAAGGACCTCACAACAGGCTGAGGA 2028
QY 2402 CTATGACCGCTTCCCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2461
DB 2029 CACAACTGCTCTCATGTAACCAACCAAGATTTATTCACCGAATTAAGTGTACCAATGCT 2088
QY 2462 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2521
DB 2089 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2148
QY 2522 GZAGGAGCTCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2581
DB 2149 GZAGGAGAGCTCTGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2208
QY 2582 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2641
DB 2209 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2268
QY 2642 GCTG 2701
DB 2269 TACGAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2304
QY 2702 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2761
DB 2305 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2364
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DB 2365 ACTTATGAGCGCAACACCATCACCATTGATTCACCAACACACTG 2407

RESULT 14

US-09-978-191A-374
; Sequence 374, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferraro, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A.
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05

Query Match	19.5%	Score 912.2	DB 11	Length 3113
Best Local Similarity	64.7%	Prod. No. 1.4e-213		
Matches 1503	Conservative 0	Mismatches 748	Indels 72	Gaps 7
QY	527	CGGGAGAGCGCTTCCCGGTGGTGAACAGGCCCTACGGCGCATGCGCGGTGTGCGCGC	586	
Db	112	CAGCCAGCACAGTATCAGTTGTCACACAAATTTGGCAAAATCCGGGGCCCTAAGAAC	171	
QY	587	CGAGCTCAACAAACGAGATCTCTGGCCCGCTGCTGTCAGTTCTTGGCGCGTGCCTTACGCCAC	646	
Db	172	ACGGTTACCCAATGAGATCTTGGTGTCAGTGGAGCAGTACTTATGGGGTCCCTATGCTC	231	
QY	647	CGCGCCCTCGGGCGCCGCGCTTCCAGCGCCCTGAGCGGCCCGCTCTGTGGCCCGCGGT	706	
Db	232	ACCCCCACTGGAGAGAGGGCGTTTCAGCCCCAGAAACCCCGCTCTCTGGAGATGGCAT	291	
QY	707	GGCGAAGCCACCAACCTGCGCCCGCTCCGCGAGAACCTGCACG--GGGCGCTGCC	763	
Db	292	CCGAAATACTACTCAGTTTGTGTCGTGTGCCCCAGCACCTGATGAGAGATCCTTACT	351	
QY	764	CGCCATCATCTCGCTGTGTGTTTCAACGACAACTTGGAGCGGCCCGCCACCTACGTGCA	823	
Db	352	GCATGACATGCTGCCATCTGGTTTACCGGCAATTTGGATACTTGTATGACCTATGTTCA	411	
QY	824	GAACGAGCGAGGACTGCTGTACCTCAACCTCTAGTCCCAACCGAGACCGTCCGCT	883	
Db	412	AGATCAAAATGAAGACTGCCCTTTACTTAAACATCTACGTGCCCAACGAAAGTGAACCA	471	
QY	884	CACAAAAAACGTGACGAGCGG-----ACGCTCAATCCGCCAGACAGATATCCG	934	
Db	472	CACAAAGAAAACGAGATGATATACGAGTAATACCGGTGGTGAAGACGAAGATATCA	531	
QY	935	TGACCCCTG--GGAAGAAGCCTGTGATGCTGTTTCTCCATGGCGGCTCTACATGAGGG	991	

Db	532	TCATCAGAACAGTAGAAGCCCGTCATGGTCTATATCCATGGGGAGTCTTACATGGAGGG	591
Qy	992	GACCGGAACATGTTTCGATGGCTCAGTCCCTGGCTGCTATGGCAACGTCATTTGAGCCAC	1051
Db	592	CACCGCAACATGATTGACGGCAGCATTTTGGCAAGCTACGGAAA	651
Qy	1052	GCTCAACTACCGTCTTGGGTGCTCGGTCTTTCTAGCACCGGGGA	1111
Db	652	CATTAACTACCGTCTGGGAATCTAGGGTTTTAAGTACCGGTGAC	711
Qy	1112	CAACTATGGGCTCTCGACACAGATCCAGGCGCTCGCTGCTCAGTCAAAACATCGCCA	1171
Db	712	CAACTATGGGCTCTCGATCAGATTCAAGCACTGCGGTGATTTAGAGAAATGTGGAGC	771
Qy	1172	CTTTGGGGGCGACCCCGAGCGTATCAACTCTTTTGGTTCGGGGCAGGGGCTCTCTCGCT	1231
Db	772	CTTTGGGGGGGACCCCAAGAGATGACCATCTTTGGCTCGGGGCTGGGCGCTCTCTGT	831
Qy	1232	CAACCTTCTGATCTCTCCCAACCATTTCAAGAGGGCTGTTCCAGAAAGCCATGCCCAGAG	1291
Db	832	CAGCTCTTTGACCTGTCCCACTACTCAAGAGTCTCTTCCAGAAAGCCATATTCAAG	891
Qy	1292	TGGCACCGCCATTTCCAGCTGGTCTGTCAACTACCAAGCGCTCAAGTACACGGGCTGT	1351
Db	892	CGGCACCGCCCTGTCCAGCTGGGCACTGAACCTACCAAGCGGCCAAGTACACTCGGATTT	951
Qy	1352	GGCAGCCAAAGGTGGGCTGTGACCGAAGACAGTGTGAAGTGTGAGTGTCTGGCGG	1411
Db	952	GGCAGAAAGGTGGGTGTGCAACTGTGACACCAAGTGTGAGTGTGAGTGTCTGGAA	1011
Qy	1412	GAAGCCCTCCCGGAGCTGGTGACACGAGCGTGCAGCTGCCGCTACCAATCGCCTT	1471
Db	1012	CAAGAACTACAAGAGCTCATCCAGCAGACCATCACCCCGGCCACTTCCATAGACCTT	1071
Qy	1472	TGGGCCGTGGTGATGGCGACGTGGTCCCGATGACCTGAGATCTCTATGACAGAGG	1531
Db	1072	CGGGCCCGTGTATCGACGGGAGCGTTCATCCAGACGACCCCAAGTCTGTATGGAGCAAG	1131
Qy	1532	AGAAATTCCTCAACTAGCAGTCTCATCGCGCTCAACAGGAGAGGGCTCAAGTCTGT	1591
Db	1132	CGAGTTCTTCACTACGACATCATGCTGGGCGTCAACGAGGGAGGCTCTGAATCTGT	1191
Qy	1592	GGAGGACTGTGACAGAGCGAGGACGGTGTCTCCAGCGCTTTGACTTCACCTGTCTC	1651
Db	1192	GGACGCGCATCGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCGCTGC	1251
Qy	1652	CAACTTTGTGGACACCTGTATGGCTACCCGGAAGCGAAGTGTGCTTCGGGAGACCAT	1711
Db	1252	CAACTTCGTGGACACCTTTACGGTACCCCTGAAGGGAAAGACATTTTCGGGAGACTAT	1311
Qy	1712	CAAGTTTATGTACAGACTGGGGCGACCGGGAACAATGGCGAAATGCGCCGCCAAAACCTT	1771
Db	1312	CAAGTTTCATGTACAGACTGGCGCGATAAGGAAAACCCGAGAGCGCGCGGAAAACCTT	1371
Qy	1772	GCTGGCGCTTTTACTGACCAATAGGTTGGCACCAAGCTGTGGGCACTGCCAAGCTGCA	1831
Db	1372	GGTGGCTCTCTTTACTGACCAACCAAGTGGGTGGCGCCCGCCCGTGGCC--GCCGACCTGCA	1438
Qy	1832	CGCGACTACCACTCTCCGCTCTACTTTTACACTTCTTACCACCACTGCCAGCGGAGGG	1891
Db	1429	CGGCGAGTACGGCTCCCCCACTACTTCTATGCTTATCATCTACCTGCCAAGCGAAT	1488
Qy	1892	CGGCGCTGATGGGAGATGGCGGCAACGGGATGAATGCGCCCTATGCTTTGGCGTGCC	1951
Db	1489	GAAGCCCAAGCTGGGAGATTCGGGCCATGGTGTATGAGTCCCTATGCTTCGGCATCCC	1548
Qy	1952	CATGTTGGGTGCAACCGACCTCTTCCCTGTGAATTTCTCCAGATGACGTCATGCTCAG	2011
Db	1549	CATGATCGGTCCACCCGAGCTCTTACGTTGTAACTTTTCAAGAAACGACGTCATGCTCAG	1608
Qy	2012	TGCCGTGTGATGACCTACTGGACCAACTTGGCCAGACTGGGACCGCCCAACCAAGCCGGT	2071

Db 1609 CGCGTGGTCTATGACCTACTGGACGAACTTCGCAAAACTGGTGATCCAAATCAACCACT 1668
QY 2072 GCGCAGGATACCAAGTTCATCCACCAAGCCCAATCGCTTCGAGGAGGTGGTGGAG 2131
Db 1669 TCCTCAGGATACCAAGTTCATCCACCAAAACCCACCGCTTTGAAGAAGTGGCGTGGC 1728
QY 2132 CAAATTCACAGAGGAGAGACGATATCTGCATAGGCTTGAAGCCACGCGTGGTGA 2191
Db 1729 CAAGTATAATCCCAAGACGAGCTATCTGCATATTTGGCTTGAACCCACAGGTGAGAGA 1788
QY 2192 CAACTACCGCGCAACAAGGTGGCTTCCTGGGTGGAGTCTGGTCCACCTGCACAACT 2251
Db 1789 TCCTACCGGGCAACGAAGTGGCTTCCTGGGTGGAGTCTGGTCCATTTGGCAACTT 1848
QY 2252 GCA-----CACGGAGCTTTCACCAACCAACGCGCTGCTCCCTACGCGCAGCG 2302
Db 1849 GAACGAGATATTCAGTATGTTTCAACAACCAACCAAGGTTCTCCACGAGATGACATC 1908
QY 2303 CTGGCGGCTCTGCTCCCGCTGGCGCGCCCGGGGACACGCGGCGCCCGCGCTGGCAC 2362
Db 1909 ATTTCCTATGACACCGCGGATCTCCCGGCCAAGATATGGCCAAACCAACGCGCCAGC 1968
QY 2363 CTGCTCTCCGAGCGCGCGCGAGC-----CCGCGCCCAAGGCG 2401
Db 1969 ATCACTCTCTGCAACAATCCCAACACTCTAAGGACCTCACAACAGGCGCTGAGGA 2028
QY 2402 CTATGACGCTTCCCGGGGACTCAGGAGTACTTCACGAGGTGAGCGTCACTGGC 2461
Db 2029 CACAATCTCTCTCAATTGAACCAACAGAGATTTCCACCGAATTAAGTGTCACTTGC 2088
QY 2462 CTGGGTGCTCTCTCTCTCTCTCAACATCTGCGCTTCTGCTGCTCTCTCTCTCTCTCT 2521
Db 2089 CTGCGGGCGTCT 2148
QY 2522 GACCGCGGCGAGGAGTGGCGGTGAGCGGCTTAGCCCACTTGGCGGCTCAGGCTCTGG 2581
Db 2149 GGACAAGAGCGCCATGAGACTCAAGCGCGCCAGTCCCGAGAGAAACCAACCAATGA 2208
QY 2582 CTGCTCTGGTGGGCGCCCTCTGCTCCCGCGCGCGCGTGGTGGTGGTGGTGGTGGTGG 2641
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Db 2305 GAGGTCTACCTGCG 2364
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Db 2365 ACTTATGAGCGCAACACCATCATCATGATTCGAACACACTG 2407

RESULT 15

US-09-978-403A-374
; Sequence 374, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 19.5%; Score 912.2; DB 11; Length 3113;
 Best Local Similarity 64.7%; Pred. No. 1.4e-213;
 Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;

QY	527	CGCGGAGGAGCGCTTCCCGGTGTAACACAGCGCTTACGGCGGAGTGGCGGTGTGGCGG	586
DB	112	CAGCCAGCACAGTATCCAGTTGTCAACAAATATGCAAAATCCGGGGCTTAAGAAC	171
QY	587	CGAGCTCAACACAGATCTCGGCCCGCTCGTGAGTTCTTTGGCGTGCCCTACGCCAC	646
DB	172	ACCGTTACCCAATGAGATCTTGGTCCAGTGGAGCAGTACTTAGGGTCCCTATGCCCTC	231
QY	647	GGCGCCCTGGGGCGCGCTTCCAGCGCTTACGGCGGCGGCTGTGGCCCGGGCT	706
DB	232	ACCCCGCTGGAGAGAGCGGTTCAGCCCCAGAACCCCGCTCTCTGAGATGGCAT	291
QY	707	GGCAACGCCACACCTCGCGCCCTGCGCCGAGAACCTTGACG--GGCGCTGCC	763
DB	292	CGAAATACTACTCAGTTTGTGTGTGCCCCAGCACCTGGATGAGATCCTTACT	351
QY	764	CGCCATCATGCTGCTGTGTGTTACCGACAACTTGAGGGCGGCCCACTACGTGCA	823
DB	352	GCATGACATGTGCCCATCTGGTTTACCGCCAAATTTGGATATCTTTGATGACCTATGTTCA	411
QY	824	GAACGAGAGCGAGGACTGCTGTACTCAACTCTACGTGCCACCGAGGAGCGGTCCGCT	883
DB	412	AGATCAAAATGAAGACTGCTTTACTTTAAACATCTACGTGCCACCGAAGATGAGCCAA	471
QY	884	CACAAAAAAGTGCAGAGGGG-----ACGCTCAATCCGCCAGACACAGATATCCG	934
DB	472	CACAAAGAAAAACCGAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGATATCA	531
QY	935	TGACCCCTG---GGAAGAGCGCTGTGATGCTGTTCTCCATGGCGGCTCTACATGGAGG	991

Db 532 TGATCAGAACAGTAGAAGCCGTCATGGTCTATATCCATGGGGATCTTACATGGAGGG 591
Qy 992 GACCGAAACATGTTGATGCTCAGTCTCGTGGCTCTATGGCAACGTCATTTAGCCAC 1051
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Db 712 CAACTATGGGCTCTGGATCAGATTAAGCACTCGGCTGATTCAGGAGATGTGGGAGC 771
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Qy 2762 TCTCTTGGCCCGCGGGGCGCTGACCTGCTGCCAGTGGGCTG 2804
Db 2365 ACTTATGACGCGCAACACCATCAGCATGATTCCAAACACACTG 2407

Search completed: February 19, 2004, 11:54:03

Job time : 1528.21 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 17:13:07 ; Search time 9101.14 Seconds
(without alignment)
12463.166 Million cell updates/sec

Title: US-09-934-323-1

Perfect score: 4667

Sequence: 1 ggcacaggaacttggtctt.....ttgccttgactgccttc 4667

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*

2: em_esthm:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrt:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91.8	21.3	3853	11 AK039018	AK039018 Mus musculus
2	78.8	16.9	1058	12 BM800364	BM800364 AGENCOURT
3	781.2	16.7	945	12 BI861707	BI861707 60338389
4	756.4	16.2	887	13 BQ437258	BQ437258 AGENCOURT

5	741.2	15.9	1884	11 BC028738	Homo sapi
6	733.6	15.7	1157	12 BM477185	BM477185 AGENCOURT
7	699.8	15.0	790	14 CA324321	CA324321 UI-M-FYO
8	682.8	14.6	981	13 BU542698	BU542698 AGENCOURT
9	676.6	14.5	942	13 BU173291	BU173291 AGENCOURT
10	674.6	14.5	919	13 BQ891968	BQ891968 AGENCOURT
11	667.6	14.3	766	14 CA749282	CA749282 UI-M-FYO
12	667.2	14.3	735	10 BF058856	BF058856 7k3e09-X
13	665.8	14.3	1073	10 BF529926	BF529926 602042317
14	661.8	14.2	879	13 BQ947939	BQ947939 AGENCOURT
15	656.4	14.1	708	14 CD349431	CD349431 UI-M-FYO
16	652.6	14.0	799	13 BQ769293	BQ769293 UI-M-FYO
17	645.8	13.8	755	14 CD348520	CD348520 UI-M-FYO
18	643.4	13.8	1155	13 BQ278029	BQ278029 AGENCOURT
19	638.2	13.7	727	12 BI915486	BI915486 603177425
20	636.8	13.6	784	14 CB526398	CB526398 UI-M-FYO
21	636.6	13.6	807	14 CD348683	CD348683 UI-M-FYO
22	635.2	13.6	719	13 BQ180305	BQ180305 UI-M-FYO
23	631.2	13.5	1133	12 BM467133	BM467133 AGENCOURT
24	629.4	13.5	729	13 BQ771190	BQ771190 UI-M-FYO
25	628.4	13.5	796	14 CA316129	CA316129 UI-M-FWO
26	628.2	13.5	660	12 BI046856	BI046856 MR3-FN020
27	626.2	13.4	1066	13 BQ920779	BQ920779 AGENCOURT
28	621.2	13.3	804	14 CD355788	CD355788 UI-M-FYO
29	620.8	13.3	910	13 BU931333	BU931333 AGENCOURT
30	619.2	13.3	873	12 BG920355	BG920355 602825882
31	618.2	13.2	770	12 BM944282	BM944282 UI-M-EHOP
32	617.6	13.2	741	14 CA328689	CA328689 UI-M-FYO
33	614	13.2	715	13 BQ180670	BQ180670 UI-M-FYO
34	613.4	13.1	780	14 CA316667	CA316667 UI-M-FWO
35	609.6	13.1	881	12 BI766799	BI766799 603056710
36	606.4	13.0	989	13 BU501135	BU501135 AGENCOURT
37	606.2	13.0	692	10 BR952199	BR952199 UI-M-CDO
38	603.8	12.9	994	10 BG026604	BG026604 602293726
39	602.8	12.9	727	14 CB526164	CB526164 UI-M-FYO
40	597.8	12.8	602	12 BM700081	BM700081 UI-E-DW1
41	597.8	12.8	689	13 BU708515	BU708515 UI-M-FYO
42	585.2	12.5	736	14 CB249514	CB249514 UI-M-FYO
43	573.6	12.3	679	14 CB248107	CB248107 UI-M-FYO
44	573.2	12.3	733	14 CA318458	CA318458 UI-M-FWO
45	567.2	12.2	714	12 BM963021	BM963021 UI-M-EQO

ALIGNMENTS

RESULT 1	AK039018	3853 bp	mRNA	linear	HTC 05-DEC-2002
LOCUS	AK039018	Mus musculus adult male hypothalamus cDNA, RIKEN full-length			
DEFINITION	AK039018	enriched library, clone: A230085M13 product: NEUROLIGIN 3 ISOFORM			
ACCESSION	AK039018	HNL3 homolog [Homo sapiens], full insert sequence.			
VERSION	AK039018.1	GI:26332978			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				

QY 902 ----GGCGAGCCTCAATCGGCCAGACACAGATATCCGTGACCCCTGGGAAAGACCTGTGA 957
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 VERSION
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 EST.
 SOURCE
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 ORGANISM
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 1058)

AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence stop: 649.

FEATURES
source

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Query Match 16.9%; Score 789.8; DB 12; Length 1058;
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Matches 855; Conservative 0; Mismatches 33; Indels 6; Gaps 4;
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LOCUS

DEFINITION 603389389F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5398199 5', mRNA sequence.
ACCESSION BI861707
VERSION BI861707.1 GI:16002454
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 945)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTP/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12015 row: b column: 24
High quality sequence stop: 753.

FEATURES
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BASE COUNT 189 a 268 c 311 g 175 t 2 others
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Query Match 16.7%; Score 781.2; DB 12; Length 945;
Best Local Similarity 94.4%; Fred. No. 2.9e-138;
Matches 874; Conservative 0; Mismatches 45; Indels 7; Gaps 6;
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3701 GTGATGTGTGTTTCCCGAGGAGCGCCCTCTCTCCAGACTTCCCTGCTCC 3760
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 VERSION BQ437258.1 GI:21176334
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 887)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
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 Average insert size 1.75 kb. Library constructed by Life
 Technologies."
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Db      601  CTGGAAGGCTTAAGGACACAGTGAGCGAGGGAGAGTCTCATCTGCTGCAATTTGT 660
Qy      4558  GGCGGTGTAGTGCCAAACTTGAATA-GGGGCTGGGGTGTCTTCCACTGACACCCAAA 4616
Db      661  GGGGTGTAGTGCCAAACTTGAATAGGGGCTGGGGTGTCTTCCACTGACACCCAAA 720
Qy      4617  TCAGAAATCCCTGGTCTTGAAGTCCAGAACTTTGGCTCTTGAAGTCTTCCCT 4666
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RESULT 5
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VERSION BC028738
KEYWORDS HTC.
SOURCE  Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS Strausberg, R.
TITLE   Direct Submission
JOURNAL Submitted (29-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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This clone has the following problem: frame shifted.
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Matches 1080; Conservative 0; Mismatches 463; Indels 51; Gaps 1;

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 Db 1716 TTTACGCGCTTCTATCATCATCTGCGAGGCGCTCATGAAGCTGCTTGTGATGAGCT 1775
 QY 1917 CACGGGATGAACTGCGCTATGCTTTGGCGTGCCATGCTGGGTGCGCAGCAGCTTTC 1976
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RESULT 6
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 BM477185
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)

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 1 (bases 1 to 1157)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-rcmail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Cloning Distribution: Agencourt Bioscience Corporation
 Cloning Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

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 Average insert size 1.867 Kb. Library enriched for
 full-length clones and constructed by Life Technologies.

FEATURES
 source

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 Best Local Similarity 93.6%; Pred. No. 3.4e-129;
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 Db 193 CTGCCAGGCGAGGCGCGGCTGAGTGGGAGATGCGGCGACGGGGATGAATGCCCTTA 252
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Query Match      14.6%; Score 682.8; DB 13; Length 981;
Best Local Similarity 90.4%; Pred. No. 1.5e-119;
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DB 13 GCTCATCGGCTCAACACGAGGAGGCGCTCAAGTTCTGTGGAGGACTCTGCAGAGCGA 72
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DB 193 GGCAGACCGGGCAATATGGGAAATGGCGCGCAAAACCTTGCTGGCGCTCTTTACTGACCA 252
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ACCESSION BUI73291
VERSION BUI73291.1 GI:22687275
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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 942)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUAM13543 row: c column: 09
High quality sequence stop: 482.
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Best Local Similarity 92.1%; Pred. No. 2.2e-118;
Matches 791; Conservative 0; Mismatches 56; Indels 12; Gaps 7;
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ACCESSION      B0891968
VERSION        B0891968.1 GI:22283982
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE         1 (bases 1 to 919)
JOURNAL       NIH-MGC http://mgs.nci.nih.gov/.
COMMENT       National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-f@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Rubin Laboratory
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution: Agencourt Bioscience Corporation
              found through the I.M.A.G.E. Consortium/LLNL at:
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             the laboratory of Gerald M. Rubin (University of
             California, Berkeley) using ZAP-cDNA synthesis kit
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BASE COUNT  187 a 290 c 275 g 167 t
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Query Match      14.5%; Score 674.6; DB 13; Length 919;
Best Local Similarity 98.0%; Pred. No. 5.4e-118;
Matches 683; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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FEATURES

[illegible]

FEATURES
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VERSION BQ947939.1 GI:22363417
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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3	4246.6	Novel human coding
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5	2452.6	Human MBSP4 poly
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2221 GGTGAGCTGCTGCGCACTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTG 2280
2281 GCCTGCTTCCCTAGCCACGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
2281 GCCTGCTTCCCTAGCCACGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
2341 GCGGCGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
2341 GCGGCGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
2401 CCTATGACCGCTTCCCGGAGCTACCGGACTACTCCACGAGCTGAGCTGACCGTGG 2460
2401 CCTATGACCGCTTCCCGGAGCTACCGGACTACTCCACGAGCTGAGCTGACCGTGG 2460
2461 CCGTGGGTGCTTCCCTCTCTTCTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
2461 CCGTGGGTGCTTCCCTCTCTTCTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
2521 GGGACCGCGGAGAGCTGCGGTGCGGCTTAGCCCACTGCGGCTGCGGCTGCGGCTGCGGCTG 2580
2521 GGGACCGCGGAGAGCTGCGGTGCGGCTTAGCCCACTGCGGCTGCGGCTGCGGCTGCGGCTG 2580
2581 GCGTCCCTGCTGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
2581 GCGTCCCTGCTGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640

2641 AGCTGCTGCTCACTGACGCTGAAGCGGGTGGTGGCTGCGGGCGGACCCCTGCGAGGCTC 2700
2641 AGCTGCTGCTCACTGACGCTGAAGCGGGTGGTGGCTGCGGGCGGACCCCTGCGAGGCTC 2700
2701 TGCGCCTTGCCTGCGCGCGCTGACCTGCTGCGCGCTGCGCGCGGACCCGACGATGTGC 2760
2701 TGCGCCTTGCCTGCGCGCGCTGACCTGCTGCGCGCTGCGCGCGGACCCGACGATGTGC 2760
2761 CTCTCTTGGCGCGCGCGCTGACCTGCTGCGCGCTGCGCGCGGACCCGACGATGTGC 2820
2761 CTCTCTTGGCGCGCGCGCTGACCTGCTGCGCGCTGCGCGCGGACCCGACGATGTGC 2820
2821 CACCGCGCGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
2821 CACCGCGCGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
2881 GCGCAACGACGCTTACCGCGCGCGCTTACCGCGCGCTTACCGCGCGCTTACCGCGCGCTTAC 2940
2881 GCGCAACGACGCTTACCGCGCGCGCTTACCGCGCGCTTACCGCGCGCTTACCGCGCGCTTAC 2940
2941 AGCGCCTTCT 3000
2941 AGCGCCTTCT 3000
3001 CAACTGGCTTTTCT 3060
3001 CAACTGGCTTTTCT 3060
3061 GGAATCT 3120
3061 GGAATCT 3120
3121 TCTGGCGCTTTGAAACAACTGCGGGGCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3180
3121 TCTGGCGCTTTGAAACAACTGCGGGGCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3180
3181 TGTGTGGATGTTGTTTCT 3240
3181 TGTGTGGATGTTGTTTCT 3240
3241 CCAATGTGAGGCTGAGGTTTCT 3300
3241 CCAATGTGAGGCTGAGGTTTCT 3300
3301 ATTTCTGTGGGATTTGTACCCAGAACTCTGTTTCCCGATCTCTCTCTCTCTCTCTCTCTCTCTCT 3360
3301 ATTTCTGTGGGATTTGTACCCAGAACTCTGTTTCCCGATCTCTCTCTCTCTCTCTCTCTCTCTCT 3360
3361 CTTCT 3420
3361 CTTCT 3420
3421 CAGACCAACAGAGATGAGGCTGAGAGCAGAGGAGAAATCAGAGCCCTCTGCGCCCTG 3480
3421 CAGACCAACAGAGATGAGGCTGAGAGCAGAGGAGAAATCAGAGCCCTCTGCGCCCTG 3480
3481 CTTCT 3540
3481 CTTCT 3540
3541 AGATGAAGCACTTCTGCGGGGCGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3600
3541 AGATGAAGCACTTCTGCGGGGCGCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3600
3601 CTGCTGGGGAGGAGGCTCCACGATCT 3660
3601 CTGCTGGGGAGGAGGAGTCCACGATCT 3660
3661 GCGAGGACCACTTCTCTGAGTGGAAACAGGTTCTTGTATGTGGATGTGTGTCTCTCTCTCTCTCTCT 3720
3661 GCGAGGACCACTTCTCTGAGTGGAAACAGGTTCTTGTATGTGGATGTGTGTCTCTCTCTCTCTCTCT 3720

CC analyse the proteome of a tissue or cell type. The invention is useful
 CC for creating knock-in humanised animals or transgenic animals to model
 CC human diseases, in somatic or germline gene therapy, to generate a
 CC transcript image of a tissue or cell type, for detecting differences in
 CC the chromosomal location due to translocation, inversion, etc. among
 CC normal, carrier or affected individuals, and as hybridisation probes for
 CC mapping naturally occurring genomic sequences. The present sequence is
 CC human DME-5 cDNA.
 XX
 SQ Sequence 4763 BP; 871 A; 1601 C; 1364 G; 927 T; 0 other;
 Query Match 92.8%; Score 4332.4; DB 24; Length 4763;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 4396; Conservative 0; Mismatches 26; Indels 8; Gaps 4;
 QY 238 GAGAGGAACAGACCCCTTCTCTGTCCTCAAGTCTAAACCCAGGTCCCTCCCAACCCCTCTCTC 297
 DB 1 GAGAGAAATAGACTCTCTTCTGTCCTCTTCTAAACCCAGGTCCCTACCCGTACCCCTCTCTC 60
 QY 298 CTTCTTTCCTCCCT 357
 DB 61 CTTCTTTCCTCCCT 119
 QY 358 CTTCTTTCCT 417
 DB 120 CTTCTTTCCT 174
 QY 418 GCATGTGCT 477
 DB 175 GCATGTGCT 234
 QY 478 GTCCCG 537
 DB 235 GTCCCG 294
 QY 538 GCTTCCCGGTGTGAACACAGCGCTTACCGCGGAGTGTGCGCGGAGTGTGCGCGGAGTGTGAACA 597
 DB 295 GCTTCCCGGTGTGAACACAGCGCTTACCGCGGAGTGTGCGCGGAGTGTGCGCGGAGTGTGAACA 354
 QY 598 ACGAGATCTCTGGCGCGCGTGTGAGTCTTGGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCG 657
 DB 355 ACGAGATCTCTGGCGCGCGTGTGAGTCTTGGCGTGTGCGCGTGTGCGCGTGTGCGCGTGTGCGCG 414
 QY 658 GCGCGCGCGGTCTCAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAG 717
 DB 415 GCGCGCGCGGTCTCAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAG 474
 QY 718 CCACTCTGCGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGT 777
 DB 475 CCACTCTGCGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGT 534
 QY 778 CTGTGTGCTTCACTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAG 837
 DB 535 CTGTGTGCTTCACTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAG 594
 QY 838 ACTGCTGTACCTCACTCTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGT 897
 DB 595 ACTGCTGTACCTCACTCTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGT 654
 QY 898 ACGAGCGAGCTCAATCCCGCAGACACAGATATCGTGACCTCGTGGAGAGAGCTGTGA 957
 DB 655 ACGAGCGAGCTCAATCCCGCAGACACAGATATCGTGACCTCGTGGAGAGAGCTGTGA 714
 QY 958 TGCTGTCTTCTCACTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAG 1017
 DB 715 TGCTGTCTTCTCACTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAGCGCGTGTGAG 774
 QY 1018 TCTGTGTCTATGGAACAGTCAATGTAGCCAGCTCAACTACCTCTTGGGTGCTCG 1077
 DB 775 TCTGTGTCTATGGAACAGTCAATGTAGCCAGCTCAACTACCTCTTGGGTGCTCG 834
 QY 1078 GTTTTCTCAGCGCGGACAGGCTGCAAGGCAACTATGGCTCTCTGGACAGATCC 1137

DB 835 GTTTTCTCAGCACCCGGGACACAGCTGCAAAAGCAACTATGGCTCTCTGGACACAGATCC 894
 QY 1138 AGCCCTCGCTGGCTCAGTGAACATCGCCACTTTTGGGGGCGACCCCGAGCGTATCA 1197
 DB 895 AGCCCTCGCTGGCTCAGTGAACATCGCCACTTTTGGGGGCGACCCCGAGCGTATCA 954
 QY 1198 CCACTCTTGGTTCGGGGGAGGGGCTCTCTGCGTCAAACTTCTGATCTCTCTCCACCAT 1257
 DB 955 CCACTCTTGGTTCGGGGGAGGGGCTCTCTGCGTCAAACTTCTGATCTCTCTCCACCAT 1014
 QY 1258 CAGAGGGCTGTTCAGAAAGGCTCGCCAGAGTGGACACCGCCATTTCCAGCTGGTCTG 1317
 DB 1015 CAGAAAGGCTGTTCAGAAAGGCTCGCCAGAGTGGACACCGCCATTTCCAGCTGGTCTG 1074
 QY 1318 TCAACTACAGCGCTCAAGTACACCGCTCTGCTGCGAGCAAGTGGCTGTGACCGAG 1377
 DB 1075 TCAACTACAGCGCTCAAGTACACCGCTCTGCTGCGAGCAAGTGGCTGTGACCGAG 1134
 QY 1378 AGGACAGTGTGAAGTGTGAGTGTCTGCGCGGAGACCTCTCCGGGAGTGTGTGGACC 1437
 DB 1135 AGGACAGTGTGAAGTGTGAGTGTCTGCGCGGAGACCTCTCCGGGAGTGTGTGGACC 1194
 QY 1438 AGGAGTGTGAGCTGTGAGTGTCTGCGCGGAGACCTCTCCGGGAGTGTGTGGACC 1497
 DB 1195 AGGAGTGTGAGCTGTGAGTGTCTGCGCGGAGACCTCTCCGGGAGTGTGTGGACC 1254
 QY 1498 TCCCGATGACCTGAGATCTCTATGACGAGGAGAAATTCCTCAACTACGACATGCTCA 1557
 DB 1255 TCCCGATGACCTGAGATCTCTATGACGAGGAGAAATTCCTCAACTACGACATGCTCA 1314
 QY 1558 TCGGCGTCAACGAGGAGAGGCTCAAGTTCGTGGAGACTCTGACAGAGAGGAGGAG 1617
 DB 1315 TCGGCGTCAACGAGGAGAGGCTCAAGTTCGTGGAGACTCTGACAGAGAGGAGGAG 1374
 QY 1618 GTGTGTCTGCGAGCGCTTTCACCTTCTGCTCTCAACTTTTGTGACAACTGTATGCT 1677
 DB 1375 GTGTGTCTGCGAGCGCTTTCACCTTCTGCTCTCAACTTTTGTGACAACTGTATGCT 1434
 QY 1678 ACCCGAAGGAGAGTGTCTGCGGAGACATCAAGTTTATGTAACAGACTGGGCG 1737
 DB 1435 ACCCGAAGGAGAGTGTCTGCGGAGACATCAAGTTTATGTAACAGACTGGGCG 1494
 QY 1738 ACCCGAAGTGTGCGGAGTGTGCGGAGACATCAAGTTTATGTAACAGACTGGGCG 1797
 DB 1495 ACCCGAAGTGTGCGGAGTGTGCGGAGACATCAAGTTTATGTAACAGACTGGGCG 1554
 QY 1798 GGTGTGACACAGCTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGG 1857
 DB 1555 GGTGTGACACAGCTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGG 1614
 QY 1858 TTTACACCTTCTACACACCTGCGGAGGAGGCGCGCTGAGTGGGAGATGGGCG 1917
 DB 1615 TTTACACCTTCTACACACCTGCGGAGGAGGCGCGCTGAGTGGGAGATGGGCG 1674
 QY 1918 ACGGGATGAATGCTCTATGCTTTTGGCGTGGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1977
 DB 1675 ACGGGATGAATGCTCTATGCTTTTGGCGTGGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1734
 QY 1978 CTTGTAACTTCTCAAGAAATGACGTCTGCTGAGTGTGCGTGTGATGACCTTCTGAGACCA 2037
 DB 1735 CTTGTAACTTCTCAAGAAATGACGTCTGCTGAGTGTGCGTGTGATGACCTTCTGAGACCA 1794
 QY 2038 ACTTCCGCAAGACTGGGAGACCCCAACAGCGGTGCGGAGTACCAAGTTTCAATCCACA 2097
 DB 1795 ACTTCCGCAAGACTGGGAGACCCCAACAGCGGTGCGGAGTACCAAGTTTCAATCCACA 1854
 QY 2098 CAAAGCCCAATCGTTTCGAGAGTGTGTGAGCAAAATTCACAGCAAGGAGAGAGT 2157
 DB 1855 CAAAGCCCAATCGTTTCGAGAGTGTGTGAGCAAAATTCACAGCAAGGAGAGAGT 1914
 QY 2158 ATCTGCAATAGGCTGAGCCAGCGCTGAGTGTGAGCAACTACCGCGCCAAAGAGTGGCT 2217
 DB 1915 ATCTGCAATAGGCTGAGCCAGCGCTGAGTGTGAGCAACTACCGCGCCAAAGAGTGGCT 1974

Db 4134 GAAACAGATGGAGGCGCAGTGGGACAGCGCTTGGGACAGACACAGCAGGAGTAATTTGA 4193
 QY 4438 AATGTGTAGTGTACTCCCGAGGCGCTTGGGCTTGGGCAATTTGGGAAAGATGATGT 4497
 Db 4194 AATGTGTAGTGTACTCCCGAGGCGCTTGGGCTTGGGCAATTTGGGAAAGATGATGT 4253
 QY 4498 CTGGAAGGGCTTAAGGACACAGTGGACGAGGGGAGAGTCCCTCATCTGTGCGCATTTTGT 4557
 Db 4254 CTGGAAGGGCTTAAGGACACAGTGGACGAGGGGAGAGTCCCTCATCTGTGCGCATTTTGT 4313
 QY 4558 GGGGTGTAGTGTCCAACTTGAATAGGGGCTGGGGTGTCTTCCACTGACACCCAAAT 4617
 Db 4314 GGGGTGTAGTGTCCAACTTGAATAGGGGCTGGGGTGTCTTCCACTGACACCCAAAT 4373
 QY 4618 CCAGAATCCCTGGTCTTGAAT-CCAGAACTTTGCCCTCTTCACTGTCCCT 4666
 Db 4374 CCAGAATCCCTGGTCTTGAATGCCAGAACTTTGCCCTCTTCACTGTCCCT 4423

RESULT 3
 AEN59628
 ID AEN59628 standard; cDNA; 4622 BP.
 AC AEN59628;
 XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Novel human coding sequence SEQ ID NO: 39.
 XX
 KW Human; anti-nausea; vulnary; anti-inflammatory; immunomodulator;
 KW anti-infectivity; cerebroprotective; cytostatic; rheumatic; gene therapy;
 KW neuroprotective; antiparkinsonian; protein therapy; EST;
 KW expressed sequence tag; gene; ss.

OS Homo sapiens.
 XX
 PN WO200222660-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US26015.
 XX
 PR 11-SEP-2000; 2000US-0659671.
 XX
 PA (HYSE-) HYSBQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX
 DR WPI: 2002-292408/33.
 DR P-PSDB; ABB97215.
 XX
 FT An isolated polynucleotide for treating diseases associated with its
 PT encoded polypeptide such as cancer and multiple sclerosis -
 XX
 PS Claim 1; SEQ ID NO 39; 509pp; English.
 XX
 CC The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat
 CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
 CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
 CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
 CC Parkinson's disease. The present sequence is a coding sequence of the
 XX
 SQ Sequence 4622 BP; 850 A; 1540 C; 1344 G; 888 T; 0 other;
 Query Match 91.0%; Score 4246.6; DB 24; Length 4622;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 4282; Conservative 0; Mismatches 4; Indels 3; Gaps 3;
 QY 380 GGGGGGGTCCCAAGGAGGAGGGGGGTCCCGCATGACATGTGCTCTCGCGCTGTG 439
 Db 1 GGGGGGGTCCCAAGGAGGAGGGGGGTCCCGCATGACATGTGCTCTCGCGCTGTG 60
 QY 440 TCTGTGGGGCTTGGGGGGGTCAACGCGGGGGAGGGGTCCCGCGGGCGCGCCCGGG 499
 Db 61 TCTGTGGGGCTTGGGGGGGTCAACGCGGGGGAGGGGTCCCGCGGGCGCGCCCGGG 120
 QY 500 CGGCCCCCGGCTTGGGGCTTGGGAGCTTGGGAGAGCGCTTCCCGGTGTGAAACACGGC 559
 Db 121 CGGCCCCCGGCTTGGGGCTTGGGAGCTTGGGAGAGCGCTTCCCGGTGTGAAACACGGC 180
 QY 560 CTACGGGGGAGTGGCGGTGGCGGCGGAGCTCAACACGAGATCCTGGGGCCCCGTGT 619
 Db 181 CTACGGGGGAGTGGCGGTGGCGGCGGAGCTCAACACGAGATCCTGGGGCCCCGTGT 240
 QY 620 GCAGTTCTTGGGGCTTACGCCACCGCCCTTGGGGCGCCCGCGCTTCCAGCCGCC 679
 Db 241 GCAGTTCTTGGGGCTTACGCCACCGCCCTTGGGGCGCCCGCGCTTCCAGCCGCC 300
 QY 680 TGAGGGGGGGCTTGGGGCTTGGGAGAGCGCTCAACGCGGCGCGCCCGCGCTTCCCG 739
 Db 301 TGAGGGGGGGCTTGGGGCTTGGGAGAGCGCTCAACGCGGCGCGCCCGCGCTTCCCG 360
 QY 740 GCAGAACTTGCACGGGGGGCTTGGGGCTTGGGAGAGCGCTTGGGGTTCACGCAACTT 799
 Db 361 GCAGAACTTGCACGGGGGGCTTGGGGCTTGGGAGAGCGCTTGGGGTTCACGCAACTT 420
 QY 800 GGAGGGGGGGCTTGGGGCTTGGGAGAGCGCTTGGGAGAGCGCTTGGGGTTCACGCAACTT 859
 Db 421 GGAGGGGGGGCTTGGGGCTTGGGAGAGCGCTTGGGAGAGCGCTTGGGGTTCACGCAACTT 480
 QY 860 CGTGGCCCGGAGGAGCGTGGCTTCAAAAAGAGTGCAGAGGGGAGCGTCAATCCGCG 919
 Db 481 CGTGGCCCGGAGGAGCGTGGCTTCAAAAAGAGTGCAGAGGGGAGCGTCAATCCGCG 540
 QY 920 AGACACAGATATCCGTGACCTTGGGAGAGCGCTTGGTGTCTTCTTCTTCCATGGCGGTC 979
 Db 541 AGACACAGATATCCGTGACCTTGGGAGAGCGCTTGGTGTCTTCTTCTTCCATGGCGGTC 600
 QY 980 CTACATGGAGGGGAGCGGAAACATGTTGATGGCTCAGTCTGGTGTGCTATGGCAAGT 1039
 Db 601 CTACATGGAGGGGAGCGGAAACATGTTGATGGCTCAGTCTGGTGTGCTATGGCAAGT 660
 QY 1040 CATTTAGCCAGCTCAACTACCGTCTTGGGGTGTCTGGTCTTCTCAGCACCGGGGACCA 1099
 Db 661 CATTTAGCCAGCTCAACTACCGTCTTGGGGTGTCTGGTCTTCTCAGCACCGGGGACCA 720
 QY 1100 GGCTGCAAAAGCAACTATGGGCTTCTGGACAGATCCAGGCCCTTGGCTGAGTGA 1159
 Db 721 GGCTGCAAAAGCAACTATGGGCTTCTGGACAGATCCAGGCCCTTGGCTGAGTGA 780
 QY 1160 AAACATCGCCCACTTTGGGGGCGACCCGAGCGTATCACCATCTTGGTTCGGGGGAGG 1219
 Db 781 AAACATCGCCCACTTTGGGGGCGACCCGAGCGTATCACCATCTTGGTTCGGGGGAGG 840
 QY 1220 GGCTTCTCGGTCACCTTCTGATCTCTCCCACTTCCAGAGGGCTTGGTTCAGAAAGC 1279
 Db 841 GGCTTCTCGGTCACCTTCTGATCTCTCCCACTTCCAGAGGGCTTGGTTCAGAAAGC 900
 QY 1280 CATCGCCAGAGTGGCACCGCATTTCCAGTGTCTGCTCACTACAGCGCTCAAGTA 1339
 Db 901 CATCGCCAGAGTGGCACCGCATTTCCAGTGTCTGCTCACTACAGCGCTCAAGTA 960
 QY 1340 CACGGGGCTTGGCAGCAAGGTGGGCTGTGACCGAGAGGAGTGTGCTGAAGCTGTGGA 1399
 Db 961 CACGGGGCTTGGCAGCAAGGTGGGCTGTGACCGAGAGGAGTGTGCTGAAGCTGTGGA 1020
 QY 1400 GTGTCTGGCGGAGAGCCCTTCCCGGAGCTGGTGGACCGAGAGCGTGGCCGCTA 1459

Db 1021 GTGTCTGGCCCGGAAGCCCTCCCGGGAGCTGGTGGACAGAGACGTGACGCTGCGCGCTA 1080
 QY 1460 CCATACGCTTTGGGCGCGTGGTGGATGGCGAGTGGTCCCCGATGACCCCTGAGATCCT 1519
 Db 1081 CCATACGCTTTGGGCGCGTGGTGGATGGCGAGTGGTCCCCGATGACCCCTGAGATCCT 1140
 QY 1520 CATGACGAGGAGAAATTCCTCACTAGGACATGCTCATGGCGTCAACAGGAGAGGG 1579
 Db 1141 CATGACGAGGAGAAATTCCTCACTAGGACATGCTCATGGCGTCAACAGGAGAGGG 1200
 QY 1580 CCTCAAGTTCGTGAGGACTCTGACAGAGAGGAGAGCGGTGTGTCTGCCAGCGCTTTGA 1639
 Db 1201 CCTCAAGTTCGTGAGGACTCTGACAGAGAGGAGAGCGGTGTGTCTGCCAGCGCTTTGA 1260
 QY 1640 CTTCACTGTCTCCAACTTTGTGGACAACTCTGATATGGCTA CCGGAGGCAAGATGTGCT 1699
 Db 1261 CTTCACTGTCTCCAACTTTGTGGACAACTCTGATATGGCTA CCGGAGGCAAGATGTGCT 1320
 QY 1700 TCGGAGAGACCAATCAAGTTTATGACAGACTGGGCGGACCGGAGCAATGGCGAAATGCG 1759
 Db 1321 TCGGAGAGACCAATCAAGTTTATGACAGACTGGGCGGACCGGAGCAATGGCGAAATGCG 1380
 QY 1760 CCGCAAAACCCCTGTGGCGCTTTTATGACCAACCAATGGGTGGCAACAGCTGTGCCAC 1819
 Db 1381 CCGCAAAACCCCTGTGGCGCTTTTATGACCAACCAATGGGTGGCAACAGCTGTGCCAC 1440
 QY 1820 TGCCAAAGTGCACCGGACTACCACTCTCCGCTCTACTTTTACCTTTACCAACCACTG 1879
 Db 1441 TGCCAAAGTGCACCGGACTACCACTCTCCGCTCTACTTTTACCACTTTTACCAACCACTG 1500
 QY 1880 CCAGCGAGGCGCGGCTGAGTGGGAGATGCGGCGCAGCGGAGTGAATGCGCCCTATGT 1939
 Db 1501 CCAGCGAGGCGCGGCTGAGTGGGAGATGCGGCGCAGCGGAGTGAATGCGCCCTATGT 1560
 QY 1940 CTTTGGGCTGCCATGTGGTGCACCGGACTCTTCCCTGTAACTTCTCCAAAGATGA 1999
 Db 1561 CTTTGGGCTGCCATGTGGTGCACCGGACTCTTCCCTGTAACTTCTCCAAAGATGA 1620
 QY 2000 CGTCATGCTCAGTCCGCTGGTCTAGTACTGTGACCAACTTGCACAAAGCTGGGACCC 2059
 Db 1621 CGTCATGCTCAGTCCGCTGGTCTAGTACTGTGACCAACTTGCACAAAGCTGGGACCC 1680
 QY 2060 CAACAGCGGCTGCCAGGATACCAAGTTCAATCCACCAAGCCCAATCGCTTCGAGGA 2119
 Db 1681 CAACAGCGGCTGCCAGGATACCAAGTTCAATCCACCAAGCCCAATCGCTTCGAGGA 1740
 QY 2120 GGTGCTGGAGCAATTCACAGCAAGGAGAGCAGTATCTGCATAGGCGCTGAGGCC 2179
 Db 1741 GGTGCTGGAGCAATTCACAGCAAGGAGAGCAGTATCTGCATAGGCGCTGAGGCC 1800
 QY 2180 ACGGCTGCTGACAACTACCGCGCCAAACAAGGTGGCCTTCTGGCTGGAGCTCGTGCCCA 2239
 Db 1801 ACGGCTGCTGACAACTACCGCGCCAAACAAGGTGGCCTTCTGGCTGGAGCTCGTGCCCA 1860
 QY 2240 CTTGCAACCTGACAGGAGCTTCTCAACAGCAGGAGAGCAGTATCTGCATAGGCGCTGAGGCC 2299
 Db 1861 CTTGCAACCTGACAGGAGCTTCTCAACAGCAGGAGAGCAGTATCTGCATAGGCGCTGAGGCC 1920
 QY 2300 GCGCTGCGCGCTCGTCCCGCGCTGGCGCCCGGAGCAGCGCGGCGCCCGCGCGCTGC 2359
 Db 1921 GCGCTGCGCGCTCGTCCCGCGCTGGCGCCCGGAGCAGCGCGGCGCCCGCGCGCTGC 1980
 QY 2360 CACCTGCTCCGAGCGCGAGCCGAGCCGAGCCGAGCCCAAGGCGCTATGA CCGCTTCCCGG 2419
 Db 1981 CACCTGCTCCCGAGCCGAGCCGAGCCGAGCCGAGCCCAAGGCGCTATGA CCGCTTCCCGG 2040
 QY 2420 GGACTCAGGAGCTACTCCAGGAGCTGAGCTACCGTGGCGCTGGGTCCTTCCCTCT 2479
 Db 2041 GGACTCAGGAGCTACTCCAGGAGCTGAGCTACCGTGGCGCTGGGTCCTTCCCTCT 2100
 QY 2480 CTTCTCAACATCTGCGCTTTGTGCTCTACTACAAGCGGAGCCGCGGAGGAGCT 2539
 Db 2101 CTTCTCAACATCTGCGCTTTGTGCTCTACTACAAGCGGAGCCGCGGAGGAGCT 2160

QY 2540 GCGGTGACAGGCGGCTTAGCCACCTGGCGGCTCAGGCTCTGCGTGCCTGTGGGGGCC 2599
 Db 2161 GCGGTGACAGGCGGCTTAGCCACCTGGCGGCTCAGGCTCTGCGTGCCTGTGGGGGCC 2220
 QY 2600 CTTGCTCCCGCGCGGCGGCTGAGCTGCACACAGAGAGAGCTGGTGTCACTGCAGCT 2659
 Db 2221 CTTGCTCCCGCGCGGCGGCTGAGCTGCACACAGAGAGAGCTGGTGTCACTGCAGCT 2280
 QY 2660 GAAAGCGGCTGTGCTGCGGCGGAGCCCTGCGGAGCTCTGCGCCCTGCTGCGCCGCC 2719
 Db 2281 GAAAGCGGCTGTGCTGCGGCGGAGCCCTGCGGAGCTCTGCGCCCTGCTGCGCCGCC 2340
 QY 2720 CGACTACACCTGTGGCCCTGTGGCGGCGGAGCCGAGATGTGCTCTTGTGGCCCCCGGGC 2779
 Db 2341 CGACTACACCTGTGGCCCTGTGGCGGCGGAGCCGAGATGTGCTCTTGTGGCCCCCGGGC 2400
 QY 2780 CTTGACCTGTGCTGCGGCTGGGCGGAGCCGAGCTGGGCGGAGCTGGGCGGAGCTGGGCGG 2839
 Db 2401 CTTGACCTGTGCTGCGGCTGGGCGGAGCCGAGCTGGGCGGAGCTGGGCGGAGCTGGGCGG 2460
 QY 2840 TCCCTTGGGCGGCTTTCGCCCGCGCCCTTCCCAACCGGCGGAGCCGAGCAACAAAGCTACC 2899
 Db 2461 TCCCTTGGGCGGCTTTCGCCCGCGCCCTTCCCAACCGGCTACCGGCGGAGCAACAAAGCTACC 2520
 QY 2900 CCACCCCGGCTTTCGCCCGCGGCTTTCGCCCGGAGGCTTGGCAACTGGCTTTTCTCCTGT 2959
 Db 2521 CCACCCCGGCTTTCGCCCGCGGCTTTCGCCCGGAGGCTTGGCAACTGGCTTTTCTCCTGT 2580
 QY 2960 TCCCTTGGGCGGCTTTCGCCCGGCTTTCGCCCGGAGGCTTGGCAACTGGCTTTTCTCCTGT 3019
 Db 2581 TCCCTTGGGCGGCTTTCGCCCGGCTTTCGCCCGGAGGCTTGGCAACTGGCTTTTCTCCTGT 2640
 QY 3020 GGAGTGTGTACACGCGCTACAGAGCGCTAAGGTGGAGCATGGGATTCCTCCCTGGAGTC 3079
 Db 2641 GGAGTGTGTACACGCGCTACAGAGCGCTAAGGTGGAGCATGGGATTCCTCCCTGGAGTC 2700
 QY 3080 GTGTCTTTCGCCCGGAGGCGGCTTTCCTCTCTGGATCTGGGCGCTTGGCAACT 3139
 Db 2701 GTGTCTTTCGCCCGGAGAGG-CCAGTCTCTCTCTGGATCTGGGCGCTTGGCAACT 2759
 QY 3140 GGGGGCGGCTTTTCTCCCGCGGCTTTCGCCCGGAGGCTTTCGGTGTGGATTTGCTATTT 3199
 Db 2760 GGGGGCGGCTTTTCTCCCGCGGCTTTCGCCCGGAGGCTTTCGGTGTGGATTTGCTATTT 2819
 QY 3200 TCCCGCTGGAGGTGTGCTTTCACAAAGGCGGCTTTCGCCCGGAGGCTTTCGCCCGGAGG 3259
 Db 2820 TCCCGCTGGAGGTGTGCTTTCACAAAGGCGGCTTTCGCCCGGAGGCTTTCGCCCGGAGG 2879
 QY 3260 TTTTTCGCCCGGAGGAGGCTTTCGCCCGGCTTTCGCCCGGAGGCTTTCGCCCGGAGG 3319
 Db 2880 TTTTTCGCCCGGAGGAGGCTTTCGCCCGGCTTTCGCCCGGAGGCTTTCGCCCGGAGG 2939
 QY 3320 CCGGAGGAGGCTTTCGCCCGGAGGCTTTCGCCCGGCTTTCGCCCGGAGGCTTTCGCCCGGAG 3379
 Db 2940 CCGGAGGAGGCTTTCGCCCGGAGGCTTTCGCCCGGCTTTCGCCCGGAGGCTTTCGCCCGGAG 2999
 QY 3380 ACCCTGGAAGTGGTGTGTTTACATACAGTACCTTGGGCGGAGGCTTTCGCCCGGAGG 3438
 Db 3000 ACCCTGGAAGTGGTGTGTTTACATACAGTACCTTGGGCGGAGGCTTTCGCCCGGAGG 3059
 QY 3439 AGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3498
 Db 3060 AGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3119
 QY 3499 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3558
 Db 3120 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3179
 QY 3559 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3618
 Db 3180 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3239

QY 3619 GTCCAGCATCTCTGATGCTGCTGGAAGCTTATTTTCCGTTGGCCAGACGATTTCTCT 3678
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 3679 GAGTGAACACAGGTTCTTTCATGTGTGATGTGTGTTTCCAGGAGACGCGCCCTCTCTT 3738
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 3739 CCCAGCACTTCCCTGCTCCCTCCAGCCCTCAGGCCACGACCCAGTTCCTCTCTCATG 3798
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 3799 CAGGTGAGCACAGACTTCTAGTTGACAGAGCTGAGGAGGTGACAAACCCCGAGGAG 3858
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 3859 GCCCGGCTTCTCTCCAGTTGGGGGAGGGGGTGTGGCAACGTTGCCCTCCCGCAGAGGC 3918
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 3919 CACGATGTTTGACCAAGCCCTATTGTTGTCGAGACAGACCTTTTCCCGAGGCTCA 3978
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 3979 GAGCATTTCTCATCGTCCAAACTGGGTAGGTGATTTGAGCGGAAAGACTCCCAAAAT 4038
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4039 GTGCCAAGAAATTTCCAGTCCAGCAGGAGGAGGAACTAAGGCAAGCAGATACAG 4098
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4099 GCGAGGAGTGTGGCAGGTGAGGGGGTCCCGCTGTGCGCTTCTCTCACCATTGCTC 4158
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4159 CCCACCTGCTCAGTTCTCGTTTCCCTTCACTCGTCCCTCTTTTGAAGCTGTCC 4218
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4219 CCATCTCAGTGTACAGCAGCTTCTCTCATCTGACCACTCTCTGACCAAGCCCTC 4278
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4279 CTCCTTGTCTCAAAAGAGGAGCCCTTGAATGGTGGAGGAGGAGTGGGAGAAAGTCT 4338
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4339 CACCGACAGTTGGGAGATGAGTGTGAGTGTCTGGGAAACAGATGGAGGGGAGTG 4398
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4399 GGGACAGGCTTGGGACAGACACAGCAGGAGTATTTGAATGTGTGAGTGTCTCCCG 4458
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4459 GAGGCTTGGGCTTGGGCAATTTGGGAAAGATGATGTCTGAAGGCTTAAAGGACAC 4518
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4519 AGTGACAGGGGAGTCTCTCATCTGCTGCACTTTTGGGGTGTAGTCCAACTTG 4578
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4579 AATAGGGCTGGGTGTGTCTTCCATGACCCCAATCCAGATCCCTGTGCTTGTAGT 4638
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4639 -CCAGAACTTGGCTCTTGTGCTTCTT 4666
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 4666 CCCAGAACTTGGCTCTTGTGCTTCTT 4688
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
 ID ABA95200 standard; cDNA; 2508 BP.
 AC ABA95200;
 XX 10-JUN-2002 (first entry)
 DT Human carboxylesterase family member, 33410 coding sequence.
 DE Carboxylesterase; 33410; cytostatic; cardiant; dermatological; human;
 XX antidiabetic; antirheumatic; antiarthritic; antiallergic; vasotropic;
 XX vulnary; neuroprotective; antinflammatory; antitumor; antitumor;
 XX antiallergic; antiviral; hepatotropic; nephrotropic; anti-HIV; gene;
 XX antiparkinsonian; tuberculostatic; hypotensive; antithrombotic;
 XX nootropic; antisense therapy; angiogenesis; gene therapy; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2508
 FT /*tag= a
 FT /product= "33410 polypeptide"
 XX
 PN WO200216616-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 21-AUG-2001; 2001WO-US26091.
 XX
 PR 21-AUG-2000; 2000US-226774P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAJ;
 XX
 DR WPI; 2002-257916/30.
 DR P-PSDB; ABB07675.
 XX
 PT New carboxylesterase nucleic acid 33410, useful for the treatment and
 PT diagnosis of immune, cardiovascular, reproductive and cancerous
 PT disorders -
 XX
 PS Claim 1; Page 108-110; 123pp; English.
 XX
 CC The invention provides a novel carboxylesterase family member, designated
 CC 33410. Compounds that binds to or modulate the activity or expression of
 CC 33410, are useful for treating or preventing a disorder such as cellular
 CC proliferative or differentiative, neural, cardiovascular, prostatic, skin
 CC brain and skeletal muscular disorders, protein-protein interaction
 CC disorders, signal transduction disorders, immune (e.g. diabetes and
 CC rheumatoid arthritis), reproductive, cardiovascular (e.g. hypertension,
 CC atherosclerosis, coronary artery disease, arrhythmia, ischaemic heart
 CC disease and angina pectoris), vascular disorders (e.g. varicose veins,
 CC Wegener's granulomatosis and wound healing) or cancerous disorders,
 CC multiple sclerosis, Crohn's disease, ulcers, asthma, allergy, infection,
 CC kidney disease (glomerulonephritis), idiopathic thrombocytopenic purpura,
 CC hepatitis, tuberculosis, human immunodeficiency virus, Alzheimer's and
 CC Parkinson's. The 33410 polynucleotide and polypeptide are useful for
 CC diagnosis of a predisposition to a disorder, for evaluating the efficacy
 CC of a therapeutic or prophylactic disorder, for chromosome mapping, as
 CC immunogens, for drug screening, for the detection of mutations in the
 CC gene and for tissue typing. The present sequence represents the coding
 CC sequence of the human carboxylesterase family member, 33410.
 XX
 SQ Sequence 2508 BP; 425 A; 906 C; 751 G; 426 T; 0 other;

Query Match 53.7%; Score 2508; DB 24; Length 2508;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 420 ATGTGGCTCTGGCGCTGTCTGTCTGGCTGGCGGCTCAACGGGGGGGGT 479

Db 1 ATGTGGCTCTGGCGCTGTGTCTGTGTGGGGTGTGGGGGCTCAACGCGGGGGAGGGGT 60
 QY 480 CCG 539
 Db 61 CCG 120
 QY 540 TTCCCGGTGTGAACACGGCTTACGGGCGAGTGTGGCGGTGTGGCGCGGAGCTCAACAAC 599
 Db 121 TTCCCGGTGTGAACACGGCTTACGGGCGAGTGTGGCGGTGTGGCGCGGAGCTCAACAAC 180
 QY 600 GAGATCTTGGGCGCGCGCTGT 659
 Db 181 GAGATCTTGGGCGCGCGCTGT 240
 QY 660 GCGCGCGCGCTTCCAGCGCTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
 Db 241 GCGCGCGCGCTTCCAGCGCTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
 QY 720 ACCCTGCGCGCGCGCTGCGCGCAGAACCTGACGCGCGCGCTGCGCGCGCGCGCGCGCGCT 779
 Db 301 ACCCTGCGCGCGCGCTGCGCGCAGAACCTGACGCGCGCGCTGCGCGCGCGCGCGCGCGCT 360
 QY 780 GTGTGGTTCAACGCAACTTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 839
 Db 361 GTGTGGTTCAACGCAACTTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
 QY 840 TGCCTGTACCTCAACCTCTAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 899
 Db 421 TGCCTGTACCTCAACCTCTAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
 QY 900 GAGCGCGCGCTCAATCCCGCAGACACAGATATCGGTGACCGCTGCGGAGAGAGCGCTGTGATG 959
 Db 481 GAGCGCGCGCTCAATCCCGCAGACACAGATATCGGTGACCGCTGCGGAGAGAGCGCTGTGATG 540
 QY 960 CTGTTTCTCATGTGGCGCTCCTACATGAGAGGGGACCGGAAACATGTTCGATGGCTCAGTC 1019
 Db 541 CTGTTTCTCATGTGGCGCTCCTACATGAGAGGGGACCGGAAACATGTTCGATGGCTCAGTC 600
 QY 1020 CTGGCTGCTATGGCAAGCTCATTTGTAGCCAGCTCAACTACCGCTTTGGGGTGTCTCGGT 1079
 Db 601 CTGGCTGCTATGTGACAGCTCATTTGTAGCCAGCTCAACTACCGCTTTGGGGTGTCTCGGT 660
 QY 1080 TTTCTCAGCACCGGGACCGAGCTGCAAAAGGCAACTATGGGTCTCTGGACCAAGATCCAG 1139
 Db 661 TTTCTCAGCACCGGGACCGAGCTGCAAAAGGCAACTATGGGTCTCTGGACCAAGATCCAG 720
 QY 1140 GCGCTGCGCTGCTCAGTGAACATCGCCACATTTGGGGCGACCGCGAGCGTATCACC 1199
 Db 721 GCGCTGCGCTGCTCAGTGAACATCGCCACATTTGGGGCGACCGCGAGCGTATCACC 780
 QY 1200 ATCTTTGGTTCCGGGGCAGGGGCGCTCTGTGCTCAACCTTCTGTATCTCTCCACCATTTCA 1259
 Db 781 ATCTTTGGTTCCGGGGCAGGGGCGCTCTGTGCTCAACCTTCTGTATCTCTCCACCATTTCA 840
 QY 1260 GAAGGGCTTTCCAGAGGCGCATGCGCCAGAGTGGGACCGGCATTTCCAGTGTGTGTGTC 1319
 Db 841 GAAGGGCTTTCCAGAGGCGCATGCGCCAGAGTGGGACCGGCATTTCCAGTGTGTGTGTC 900
 QY 1320 AACTACAGCGCTCAAGTACAGCGGCTGTGGCAGCAAGGTGGGCTGTGACCGAGAG 1379
 Db 901 AACTACAGCGCTCAAGTACAGCGGCTGTGGCAGCAAGGTGGGCTGTGACCGAGAG 960
 QY 1380 GACAGTGTGAAGTGTGAAGTGTGTGCGCGGAAGCGCTCCCGGAGCTGTGGACCGAG 1439
 Db 961 GACAGTGTGAAGTGTGAAGTGTGTGCGCGGAAGCGCTCCCGGAGCTGTGGACCGAG 1020
 QY 1440 GACGTGACGTGCGCGCTACCATCGCTTTGGGCGCGCTGTGGTGTGATGCGAGCTGTGTC 1499
 Db 1021 GACGTGACGTGCGCGCTACCATCGCTTTGGGCGCGCTGTGGTGTGATGCGAGCTGTGTC 1080
 QY 1500 CCCGATGACCTTGATCTCTATGACAGCAGGAGAAATTCCTCAACTACGACATGCTCATC 1559
 Db 1081 CCCGATGACCTTGATCTCTATGACAGCAGGAGAAATTCCTCAACTACGACATGCTCATC 1140

QY 1560 GCGCTCAACACGAGGAGAGGGGCTCAAGTTCTGTGGAGGACTCTGCAGAGAGCGAGACGGT 1619
 Db 1141 GCGCTCAACACGAGGAGAGGGGCTCAAGTTCTGTGGAGGACTCTGCAGAGAGCGAGACGGT 1200
 QY 1620 GTGTCTGCCAGCGCTTTGACTTCACTGTCTCCAACTTTGTGGACAACTGTATGGCTAC 1679
 Db 1201 GTGTCTGCCAGCGCTTTGACTTCACTGTCTCCAACTTTGTGGACAACTGTATGGCTAC 1260
 QY 1680 CCGGAAGGCAAGGATGTCTTCCGAGAGACCAATCAAGTTTATGTACACAGACTTGGGCGCGAC 1739
 Db 1261 CCGGAAGGCAAGGATGTCTTCCGAGAGACCAATCAAGTTTATGTACACAGACTTGGGCGCGAC 1320
 QY 1740 CCGGACATGTGGGCAATGTGGCGCGCAAAACCTGTCTTGTGGCGCTTTTACTGACCAATGG 1799
 Db 1321 CCGGACATGTGGGCAATGTGGCGCGCAAAACCTGTCTTGTGGCGCTTTTACTGACCAATGG 1380
 QY 1800 GTGGCACAGCTGTGGCGCACTGCCAAGCTGACGCGCGACTACAGCTTCCCGTCTACTTT 1859
 Db 1381 GTGGCACAGCTGTGGCGCACTGCCAAGCTGACGCGCGACTACAGCTTCCCGTCTACTTT 1440
 QY 1860 TACACCTTCTACCACTGCGCAGCGGAGGGCGCGCTGTAGTGGGCGAGATGCGGCGGAC 1919
 Db 1441 TACACCTTCTACCACTGCGCAGCGGAGGGCGCGCTGTAGTGGGCGAGATGCGGCGGAC 1500
 QY 1920 GGGGATGAACTGCGCTTATGTCTTTGGCGTGGCCATGTGGTGGGTGCCACCGACTCTTCCCG 1979
 Db 1501 GGGGATGAACTGCGCTTATGTCTTTGGCGTGGCCATGTGGTGGGTGCCACCGACTCTTCCCG 1560
 QY 1980 TGTAACTTCTCAGAATGACGTCACTGTCTCAGTGTGGTGGTCAATGACCTTCTGGAACCAAC 2039
 Db 1561 TGTAACTTCTCAGAATGACGTCACTGTCTCAGTGTGGTGGTCAATGACCTTCTGGAACCAAC 1620
 QY 2040 TTCGCGAGACTTGGGACCCCAACAGCGGCTGCCGAGGATACCAAGTTCTATCCACACC 2099
 Db 1621 TTCGCGAGACTTGGGACCCCAACAGCGGCTGCCGAGGATACCAAGTTCTATCCACACC 1680
 QY 2100 AAGCCCAATCGCTTCGAGGAGTGTGTGGAGCAATTCACAGCAAGAGAGAGCAGTAT 2159
 Db 1681 AAGCCCAATCGCTTCGAGGAGTGTGTGGAGCAATTCACAGCAAGAGAGAGCAGTAT 1740
 QY 2160 CTGCATATAGGCTTGAAGCCAGCGCTGTGTGACAACTACCGCGCCAAACAGGTGGCTTTC 2219
 Db 1741 CTGCATATAGGCTTGAAGCCAGCGCTGTGTGACAACTACCGCGCCAAACAGGTGGCTTTC 1800
 QY 2220 TGSCTGGAGCTGTGCCCGCCACCTGACACCTGTGACAGCGGCTCTTCCACCAACCAAG 2279
 Db 1801 TGSCTGGAGCTGTGCCCGCCACCTGACACCTGTGACAGCGGCTCTTCCACCAACCAAG 1860
 QY 2280 GCGCTGCTCTCTACGCCACCGCTTGGCGCGCTCGTCTCCCGCGCTGGCGCGCCCGGGGACA 2339
 Db 1861 GCGCTGCTCTCTACGCCACCGCTTGGCGCGCTCGTCTCCCGCGCTGGCGCGCCCGGGGACA 1920
 QY 2340 GCGCGCGCGCGCGCGCTGCGACCTGCTTCCGAGCGCGAGCGCGAGCGCGCGCGCGCGAGG 2399
 Db 1921 GCGCGCGCGCGCGCGCTGCGACCTGCTTCCGAGCGCGAGCGCGAGCGCGCGCGCGCGAGG 1980
 QY 2400 GCGCTATGACCGCTTCCCGGGGACTCAGCGGACTACTCCAGGAGCTTCCAGGAGCTCAGCGGTG 2459
 Db 1981 GCGCTATGACCGCTTCCCGGGGACTCAGCGGACTACTCCAGGAGCTTCCAGGAGCTCAGCGGTG 2040
 QY 2460 GCGGTGGGTGCTTCCCTCTCTTCTCAACATCTGTGGCTTGTGTGCGCTTCTATACAG 2519
 Db 2041 GCGGTGGGTGCTTCCCTCTCTTCTCAACATCTGTGGCTTGTGTGCGCTTCTATACAG 2100
 QY 2520 CCGGACCGCGCGGAGCTGCGGTGCGAGGCGGCTTAGCCACCTGGCGGCTCAGGCTCT 2579
 Db 2101 CCGGACCGCGCGGAGCTGCGGTGCGAGGCGGCTTAGCCACCTGGCGGCTCAGGCTCT 2160
 QY 2580 GCGGTGCTGTGTGGGGCGCGCTGCTTCCCGCGCGCGGCGGTGAGCTGCCACCAAGAGAG 2639
 Db 2161 GCGGTGCTGTGTGGGGCGCGCTGCTTCCCGCGCGCGGCGGTGAGCTGCCACCAAGAGAG 2220

Db 901 AACTACAGCGCTCAAGTACACGCGCTGTGGCAGCAAGGTGGCGTGTGACCGGAG 960
 Qy 1380 GACAGTGTGAAGCTGTGAAGTGTCTGCGCGGAGAGCCCTCCCGGAGCTGTGAGACGAG 1439
 Db 961 GACAGTGTGAAGCTGTGAAGTGTCTGCGCGGAGAGCCCTCCCGGAGCTGTGAGACGAG 1020
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 Db 1021 GACGTGCAAGCTGTGCGGCTACCACTGCGCTTTGGGCGGCTGTGAGTGGGAGCTGTGTC 1080
 Qy 1500 CCCGATGACCTGTAGATCCTCATGACAGCAGGAGATTCCTCAACTACGACATGCTCATC 1559
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 Qy 1800 GTGCAACAGCTGTGGCGCTGCAAGCTGCAAGCGGACTACCAAGTCTCCCGCTACTTT 1859
 Db 1381 GTGCAACAGCTGTGGCGCTGCAAGCTGCAAGCGGACTACCAAGTCTCCCGCTACTTT 1440
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 Db 1621 TTCGCCAGCTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1680
 Qy 2100 AAGCCCAATCGCTTCGAGGAGTGGTGGAGCAAAATCAACAGCAAGGAGAGAGAGTAT 2159
 Db 1681 AAGCCCAATCGCTTCGAGGAGTGGTGGAGCAAAATCAACAGCAAGGAGAGAGAGTAT 1740
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 Qy 2280 CGCTGCTGCTTACGCGAGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2336
 Db 1861 CGCTGCTGCTTACGCGAGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1920
 Qy 2337 ACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2396
 Db 1921 ACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1980
 Qy 2397 AGGCGCTATGACCGCTTCCCGGCGGAGTCAAGGAGTCTCCAGCGAGCTGAGCGTCAAC 2456

Db 1981 AGGCGCTATGACCGCTTCCCGGCGGAGTCAACGCGGAGTACTCCACGAGAGTGTGACCGTACC 2040
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 Db 2041 GTGGCGCGTGGTGGCTCCCTCTCTTCAACATCTCTGGCGCTTTGGCTGCGCTCTACTAC 2100
 Qy 2517 AAGCGGAGCGGCGGAGAGTGGTGGAGCGGCTTAGCCCACTTGGCGGCTCAGGC 2576
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 Db 2221 GAGGAGCTGGTGTCTACTGAGCTGAAGCGGCGGCTGTGGCGTGGGCGGAGACCTTCCCGAG 2280
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 Qy 2934 GGT 2936
 Db 2521 GGT 2523

RESULT 6
 ABA94727
 ID ABA94727 standard; cDNA; 2863 BP.
 XX ABA94727;
 AC AC
 XX XX
 DT 23-APR-2002 (first entry)
 XX XX
 DE Human drug metabolizing enzyme (DME) cDNA (ID: 7473875CBL).
 XX XX
 KW Drug metabolizing enzyme; DME; antiallergic; antianemic; antiaesthetic;
 KW osteopathic; antirheumatic; antiarthritic; dermatological; nephrotropic;
 KW antinflammatory; vulnery; antibacterial; virucide; antiparasitic;
 KW protozoacide; fungicide; antihelminthic; cytostatic; ophthalmological;
 KW antiarteriosclerotic; hepatotropic; antidiabetic; anorectic; human;
 KW thrombolytic; metabolic; anticoagulant; antithyroid; gynecological;
 KW antiangular; antiulcer; antidiarrhoeic; laxative; enzyme; ss.
 XX OS
 XX Homo sapiens.
 XX Key
 FH Location/Qualifiers
 FT 177..2582
 FT /*tag= a
 FT /product= "DME"
 FT /transl_except= "(pos: 475..477, aa: Xaa)"
 FT /note= "Xaa = unknown"
 XX XX
 PN WO200204612-A2.
 XX XX
 PD 17-JAN-2002.
 XX XX
 PF 05-JUL-2001; 2001WO-US21324.
 XX XX
 PR 07-JUL-2000; 2000US-216804P.

Db 1435 ACCGGAAGGCAAGATGTGCTTCGGGAGACCATCAAGTTTATGTACAGACTGGGCGG 1494
 QY 1738 ACCGGACAATGGCAATGGCCGCAAAACCTGCTGCGCTCTTTACTACACCAACAT 1797
 Db 1495 ACCGGACAATGGCAATGGCCGCAAAACCTGCTGCGCTCTTTACTACACCAACAT 1554
 QY 1798 GGGTGGCAACAGCTGTGCGCACTGCAAGCTGCAAGCGGACTACAGTCTCCGCTTACT 1857
 Db 1555 GGGTGGCAACAGCTGTGCGCACTGCAAGCTGCAAGCGGACTACAGTCTCCGCTTACT 1614
 QY 1858 TTATACCTTTACACCACTGCAAGCGGAGGCGGCGCTGAGTGGGCGAGATCGGCGG 1917
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 Db 1675 ACGGGGATGAATGCGCTATGCTTTGGCGTGCCTGCGGAGTGGGCGGAGTGGGCGG 1734
 QY 1978 CCGTAACTTCTCCAAAGATGACGTGCTGCTGAGTGGCGGCTGATGACCTTACTGGACCA 2037
 Db 1735 CCGTAACTTCTCCAAAGATGACGTGCTGCTGAGTGGCGGCTGATGACCTTACTGGACCA 1794
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 Db 1795 ACTTGGCAAGACTGGGAGCCCAACCAAGCGGTCGCGAGATACCAAGTTCATCCACA 1854
 QY 2098 CCAAGCCCAATCGCTTCCAGAGAGTGTGTGAGCAATTCACAGCAAGGAGAGAGT 2157
 Db 1855 CCAAGCCCAATCGCTTCCAGAGAGTGTGTGAGCAATTCACAGCAAGGAGAGAGT 1914
 QY 2158 ATGTGCAATAGGCTGAAGCCAGCGCTGCGTGAACAATACCGGCGCAACAAAGTGGCGCT 2217
 Db 1915 ATGTGCAATAGGCTGAAGCCAGCGCTGCGTGAACAATACCGGCGCAACAAAGTGGCGCT 1974
 QY 2218 TCTGGCTGAGCTGTGCGCCACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCT 2277
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 Db 2035 CGCGCTGCTCCCTTACGCCAGCGGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 2094
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 Db 2215 TGGCGGTGGTGGCTTCCCTGCTTCCCTGCTTCCCTGCTTCCCTGCTTCCCTGCTTCCCT 2274
 QY 2518 AGCGGACCGCGGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2577
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 QY 2578 CTGGCTGCTTGGTGGGCGCGCTGCTTCCCGCGGCGGCGGCTGAGTGGTGGTGGTGGTGG 2637
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 Db 2395 AGGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2451

RESULT 7

AA05198

ID AA05198 standard; DNA; 1969 BP.

XX

AC

XX

DT 21-NOV-2001 (first entry)
 XX Human reproductive system related antigen DNA SEQ ID NO: 7886.
 DE Human reproductive system related antigen; reproductive system disorder;
 XX Human; gene therapy; ds.
 KW
 XX Homo sapiens.
 OS
 XX WO200155320-A2.
 PN
 XX 02-AUG-2001.
 PD
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 XX 17-JAN-2001; 2001WO-US01339.
 PF
 XX 31-JAN-2000; 2000US-0179065.
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 PR 08-DEC-2000; 2000US-0251989.
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 PR 11-DEC-2000; 2000US-0254037.
 PR 03-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI
 XX WPI; 2001-465570/50.
 DR
 XX
 PT Isolated nucleic acid molecule encoding a reproductive system antigen
 PT is used in preventing, treating or ameliorating a medical condition -
 XX
 PS Disclosure; SEQ ID NO 7886; 1297bp + Sequence Listing; English.
 XX
 XX The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
 XX
 SQ Sequence 1969 BP; 396 A; 594 C; 537 G; 442 T; 0 other;
 Query Match 34.7%; Score 1618.2; DB 22; Length 1969;
 Best Local Similarity 99.7%; Pred. No. 7.4e-278;
 Matches 1642; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
 QY 3021 GAGTCGTACACGCGCATCCAGCAGCGCTAAGTGGACATGGGATTCCTCCCTGCGATGCG 3080
 DB 1 GAGTCGTACACGCGCATCCAGCAGCGCTAAGTGGACATGGGATTCCTCCCTGCGATGCG 60
 QY 3081 TGTCTTTCCACGACGAGAGCCCGAGTCTTCTCTGATCTGGGCTTTGAAACAATG 3140
 DB 61 TGTCTTTCCACGACGAGAG-CCGAGTCTTCTCTGATCTGGGCTTTGAAACAATG 119
 QY 3141 GGGGGGTTTTCTCCCGCCCATTTGGACACACAGTCTTGGTGTGTGGATGTTGTTT 3200
 DB 120 GGGGGGTTTTCTCCCGCCCATTTGGACACACAGTCTTGGTGTGTGGATGTTGTTT 179
 QY 3201 CCCGGTGGAGGTGTCTTTCTCACAAGGGGTGTGTTTCCCATGTGCAGGTGAGGTT 3260
 DB 180 CCCGGTGGAGGTGTCTTTCTCACAAGGGGTGTGTTTCCCATGTGCAGGTGAGGTT 239
 QY 3261 TTTTGTGCAACCTGGACACATGTTGGCCCTCCCAAGAAATTTCTGCGGATTTGAC 3320
 DB 240 TTTTGTGCAACCTGGACACATGTTGGCCCTCCCAAGAAATTTCTGCGGATTTGAC 299
 QY 3321 CCAGAACTCTGTTCCCGCATCCCTTCTCCACCTCCCTCCCTCCCTCCCTCCCTCCCT 3380
 DB 300 CCAGAACTCTGTTCCCGCATCCCTTCTCCACCTCCCTCCCTCCCTCCCTCCCTCCCT 359
 QY 3381 CCTGGAAGTGTGTGTTCAATACAGTGACCTTGGCCACAGACACAGAGGATGAG 3440
 DB 360 CCTGGAAGTGTGTGTTCAATACAGTGACCTTGGCCACAGACACAGAGGATGAG 419
 QY 3441 CCTGGAAGTGTGTGTTCAATACAGTGACCTTGGCCACAGACACAGAGGATGAG 3500
 DB 420 CCTGGAAGTGTGTGTTCAATACAGTGACCTTGGCCACAGACACAGAGGATGAG 479
 QY 3501 GCGAAGCATGTTCCCGCGAGCGCCCTTGGCCACAGTCAAGTCAAGCATGTTCTGCGG 3560
 DB 480 GCGAAGCATGTTCCCGCGAGCGCCCTTGGCCACAGTCAAGTCAAGCATGTTCTGCGG 539
 QY 3561 GGGAGGCTTACCTTCCAGAGAGGACAGACAGATTTCTGCTGGGGAGGAGGAGT 3620
 DB 540 GGGAGGCTTACCTTCCAGAGAGGACAGACAGATTTCTGCTGGGGAGGAGGAGT 599
 QY 3621 CCACGCATCTGATGCTGCTGGAGCTTATTTTCCGTGGCCAGGACGATTTCTCTGA 3680
 DB 600 CCACGCATCTGATGCTGCTGGAGCTTATTTTCCGTGGCCAGGACGATTTCTCTGA 659

QY 3681 GTGGAAACAGGTTCTTGATGTGGATGTGTTTCCCAAGGACAGCGCCCTCTCTTCC 3740
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 QY 3741 CAGCACTTCCCTGCTTCCCAAGGCTCAGGCGCCAGCACTTCTCTCTCTCTCTCTCT 3800
 Db 720 CAGCACTTCCCTGCTTCCCAAGGCTCAGGCGCCAGCACTTCTCTCTCTCTCTCTCT 779
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 Db 780 GGTGAGCAGACACTTCTAGTTGGCAGGAGCTGAGAGGTTGAAACAAACCCGAGGAGGC 839
 QY 3861 CCGGCGCTTGTCTCCGAGTTGGGGGAGGGGTGTGCAAGTGTCCCTCCGAGGAGCA 3920
 Db 840 CCGGCGCTTGTCTCCGAGTTGGGGGAGGGGTGTGCAAGTGTCCCTCCGAGGAGCA 899
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 Db 900 CGCATGTTTGACAAAGCCCTCATTTGTCGAGGACAGGCTTTTCCCAAGGCTCAGA 959
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 Db 960 GCATTGCTCATCCGTGCGCAACTGGTAGGTGATTTGAGCGGAAAGACTCCCAATGT 1019
 QY 4041 GCCAAGAAATTTCCAGTCCAGGACAGGCGAGGGAATACTAAGGCGAAGCAGGATACAGGG 4100
 Db 1020 GCCAAGAAATTTCCAGTCCAGGACAGGCGAGGGAATACTAAGGCGAAGCAGGATACAGGG 1079
 QY 4101 CGAGGAGTGTGCGAGTGAAGGGGCTCCGCGTGTGCGGCTTCTCTCTCTCTCTCTCT 4160
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 QY 4221 ATCTCAGTGTGACACAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4280
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 QY 4401 GACAGGCTTGGGAGACACAGCAGGAGTAATTTGAAATGTGAGGTGATCTCTCTCTCT 4460
 Db 1380 GACAGGCTTGGGAGACACAGCAGGAGTAATTTGAAATGTGAGGTGATCTCTCTCTCT 1439
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 Db 1440 GGGCCTTGGGCTTGGGCAATTTGGGAAAGATGATGCTGGAAGGCTTAAGGAGACACAG 1499
 QY 4521 TGGACAGGAGAGTCT 4580
 Db 1500 TGGACAGGAGAGTCT 1559
 QY 4581 TAGGGCTTGGGCTGCTGCTTCCACTGACACCAAAATCCAGAAATCCCTGCTTGTAGT-C 4639
 Db 1560 TAGGGCTTGGGCTGCTGCTTCCACTGACACCAAAATCCAGAAATCCCTGCTTGTAGT 1619
 QY 4640 CCAGAACTTTCCTCTTGTGACTGTCCCT 4666
 Db 1620 CCAGAACTTTCCTCTTGTGACTGTCCCT 1646

RESULT 8
 ABL98083
 ID ABL98083 standard; DNA; 1969 BP.
 XX

AC ABL98083;
 XX 21-JUN-2002 (first entry)
 DT Human testicular antigen encoding DNA fragment SEQ ID NO: 2735.
 DE Human; testicular antigen; testes; cancer; metastasis; immune disorder;
 XX reproductive system disorder; urinary system disorder; gene therapy;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disease; infection; cytostatic; gene; ds.
 XX Homo sapiens.
 OS WO200155317-A2.
 XX 02-AUG-2001.
 PD 17-JAN-2001; 2001WO-US01329.
 PF 31-JAN-2000; 2000US-0179065.
 XX 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 13-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
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PR 05-DEC-2000; 2000US-0256719.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483232/52.
XX
XX Nucleic acids encoding 973 human testicular antigen polypeptides,
PT useful for preventing, diagnosing and/or treating testicular cancer
PT
XX
PS Disclosure; SEQ ID NO 2735; 765pp; English.
XX
CC The present invention provides the protein and coding sequences of 973
CC human testicular antigens, and fragments of their genomic sequences. The
CC sequences can be used in the treatment of cardiovascular, urinary system,
CC reproductive system, immune, respiratory, neurological and
CC gastrointestinal disorders, infections, and particularly cancer,
CC especially testicular cancers. The present sequence is a DNA encoding a
CC protein fragment of the invention.
XX
SQ Sequence 1969 BP; 396 A; 594 C; 537 G; 442 T; 0 other;

Query Match 34.7%; Score 1618.2; DB 23; Length 1969;
Best Local Similarity 99.7%; Pred. No. 7.4e-278; Indels 2; Gaps 2;
Matches 1642; Conservative 0; Mismatches 3;

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QY 3081 TGTCTTTCCACGAGAGAGCCAGTCTCTCTGTGATCTGGGCTTGGCAACTG 3140
DB 61 TGTCTTTCCACGAGAGAG-CCAGTCTCTCTGTGATCTGGGCTTGGCAACTG 119
QY 3141 GGGGGGTTTTCTCCGCCCATTTGGGACACCACTCTTGGTGTGGATGTGATTTT 3200
DB 120 GGGGGGTTTTCTCCGCCCATTTGGGACACCACTCTTGGTGTGGATGTGATTTT 179
QY 3201 CCCGGTGGAGTGTGCTTTCTCAACAGGGGTGTGTTTCCCATGTGAGGTGAGTT 3260
DB 180 CCCGGTGGAGTGTGCTTTCTCAACAGGGGTGTGTTTCCCATGTGAGGTGAGTT 239
QY 3261 TTTTGTGCGCCCTGGACACATGTTGGCCCTCAAGAATTTCTGTGGGATTTGTAC 3320
DB 240 TTTTGTGCGCCCTGGACACATGTTGGCCCTCAAGAATTTCTGTGGGATTTGTAC 299
QY 3321 CCAGAAATCCTGTTCCTCCCATCCTTCTCCCACTCTCCCTCTCCCTCCCTCCCTGAGA 3380
DB 300 CCAGAAATCCTGTTCCTCCCATCCTTCTCCCACTCTCCCTCTCCCTCCCTGAGA 359
QY 3381 CCTGGAAGTGTGTGTTTCAATACATGACGACCTTGGCCACAGACACAGAGGATGGAG 3440
DB 360 CCTGGAAGTGTGTGTTTCAATACATGACGACCTTGGCCACAGACACAGAGGATGGAG 419
QY 3441 CCTGGAAGCAGCAGGAAATCAGAGCCCTTCGCCCTCTCCCTCTCCCTCTCCCTGAGA 3500
DB 420 CCTGGAAGCAGCAGGAAATCAGAGCCCTTCGCCCTCTCCCTCTCCCTCTCCCTGAGA 479
QY 3501 GCGAAGCATGTTCCCTCCCGAGCCCTTGGCACAAGTCAATGAAGACGCTTCTGCGG 3560
DB 480 GCGAAGCATGTTCCCTCCCGAGCCCTTGGCACAAGTCAATGAAGACGCTTCTGCGG 539
QY 3561 GGGAGGCCCTCACCTTCCAGAGGAGCAGACAGATTTCTGTGGGGAGGAGGAGT 3620

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Db 540 GGGAGGCCCTCCTCCAGAGAGGACAGACACAGATTTCTGCTGGGGAGGAGAGT 599
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 Db 600 CCAGCATCTGATGCTGCTGGAAGCTATTTCTCCGCTGGCCAGGACGATTTCTCTCA 659
 Qy 3681 GTGGAAACAGGTTCTTGCAATGTGTGTGTTTCCCGAGGACAGCGGCCCTCTCTCC 3740
 Db 660 GTGGAAACAGGTTCTTGCAATGTGTGTGTTTCCCGAGGACAGCGGCCCTCTCTCC 719
 Qy 3741 CAGCATTCTCTCTCCCGAGGCTCAGGCCAGCAGCCAGCTTCTCTCATATGGCA 3800
 Db 720 CAGCATTCTCTCTCCCGAGGCTCAGGCCAGCAGCCAGCTTCTCTCATATGGCA 779
 Qy 3801 GGTGAGCACAGATCTTAGTGTGAGAGCTGAGAGGAGTGAACAAACCCCGAGGAGGC 3860
 Db 780 GGTGAGCACAGATCTTAGTGTGAGAGCTGAGAGGAGTGAACAAACCCCGAGGAGGC 839
 Qy 3861 CCGGCCCTTCTCCGAGTTGGGGAGGAGGAGTGTGCAACGTCGCCCGCAGAGGCCA 3920
 Db 840 CCGGCCCTTCTCCGAGTTGGGGAGGAGGAGTGTGCAACGTCGCCCGCAGAGGCCA 899
 Qy 3921 CGCATGTTTGACCAAGCCCTCATTTGTGTCCGAGGACAGCTTTTCCCGAGGCTCAGA 3980
 Db 900 CGCATGTTTGACCAAGCCCTCATTTGTGTCCGAGGACAGCTTTTCCCGAGGCTCAGA 959
 Qy 3981 GCATTGCTCATCGTGCACAACTGGGTAGTGTGATTTGACGGGAAGACTCCCAATGT 4040
 Db 960 GCATTGCTCATCGTGCACAACTGGGTAGTGTGATTTGACGGGAAGACTCCCAATGT 1019
 Qy 4041 GCCAAGAAATTTCCAGTCCAGGAGGAGGAGGAACTAAGGGCAAGCAGATACAGGG 4100
 Db 1020 GCCAAGAAATTTCCAGTCCAGGAGGAGGAGGAACTAAGGGCAAGCAGATACAGGG 1079
 Qy 4101 CGAGGATGTGGAGAGTGTGAGGAGGCTCCCGCTGTGCGCTTCTCTCAGCATGTCTCC 4160
 Db 1080 CGAGGATGTGGAGAGTGTGAGGAGGCTCCCGCTGTGCGCTTCTCTCAGCATGTCTCC 1139
 Qy 4161 CCAGCTGCTCAGTGTCTCGTCCCTTCATCTCCTGCTCCCTCTTTGAAGCTGTCCCC 4220
 Db 1140 CCAGCTGCTCAGTGTCTCGTCCCTTCATCTCCTGCTCCCTCTTTGAAGCTGTCCCC 1199
 Qy 4221 ATCTCAGTGTGAGAGGCTTCTCTCATGTACCACTCTCTGACCGAGGCGCCCT 4280
 Db 1200 ATCTCAGTGTGAGAGGCTTCTCTCATGTACCACTCTCTGACCGAGGCGCCCT 1259
 Qy 4281 CTTGTCTGAAGAAAGAGCTTTGAATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 4340
 Db 1260 CTTGTCTGAAGAAAGAGCTTTGAATGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1319
 Qy 4341 CCGACACAGTTGGGAGATGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4400
 Db 1320 CCGACACAGTTGGGAGATGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1379
 Qy 4401 GACAGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4460
 Db 1380 GACAGGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1439
 Qy 4461 GGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 4520
 Db 1440 GGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 1499
 Qy 4521 TGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4580
 Db 1500 TGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1559
 Qy 4581 TAGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 4639
 Db 1560 TAGGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1619
 Qy 4640 CCAGAACTTTGCTCTTGTGCTGCTTGTGCTGCTTGTGCTGCTTGTGCTGCTTGTGCTGCT 4665
 Db 1620 CCAGAACTTTGCTCTTGTGCTGCTTGTGCTGCTTGTGCTGCTTGTGCTGCTTGTGCTGCT 1646

RESULT 9
 AAV59639
 ID AAV59639 standard; DNA; 1446 BP.
 XX
 AC AAV59639;
 XX
 DT 19-JAN-1999 (first entry)
 XX
 DE Human secreted protein gene 129 clone HHSCV65.
 XX
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN WO9839448-A2.
 XX
 PD 11-SEP-1998.
 XX
 PF 06-MAR-1998; 98WO-US04493.
 XX
 PR 02-OCT-1997; 97US-0061060.
 PR 07-MAR-1997; 97US-0038621.
 PR 07-MAR-1997; 97US-0040161.
 PR 07-MAR-1997; 97US-0040162.
 PR 07-MAR-1997; 97US-0040163.
 PR 07-MAR-1997; 97US-0040333.
 PR 07-MAR-1997; 97US-0040334.
 PR 07-MAR-1997; 97US-0040336.
 PR 07-MAR-1997; 97US-0040626.
 PR 11-APR-1997; 97US-0043311.
 PR 11-APR-1997; 97US-0043312.
 PR 11-APR-1997; 97US-0043313.
 PR 11-APR-1997; 97US-0043314.
 PR 11-APR-1997; 97US-0043568.
 PR 11-APR-1997; 97US-0043569.
 PR 11-APR-1997; 97US-0043576.
 PR 11-APR-1997; 97US-0043578.
 PR 11-APR-1997; 97US-0043580.
 PR 11-APR-1997; 97US-0043669.
 PR 11-APR-1997; 97US-0043670.
 PR 11-APR-1997; 97US-0043671.
 PR 11-APR-1997; 97US-0043672.
 PR 11-APR-1997; 97US-0043674.
 PR 23-MAY-1997; 97US-0047492.
 PR 23-MAY-1997; 97US-0047500.
 PR 23-MAY-1997; 97US-0047501.
 PR 23-MAY-1997; 97US-0047502.
 PR 23-MAY-1997; 97US-0047503.
 PR 23-MAY-1997; 97US-0047581.
 PR 23-MAY-1997; 97US-0047582.
 PR 23-MAY-1997; 97US-0047583.
 PR 23-MAY-1997; 97US-0047584.
 PR 23-MAY-1997; 97US-0047585.
 PR 23-MAY-1997; 97US-0047586.
 PR 23-MAY-1997; 97US-0047587.
 PR 23-MAY-1997; 97US-0047588.
 PR 23-MAY-1997; 97US-0047589.
 PR 23-MAY-1997; 97US-0047590.
 PR 23-MAY-1997; 97US-0047592.
 PR 23-MAY-1997; 97US-0047593.
 PR 23-MAY-1997; 97US-0047594.
 PR 23-MAY-1997; 97US-0047595.
 PR 23-MAY-1997; 97US-0047596.
 PR 23-MAY-1997; 97US-0047597.

PR 23-MAY-1997; 97US-0047598.
 PR 23-MAY-1997; 97US-0047599.
 PR 23-MAY-1997; 97US-0047600.
 PR 23-MAY-1997; 97US-0047601.
 PR 23-MAY-1997; 97US-0047612.
 PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047632.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048974.
 PR 13-JUN-1997; 97US-0049610.
 PR 08-JUL-1997; 97US-0051926.
 PR 16-JUL-1997; 97US-0052874.
 PR 18-AUG-1997; 97US-0053724.
 PR 22-AUG-1997; 97US-0056630.
 PR 22-AUG-1997; 97US-0056631.
 PR 22-AUG-1997; 97US-0056632.
 PR 22-AUG-1997; 97US-0056636.
 PR 22-AUG-1997; 97US-0056637.
 PR 22-AUG-1997; 97US-0056662.
 PR 22-AUG-1997; 97US-0056664.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056862.
 PR 22-AUG-1997; 97US-0056864.
 PR 22-AUG-1997; 97US-0056872.
 PR 22-AUG-1997; 97US-0056874.
 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057669.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.
 XX
 (HUMA-) HUMAN GENOME SCI INC.

PA Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
 XX Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JW, Hu JS;
 PI Kyaw H, Laflair DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX WPI: 1998-506364/43.
 DR P-PSDB; AAW74857.

XX New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1; Page 364-365; 72lpp; English.

XX This sequence represents a nucleic acid molecule designated Gene 129

CC from the human cDNA clone HHSCV65 (deposited as clone ATCC 97902 and
 CC ATCC 209048) which encodes a secreted human protein. The gene can be
 CC used to generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).
 XX

SQ Sequence 1446 BP; 304 A; 419 C; 403 G; 312 T; 8 other;

Query Match 23.4%; Score 1092; DB 19; Length 1446;
 Best Local Similarity 99.0%; Pred. No. 1.5e-184;
 Matches 1133; Conservative 6; Mismatches 1; Indels 4; Gaps 4;
 3524 CCCCCTTGGCACAAGTCAGATGAAGCACGTTCTTCCGGGGAGGCCCTCACCTTCCAGAGA 3583
 Db 3 CCCCCTTGGCACAAGTCAGATGAAGCACGTTCTTCCGGGGAGGCCCTCACCTTCCAGAGA 62
 3584 GGACACACAGATTTCTCTGGGGAGGGAGAGTCCACGATCTCTGATGCTGCTGG 3643
 Db 63 GGACACACAGATTTCTCTGGGGAGGGAGAGTCCACGATCTCTGATGCTGCTGG 122
 3644 AAGCTTATTTTCCCGTGGCCAGGACGATTTCTCTGAGTGGAAACAGGTTCTTGTGATGTG 3703
 Db 123 AAGCTTATTTTCCCGTGGCCAGGATGATTTCTCTGAGTGGAAACAGGTTCTTGTGATGTG 182
 3704 GATGTGTGTTTCCCGAGGAGAGCGCCCTCTCTTCCAGAGCTTCCCTGCTCCCTCCAG 3763
 Db 183 GATGTGTGTTTCCCGAGGAGAGCGCCCTCTCTTCCAGAGCTTCCCTGCTCCCTCCAG 242
 3764 GCCTCAGGCCAGCACCCAGTTCCTCTCACATGGCAGGTGAGCAGAGACTTCTAGTTGG 3823
 Db 243 GCCTCAGG-CCAGCACCCAGTTCCTCTCACATGGCAGGTGAGCAGAGACTTCTAGTTGG 301
 3824 CAGGAGCTGAGGAGGTGAACAAACCCCGAGGAGGCCCGGCCCTTGTCTCCGAGTTGG 3883
 Db 302 CAGGAGCTGAGGAGGTGAACAAACCCCGAGGAGGCCCGGCCCTTGTCTCCGAGTTGG 361
 3884 GCGAGGGGTGGCAACGTCGCCCCCGCAGAGGCCACGATGTTTGACCAAGCCCTCA 3943
 Db 362 GCGAGGGGTGGCAACGTCGCCCCCGCAGAGGCCACGATGTTTGACCAAGCCCTCA 421
 3944 TTCTGCTCCGAGCACAGACCTTTTCCCGAGGCTTCAGAGCATTCGCTCATCCGTCGCAAACT 4003
 Db 422 TTCTGCTCCGAGCACAGACCTTTTCCCGAGGCTTCARAGCATTCGCTCATCCGTCGCAAACT 481
 4004 GGGTAGGTGGATTGAGCGGAAAGACTCCCAAAATGTGCAAGAAATTCCTCAGTCCAGG 4063
 Db 482 GGGTAGGTGGATTGAGCGGAAAGACTCCCAAAATGTGCAAGAAATTCCTCAGTCCAGG 541
 4064 CAGGGCAGGGGAAACTAAGGCAAGCAGGATACAGGGCGAGGATGTGGCAGGTGAGGGG 4123
 Db 542 CAGGGCAGGGGAAACTAAGGCAAGCAGGATACAGGGCGAGGATGTGGCAGGTGAGGGG 601
 4124 GTTCCCGCTGTGCCCTTCTCTCCTACCAATGTCCTCCACCTGCTCAGTCTCCGTT 4183
 Db 602 GTTCCCGCTGTGCCCTTCTCTCCTACCAATGTCCTCCACCTGCTCAGTCTCCGTT 661
 4184 CCGCTTCACTCGTCCCTCTTTGAAGCTGTCCCTCTCAGTGTACAGCAGGCTTC 4243
 Db 662 CCGCTTCACTCGTCCCTCTTTGAAGCTGTCCCTCTCAGTGTACAGCAGGCTTC 721
 4244 TCCTCATCTGACCACCTCTCTCTGACCGAGCGCCCTCTCTTGTCTGAAAGAGGAGCCT 4303
 Db 722 TCCTCATCTGACCACCTCTCTCTGACCGAGCGCCCTCTCTTGTCTGAAAGAGGAGCCT 780

11-APR-1997;	97US-0435801;
11-APR-1997;	97US-0436699;
11-APR-1997;	97US-043670P;
11-APR-1997;	97US-043671P;
11-APR-1997;	97US-043672P;
11-APR-1997;	97US-043674P;
23-MAY-1997;	97US-047492P;
23-MAY-1997;	97US-047500P;
23-MAY-1997;	97US-047501P;
23-MAY-1997;	97US-047502P;
23-MAY-1997;	97US-047503P;
23-MAY-1997;	97US-047581P;
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23-MAY-1997;	97US-047613P;
23-MAY-1997;	97US-047614P;
23-MAY-1997;	97US-047615P;
23-MAY-1997;	97US-047617P;
23-MAY-1997;	97US-047632P;
23-MAY-1997;	97US-047633P;
23-MAY-1997;	97US-048364P;
06-JUN-1997;	97US-048974P;
06-JUN-1997;	97US-049610P;
13-JUN-1997;	97US-051926P;
16-JUL-1997;	97US-052874P;
18-AUG-1997;	97US-055724P;
22-AUG-1997;	97US-056630P;
22-AUG-1997;	97US-056631P;
22-AUG-1997;	97US-056632P;
22-AUG-1997;	97US-056633P;
22-AUG-1997;	97US-056637P;
22-AUG-1997;	97US-056662P;
22-AUG-1997;	97US-056684P;
22-AUG-1997;	97US-056852P;
22-AUG-1997;	97US-056864P;
22-AUG-1997;	97US-056872P;
22-AUG-1997;	97US-056874P;
22-AUG-1997;	97US-056875P;
22-AUG-1997;	97US-056876P;
22-AUG-1997;	97US-056877P;
22-AUG-1997;	97US-056878P;
22-AUG-1997;	97US-056879P;
22-AUG-1997;	97US-056880P;
22-AUG-1997;	97US-056888P;
22-AUG-1997;	97US-056891P;
22-AUG-1997;	97US-056882P;
22-AUG-1997;	97US-056884P;
22-AUG-1997;	97US-056886P;
22-AUG-1997;	97US-056887P;
22-AUG-1997;	97US-056888P;
22-AUG-1997;	97US-056889P;
22-AUG-1997;	97US-056892P;
22-AUG-1997;	97US-056893P;
22-AUG-1997;	97US-056894P;

3 isoform protein encoding sequence.

Neuroprotective; immunomodulator; cancer; chromosome Xq13.1;
cytostatic; anti-inflammatory; gene therapy; nutritional supplement;
wound; burn; ulcer; Alzheimer's disease; Huntington's disease;
amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
vulnerary; gene; ss.

Homo sapiens.

WO200231111-A2.

18-APR-2002.

11-OCT-2001; 2001WO-US27760.

12-OCT-2000; 2000US-0687527.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
Xue AJ, Yang Y, Wehrman T, Drmanac RT;

WPI; 2002-426278/45.

N-PSDB; ABP43803.

New polypeptides and their encoded proteins, useful as nutritional
PT sources or supplements, or in gene therapy, particularly for treating
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
PT inflammation

Claim 1; SEQ ID # 260; 357pp + sequence listing; English.

The invention relates to 446 newly isolated polynucleotide sequences.
CC The activity of polynucleotides of the invention may be described as,
CC vulnary, neuroprotective, immunomodulator, cytostatic and
CC anti-inflammatory. Compositions comprising nucleic acids of the invention
CC are useful for treating a mammalian subject, or as nutritional sources or
CC supplements. These are useful in gene therapy, particularly for treating
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC inflammation. The nucleic acids and polypeptides are also useful in
CC diagnostic and research methods. The sequences given in records
CC AB060788-AB061233 represent polynucleotides of the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 2865 BP; 593 A; 906 C; 772 G; 594 T; 0 other;

Query Match 21.7%; Score 1014.2; DB 24; Length 2865;
Best Local Similarity 65.3%; Pred. No. 9.8e-171; Indels 63; Gaps 4;
Matches 1584; Conservative 0; Mismatches 778;

417 AGCATGTGGCTTCCTGGCGCTGTGTCCTGGTGGGCTGGCGGGGTCAACCGCGGGAGGG 476
329 AACATGTGGCTGGCGCTGGCGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 388
477 GGTCCCG 536
389 AGGAGCCTGTGCTCACCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
537 CGCTTCCTGGCTGGTGAACACCGCTACGGCGAGTGGCGCGTGGCGCGCGAGCTCAAC 596
449 CAGCACCCACAGTCAACACTCATTTGGGAGCTAAGGGGTGCCGAGTACCACTGCC 508
597 AACGAGATCTTGGGCGCGCTGGTGGAGTTCTTGGGCGTGGCGCTACGCCACCGCGCGCTG 656
509 AGTGAGATCTTGGGCGCTGTGGACCAATACCTGGGCGTGGCGCTACCGAGCTCCCGCGATC 568
657 GCGCGCGCGCTTCCAGCGCGCTGAGCGCGCGCGCTGCTGGCGCGCGCTGCGCAAGCGCC 716

Db QY 569 GGCGAGAAACGTTTCTGCCCCCTGAACACACCCCCATCTCTGTCGGGCAATCGGAAGCC 628

QY 717 ACCACCTGCGCGCGCTGCCCCGAGAACCTGACGGGGCGCTGCCCGCATCATGCTG 776

Db 629 ACACACTTTCCTCCAGTGTGCCCCAGAACATCACACAGCTGTGCCCGAAGTCATGCTG 688

QY 777 CTTGTGTGTTTACCGACAACCTTGGAGGGCGCGCGCACCTACGTGAGACACGAGCGAG 836

Db 689 CCGTCTGTGTTTCACTGCCAACTTGGATATGCTGCTGCTTACATCCAGGAGCCCAAGAA 748

QY 837 GACTGCTGTACCTCAACCTTCTACGTGCCCCACCGAGGACGCTCCGCTCAAAAAAAGCT 896

Db 749 GACTGCTCTACCTGAGAGCTGTATGTGCGAGCGAGATGATCCGCGCGCTAAGAAACAG 808

QY 897 GACGA-----GGCGAGCTCAATCCGCCAGACACAGATATCGTGACCTTGGGAAG 947

Db 809 GCGGAGGACTTAGCGGATAATGACGGGATGAAGATGAAGACATCCGGGACAGTGTGCT 868

QY 948 AAGCTCTGTATGCTGTTTCTCCATGCGGCTCTACATGAGGGGACCGGAAACATGTTT 1007

Db 869 AAACCGTCTATGCTTACATCCACGGAGCTCTTACATGGAAGGACAGGCAACATGATT 928

QY 1008 GATGCTCAGTCTGCTGCTATGGAACAGCTATTGTAGCCAGCTCACTACCTACCTT 1067

Db 929 GATGCGAGCATCTCGCCAGTTATGGCAATGTCATGCTCATCCCTCAACTATCGGGTT 988

QY 1068 GGGTGTCTGGTCTTCTCAGCACGGGACAGGCTGCAAAAGGCAACTATGGGCTCCTG 1127

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QY 1128 GACGAGATCCAGGGCTCGCTGCTCAGTGAAGAAACATCCGCCACTTTGGGGGAGACCC 1187

Db 1049 GACCAGATCCAGGGCTCGCTGCTGAGGAGATATGCTCTTCTCGGGGAGACCC 1108

QY 1188 GAGGTATCACCATCTTGGTTCGGGCGAGGGGCTCTCGCTCAACCTCTGATCCTC 1247

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QY 1308 AGTGTGTCTGCTAACCTACAGCCGCTCACTACAGCGGCTGCTGGCGACCAAGTGGGC 1367

Db 1229 AGCTGGGCTGTGAATCTACCAACAGTGAAGTACACCGCTGCTGGCAGACAAAGTGGGC 1288

QY 1368 TGTGACCGGAGGAGCAGTGTGAAGCTGTGAGTGTGTCGCCCGGAGAGCCCTCCCGGAG 1427

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QY 1428 CTGTTGACCGAGGAGCTGACGCTGCGCTGACCATGCTGCTTGGGCGCTGCTGCTGCTG 1487

Db 1349 CTGTTGAGGAGGAGCATCCAGCGAGCGCTTACCAGCTGCTGCTGCTGCTGCTGCTGCTG 1408

QY 1488 GCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1547

Db 1409 GGTGATGCTATCTGCTGATGACCTGAGATCTCTATGAGGAGGCGGCTGCTGCTGCTGCTG 1468

QY 1548 GACATGCTCATCGGCTCAACCGAGGAGGCGCTCAAGTTCTGTTGAGGAGCTTGCAGAG 1607

Db 1469 GACATCATGCTAGTGTCAACCGAGGCGAGGCTCTCAAGTTTGTGGAAGGGTGTGAGAC 1528

QY 1608 ACGGAGGAGGCTGCTGCTGCGAGCGCTTTCAGCTTCACTGCTCCCACTTTTGGGACAA 1667

Db 1529 CTTGAGGATGCTGCTGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1588

QY 1668 CTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1727

Db 1589 CTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1648

QY 1728 GACTGCGCGAGCCGAGGAGCAATGGCGAATGGCGCGCAAAACCTGCTGGCGCTGCTTACT 1787

Db 1649 GACTGCGGAGACCGTGAACAAACCTGAGACCGCGCGCTGAGAAACACACTGCTGCTTACT 1708

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 1848 CCGCTACTCTTTACACCTTTACACCACTGTCAGCGCGGAGCGGCGCTGAGTGGCA 1907
 1769 CTTACCTACTCTTACGCTTTTATCATCTACTGCAGAGCCTCATGAAGCTGCTTGGTCA 1828
 1908 GATCGCGCGACGGGATGAATGCGCCCTATGCTTTGGCGTGCCTGATGCTGGTGCAC 1967
 1829 GATGCACTCATGGGATGAATGAGTACCTATGTTTGGGGTTCCTATGATGAGCCCACT 1888
 1968 GACCTCTTCCCTGTAACTTCTCCAAAGATGAGTCACTGCTGAGTCCGCTGCTGATGACC 2027
 1889 GACCTTTTCCCTGCACTTCTCCAAAGATGATGTTATGCTCAGTCTGCTGCTGATGACC 1948
 2028 TACTGACCAACTTCGCGAAGCTGGGACCCCAACACAGCGGTGGCGAGATACCAAG 2087
 1949 TATTGACCAACTTTGCCAAGCTGGGATCCCAACAGCGGTGCCCGAGGACCAAG 2008
 2088 TTTATCCACACCAAGCCCAATCTTTCGAGGAGTGTGTGGAGCAATTCACACAGCAAG 2147
 2009 TTTATCCACACCAAGCGCACTTTCGAGGAGTGTGTGGAGTGTGTGGAGTGTGTGGAG 2068
 2148 GAGAAGCAGTATCTGCACATAGCTTGAAGCCAGCGCTGCTGAGCAACTACCGCGCAAC 2207
 2069 GACCACTCTTACCTTCACTCGGCTGAAACCAAGGCTCCGAGATCATTTACCGGCACT 2128
 2208 AAGGTGGCTTCTGGTGGAGCTGTGCGCCACCTGCACAACTGCACACGAGGCT--- 2264
 2129 AAGGTGGCTTCTGGAAACATCTGTGGCGCCACCTATACAACTGATGATGATGATGATG 2188
 2265 -----TTACACCAACCAAGCGCTGCTGCTTACGCGGCTGCGGCTGCTGCTGCTGCT 2318
 2189 TATACGTTCACCAACCAAGGCTGCGCTCGGATACCAACGCTCCACATCAC 2248
 2319 CCGCTGGCGCCCGGCGACACCGCGCGCGCGCGCTGCGGCTGCGGCTGCGGCGG 2378
 2249 CGCAGGCGCAATGCGAAGCTGCGGACCAAGCGCGCGCGCGCTGCGGCTGCGGCT 2308
 2379 GAGCGCGAGCGC-----GGCCCAAGGCGCTTATGACCGCTTCCCGCGG 2420
 2309 AAGGAGTATCCCAAGGCTGCGGACCGGACGAGATGCGAGGCTGCTGCTGCTG 2368
 2421 GACTCAGCGGACTACTCCAGGAGTGAAGTCAACCGTGGCGCTGCTGCTGCTGCTG 2480
 2369 AAGCGTGTGACTACTCACTGAATTAAGTGTCAACATCGCGCTGCGGCGCTGCTGCT 2428
 2481 TTCTCAACATCTGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2540
 2429 TTCTTTAACGTTTGTGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2488
 2541 CGGTGAGGCGGCTTATGCCCACTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 2600
 2489 CCGCTGCGGAGCGCTAGC-----CCTCAGCGGCGAGCC 2521
 2601 CTGCTCCCGCGCGCGCGCTGAGTCTCCACAGAGAGAGTGTGCTGCTGCTGCTG 2660
 2522 GGGCGCGCGAGTGTGGAGTGTCTCCAGAGGAGAGTGTGCGACATTAACATTAAC 2581
 2661 AAGCGGCGGTGTGCGCTGCGGCGCGGAGCTTCCGAGGAGTGTGCGGCGCTGCTGCT 2720
 2582 ACCACACAGAGTGTGAGCGCGGCTGCGGCGCGGCTGCGGCGCTGCTGCTGCTGCT 2641
 2721 GACTACACCTTGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2780
 2642 GACTACACCTTGGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2780
 2781 CTGACCTTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2805
 2702 ATCACTATGATCCCAACTCCCTGG 2726

RESULT 12
 AA45600
 ID AA45600 standard; cDNA; 4233 BP.
 XX
 AC AA45600;
 XX
 DT 06-APR-2000 (first entry)
 XX
 DE cDNA sequence of human neuroigin-3 (NL-3) gene clone #4.
 XX
 KW Human; PCTG4 region; X chromosome; q13 region; polymorphism;
 KW mental retardation; autism; depression; bipolar affective disorder;
 KW hypothyroidism; OPA gene; neuropsychiatric disorder; neuroigin-3;
 KW NL-3; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9955915-A2.
 XX
 PD 04-NOV-1999.
 XX
 PF 29-APR-1999; 99WO-US09365.
 XX
 PR 29-APR-1998; 98US-0083465.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Philibert RA, Gimms EI;
 XX
 DR WPI; 2000-126357/11.
 XX
 PT Identification of polymorphisms in the PCTG4 region of Xq13 for
 diagnosing mental retardation or autism -
 XX
 PS Example 7; Page 74-76; 100pp; English.
 XX
 CC The present sequence represents the cDNA sequence of a human
 CC neuroigin-3 (NL-3) clone, isolated from heart. The NL-3 gene is
 CC derived from the human PCTG4 region of chromosome Xq13. Polymorphisms
 CC in this region are associated with mental retardation, autism,
 CC depression, bipolar affective disorder or hypothyroidism. One 12 bp
 CC insertion polymorphism occurs within the coding region of the human
 CC OPA gene, and introduces a 4 amino acid insertion in a putative OPA
 CC domain. This domain has been shown to be involved in tissue specific
 CC expression. Another polymorphism consists of a pentanucleotide
 CC repeat approximately 7 kb upstream of the 12 bp polymorphism. Another
 CC polymorphism consists of a dinucleotide repeat approximately 4.5 kb
 CC downstream of the 12 bp polymorphism. The specification describes a
 CC method for screening for polymorphisms in a PCTG4 nucleic acid sequence
 CC obtained from a subject. The PCTG4 related sequences within the q13
 CC region of the X chromosome have polymorphisms associated with
 CC neuropsychiatric disorders. The methods can be used to screen for the
 CC presence of a heritably linked form of mental retardation, autism,
 CC depression, bipolar affective disorder or hypothyroidism.
 XX
 SQ Sequence 4233 BP; 945 A; 1279 C; 1097 G; 906 T; 6 other;
 Query Match 21.7%; Score 1011.2; DB 21; Length 4233;
 Best Local Similarity 65.5%; Pred. No. 3.5e-170;
 Matches 1589; Conservative 0; Mismatches 773; Indels 64; Gaps 5;
 QY 417 AGCATGTGGCTCCTGGCGCTGTGTCTGTGGGGTGGCGGGGCTCAACGCGGGGAGGG 476
 DB 404 AACATGTGGCTGCGGCTTGGCGCGCTGCTGCTGCTGAGCCCCAACGCCACGTTGGC 463
 QY 477 GGTCCCGCGGCGGCG 536
 DB 464 AGGAGCTGTGCTCCTCACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
 QY 537 CGCTTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 596

Db 524 CCAGCACCACAGTCAACTCACTTTGGGAAGCTAAGGGGTGCGCGAGTACCACCTGCCC 583
 Qy 597 AACGAGATCTGGGCGCCGCTGTCAGTTCTTTGGCGTGCCTTAGCGCACGCGCCCTG 656
 Db 584 AGTGAGATCTGGGCGCTGTGGACCAATACCTTGGGGTGCCTACGACGTCCTCCCGATC 643
 Qy 657 GGGCGCGCGCTTCAGCGGCTGAGGGCGCGGCTGTCGCGCGCGGTGGGCAACGCC 716
 Db 644 GGGGAGAAAGTTCTGCGCCCTGAAACACCCCATCTCTGTGGGCAATCCGGAACGCC 703
 Qy 717 ACCACCTGCGCGCGCTGCGCGCAGAACCTGACGCGGCGTGCCTCCCATCATGCTG 776
 Db 704 ACACATTTCCCGAGTGGCCCGCAGAACATCCACAGCTGTGCCGAGTCACTGCTG 763
 Qy 777 CCTGTGTGTTACCGACAAATTTGGAGGCGCGCGCACCTAGTGAGAACACAGAGCGAG 836
 Db 764 CCGGTCTGTTCACTGCGCAACTTGGATATCGTCGCTACTTATACATCAGAGGCCAACGAA 823
 Qy 837 GACTGCTGTACCTCAACCTTAGCTGCGCCACCGAGCGGTCCGCTCAAAAAGAAAGCT 896
 Db 824 GACTGTCTTACCTGAACTGATATGTCGCGAGCGAGATGGATCCGCGCTAAGAAACAG 883
 Qy 897 GACGA-----GGCGAGCTCAATCCGCCAGACACAGATATCCGTGAACCTGGGAAG 947
 Db 884 GCGGAGACTTAGCGGATATGACGGGATGAAGATGAAGACATCCGGGACAGTGTGCT 943
 Qy 948 AAGCTGTGATGCTGTTCTCCATGGCGGCTCCTACATGGAGGGACCGGAACATGTTTC 1007
 Db 944 AAACCCGCTATGCTTACATCCAGGAGCTTTACATGAGAGGACAGCAACATGATT 1003
 Qy 1008 GATGGCTCAGTCTGGGCTGCTATGGAACGCTCAATTTAGCCACGCTCAACTACCGTCTT 1067
 Db 1004 GATGGAGCATCTCGGAGTATGGAATGTATAGTATCATCCCTCAACTATCGGTT 1063
 Qy 1068 GGGGTGTGCTGTTCTAGCACCGGGACAGGCTGCAAAAGGCAACTATGGCTCTG 1127
 Db 1064 GGAAGTATAGTCTTCTGAGTACTGAGATCAGGCTGCCAAGGCAACTATGGGCTCCT 1123
 Qy 1128 GACAGATCCAGGCGCTGCGTGCCTGAGTGAACATCCGCCACTTTGGGGCGCACCCC 1187
 Db 1124 GACAGATCCAGGCGCTGCGTGCCTGAGGAGATATGCTCTTTCGGGGAGACCCC 1183
 Qy 1188 GAGGATACCACTTTTGGTTCCGGGCGAGGGCTCCTGCGTCAACTTCTGTATCTC 1247
 Db 1184 CGCGGATCACTGCTTTGGCTCGGCAATGGTGCATCTCGCTCAGCTCTCAGCTTG 1243
 Qy 1248 TCCACCATTCAGAGGCTTTCCAGAGGCAATCCCGAGAGTGCAACCGCATTTCC 1307
 Db 1244 TCACATCACTCAGAGGGACTTTTCCAGAGGCAATCCAGAGTGTCTGCTGTCTGTC 1303
 Qy 1308 AGCTGGTGTCAACTACAGCGCTCAAGTACACGCGCTGTGGCAGCAAGGTGGC 1367
 Db 1304 AGCTGGGCTGTGAATCAACAGTGAAGTACACCGCTGTGGCAGACAAAGTGGC 1363
 Qy 1368 TGTGACGAGAGGACAGTGTGAAGCTGTGAGTGTCTGCGCGGAAGCCCTCCCGGAG 1427
 Db 1364 TGTATGTGCTGGACACCGTGGATATGTGTGACTGTCTCGGCAAAAGAGTGCCAGGAG 1423
 Qy 1428 CTGTGGACGAGGAGCTGAGCTGCGCTACACATCGCTTTGGGCGCGTGGTGGAT 1487
 Db 1424 CTGTGAGAGGAGACATCCAGCGAGCGCTACCACTGCGTGGCTTTGGCCCTGTGATTGAT 1483
 Qy 1488 GCGAGCTGTGCTCCGATGACCTGAGATCTCTATGAGAGGAGAAATCTCTCAACTAC 1547
 Db 1484 GGTGATGTCAATCTGTGATGACCTGAGATCTCTATGAGAGGAGGAGTCTCTCAACTAT 1543
 Qy 1548 GACATGCTCATCGGCTCAACACAGGAGAGGCGCTCAAGTTCTGTGGAGACTCTGACAG 1607
 Db 1544 GACATCATCTAGTGTCAACCGAGGCGAGGCTCTCAAGTTTGTGGAAGGCTGTGAGC 1603
 Qy 1608 AGCGAGGAGGCTGTCTGCCAGCGCTTTGACTTCACTGTCTCAACTTTGTGGACAAC 1667
 Db 1604 CTTGAGGAGTGTCTCTGGCACTGACTTTGACTATTCCGTCTCCAAATTTTGTGGAACAAT 1663

Qy 1668 CTGTATGGCTTACCGGAAGGAGGATGCTTCTCGGAGACCATCAAGTTTATGTATACACA 1727
 Db 1664 CTGTATGGCTTATCTCTGAGGTAAGGACACCTCTCGAGAGACCATCAAGTTTCAIGTATACA 1723
 Qy 1728 GACTGGGCGGACCGGGAACAATGCGGAATGCGCGCAAAACCCCTGTGTGGGCTCTTTACT 1787
 Db 1724 GACTGGGACAGCGGTGACAACCTGAGACCGCGCGTAAACACTGTGGTGGCACTCTTCACT 1783
 Qy 1788 GACACCAATATGGTGGGACACAGCTGTGGCCACTGCCAAGCTGCACGCGACTACCACTCT 1847
 Db 1784 GACCACAGTGGTGGAGCCCTCAGTGGTGACAGCCGATCTGATGCCCGCTACGCTCG 1843
 Qy 1848 CCGCTCTACTTTTACACTTCTACCACTGCGAGCGGAGGCGCGCTGTAGTGGCA 1907
 Db 1844 CTTACTTACTTCTACGCTTCTATCATCTGCGAGAGCCTCATGAAGCCTGCTTGTGCA 1903
 Qy 1908 GATCGGCGACCGGGATGAATGCTCCCTATGCTTTGGCGTGCCTAGTGGTGGGTCACAC 1967
 Db 1904 GATGAGCTCATGGGATGAAGTACCTATGTTTTGGGGTTCCTATGGTAGGCCCCACT 1963
 Qy 1968 GACTCTTCCCTCTGTAATCTTCTCAAGATGAAGTCACTGCTCAGTGGCTGGTCAAGC 2027
 Db 1964 GACTTTTCCCTGCACTTCTCAAGATGATGTTATGCTCAGTGTCTGTCATGACC 2023
 Qy 2028 TACTGGACCAACTTGGCAAGACTGGGGAACCCCAACAGCGGTCGCGAGGATACCAAG 2087
 Db 2024 TATTGGACCAACTTGGCAAGACTGGGATCCCAACAGCGGTCGCCAGGACACCAAG 2083
 Qy 2088 TTCTATCCACCAAGCCCAATCGTTCGAGGAGTGTGTGGAGCAAAATCAACAGCAAG 2147
 Db 2084 TTCTATCCACCAAGCCCAACCGCTTTGAGGAATGCGCTGGTCCAAATCAATCCCGGA 2143
 Qy 2148 GAGAAGCAATATGCAATAGGCTTGAAGCCACGCTGCGTGAACAATACCGCGCAAC 2207
 Db 2144 GACAGCTCTTACTTCACTCGGCTGAACCAAGGTCGAGATCATTAACGGGCACT 2203
 Qy 2208 AAGTGGCTCTTGGCTGAGACTCGTCCCGCTGACACCTGCAACCTGCAACGAGCTC 2264
 Db 2204 AAGTGGCTCTTGGAAACATCTGGTGGCCCACTATACAACTGCAATGATGATGTCAC 2263
 Qy 2265 -----TTACCAACCAACCGCTGCTCCCTACGCGAGCGCTGCGCGCTGCTGCC 2318
 Db 2264 TATAGTCCACCAACCAAGTGCCTCGGATACCAACAGCTCCACATCACT 2323
 Qy 2319 CCGCTGCGCGCGCGGACAGCGCGCCCGCGCTGCGCTGCAACCTGCTCCCGAGCGC 2378
 Db 2324 CGCAGCGCAATGGCAAGACTGGAGCAACCAAGCGCGAGCCATCTCACCTGCTTACAGC 2383
 Qy 2379 GAG-----CCGAGCGCGCGCCCAAGGGCTATGACCGCTTC--CCCGG 2419
 Db 2384 AACGAGATGCCAGGGGTCTTGNAACGGGACCAAGGATGCCAGGCGCACTCTCTGGTGA 2443
 Qy 2420 GGAATCAGGGAGTACTCCAGGAGTGAAGCTGACCGTGAACCGTGGCGTGGTGGCTCTCT 2479
 Db 2444 GAACCTCGTGACTACTCCACTGAATTAAGTGTACCACTCGCGTGGGGGCTCTCTCTCT 2503
 Qy 2480 CTTCTCTCAACATCTGCGCTTGTGCTGCTTACTTACAAAGCGGAGCGCGCGAGGAGCT 2539
 Db 2504 GTTCTCTAACGTTTCTGGCGCTTCTGCTGCTTCTTACTTACCGTAAGGACAAACCGCGCAGGA 2563
 Qy 2540 GCGGTGCGAGCGGCTTAGCCCACTTGGCGGCTCAGGCTCTGCGGTGCTGTTGGGGGCCC 2599
 Db 2564 GCCCTCGGCGAGCTAGC-----CCTCAGCGGGGAGC 2596
 Qy 2600 CTGTCTCCCGCGCGCGCGCTGAGTGCACACAGAGGAGGAGTGTGTCACTCAGCT 2659
 Db 2597 CGGGGCGCGGAGTGGGAGTGTGCGAGAGGAGTGTGCGAGCATTACAACTGGGCCC 2656
 Qy 2660 GAAGCGGGTGTGCGTGGGGCGGACCCCTGCGAGGCTCTGCGCGCTGCTGCGCGCC 2719
 Db 2657 CACCCACACAGTGTGAGCGCGGCTCCCCCATGACACGCTGCGCTCACTGCTGCTGCTG 2716

QY 2720 CGACTACACCTGGCCCTGGCCGGGACCGAGATGTGCTCTCTTGGCCCCCGGGC 2779
 Db 2717 CGACTACACCTGGCCCTGGCCGGGACCGAGATGTGCTCTCTTGGCCCCCGGGC 2776
 QY 2780 CTTGACCTGCTGCCAGTGGCCCTGG 2805
 Db 2777 CATCACTATGATCCCACTCCCTGG 2802

RESULT 13
 AAS74457
 ID AAS74457 standard; cDNA; 4975 BP.
 XX
 AC AAS74457;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #10261.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR P-PSDB; ABG10270.
 XX
 XX

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
 Claim 1; SEQ ID No 10261; 103pp; English.
 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
 Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 4975 BP; 1159 A; 1618 C; 1170 G; 1024 T; 4 other;
 Query Match 19.9%; Score 930.4; DB 23; Length 4975;
 Best Local Similarity 91.5%; Pred. No. 7.5e-156;

Matches 1071; Conservative 0; Mismatches 22; Indels 78; Gaps 5;
 QY 1425 GAGCTGGTGGACGAGAGCTGAGCCTGCCCC---GCTACCAACATGCGCTTTGGGCCCCGTG 1481
 Db 298 GGGGTGCTCGGCCGTACTCACAGCTTGGCTTACCATGAGCTTGGGCCCCGTG 357
 QY 1482 GTGGATGGGACGTGGTCCCGATGACCTGAGATCCTCATGACGAGGAGAAATCTCTC 1541
 Db 358 GTGGATGGGACGTGGTCCCGATGACCTGAGATCCTCATGACGAGGAGAAATCTCTC 417
 QY 1542 AACTACGACATCTCATCGGCTCAACGAGGAGAGGCGCTCAAGTTGCTGAGGACTCT 1601
 Db 418 AACTACGACATCTCATCGGCTCAACGAGGAGAGGCGCTCAAGTTGCTGAGGACTCT 477
 QY 1602 GCAGAGAGGAGGAGCGGTGTCTGCCAGCGCTTTGACTTCACTGTCTCAACTTTGTG 1661
 Db 478 GCAGAGAGGAGGAGCGGTGTCTGCCAGCGCTTTGACTTCACTGTCTCAACTTTGTG 537
 QY 1662 GACAACTGTATGGCTACCCGGAAGCAAGGATGTCTTCGGGAGACCATCAAGTTTATG 1721
 Db 538 GACAACTGTATGGCTACCCGGAAGCAAGGATGTCTTCGGGAGACCATCAAGTTTATG 1721
 QY 1722 TACACAGACTGGGCGGACCGGACCAATGCGAAATGCGCGCAAAA---CCCTCTGGCGCT 1780
 Db 571 -----ACTGGCGCGACCGGACCAATGCGAAATGCGCGCAAAA---CCCTCTGGCGCT 623
 QY 1781 CTTTACTGACCAACCAATGGGTGGGACCACTGCGGCTGCGGCTGCGGCGGCTG 1840
 Db 624 CTTTACTGACCAACCAATGGGTGGGACCACTGCGGCTGCGGCTGCGGCGGCTG 683
 QY 1841 CCAGTCTCCGCTCTACTTTTACACCTTTTACACCACTTCCAGGCGGAGGGCGGCGCTGA 1900
 Db 684 CCAGTCTCCGCTCTACTTTTACACCTTTTACACCACTTCCAGGCGGAGGGCGGCGCTGA 743
 QY 1901 GTGGGAGATGCGGCGGACCGGAGTGAATGCGGCTTGTCTTTGGCGTGCCTATGTTGGG 1960
 Db 744 GTGGGAGATGCGGCGGACCGGAGTGAATGCGGCTTGTCTTTGGCGTGCCTATGTTGGG 797
 QY 1961 TGCCACCGACCTCTCCCGCTGTAACTTCTCCAGAAATGACGTGCTCAGTGGCGGTGTG 2020
 Db 798 -----GATGAGCTGCTCAGTGGCGGTGTG 824
 QY 2021 CATGACCTACTGGACCAACTTCCGAAAGTGGGACCGGCAACCGAGCGGTGCGGACGAG 2080
 Db 825 CATGACCTACTGGACCAACTTCCGAAAGTGGGACCGGCAACCGAGCGGTGCGGACGAG 884
 QY 2081 T-ACCAAGTTTATCCACACCAAGCGCTTCCGAGGAGTGTGTGGAGCAAAATTC 2139
 Db 885 TAACCAAGTTTATCCACACCAAGCGCTTCCGAGGAGTGTGTGGAGCAAAATTC 944
 QY 2140 ACAGCAAGGAGAGGAGTATCTGCACATAGGCTTGAAGCCAGCGTGTGACAACTACC 2199
 Db 945 ACAGCAAGGAGAGGAGTATCTGCACATAGGCTTGAAGCCAGCGTGTGACAACTACC 1004
 QY 2200 GCGCCAAAGGTGGCTTCTGGCTGGAGTCTGCGCCCACTGACACCTGACACGAGG 2259
 Db 1005 GCGCCAAAGGTGGCTTCTGGCTGGAGTCTGCGCCCACTGACACCTGACACGAGG 1064
 QY 2260 AGCTCTTACCAACACCAAGCGCTTCCCTAGCCACGCGCTGCGCGCTCGTCCCC 2319
 Db 1065 AGCTCTTACCAACACCAAGCGCTTCCCTAGCCACGCGCTGCGCGCTCGTCCCC 1124
 QY 2320 CCGCTGGGCGCGGCGACACGCGCGCTTCCGCGGCTGCGACCTGCTCCGAGCGCG 2379
 Db 1125 CCGCTGGGCGCGGCGACACGCGCGCTTCCGCGGCTGCGACCTGCTCCGAGCGCG 1184
 QY 2380 AGCCCGAGCGCGCGCAAGCGCTTATGACCGCTTCCCGGAGCTCACGCGGACTACTCCA 2439
 Db 1185 AGCCCGAGCGCGCGCAAGCGCTTATGACCGCTTCCCGGAGCTCACGCGGACTACTCCA 1244
 QY 2440 CGGAGCTGAGCGCTCACCGTGGCGGTGGGTCCTGCTCTCTTCTTCAACATCTGGCCT 2499
 Db 1245 CGGAGCTGAGCGCTCACCGTGGCGGTGGGTCCTGCTCTCTTCTTCAACATCTGGCCT 1304


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Db      841  CTCCTTACCAACCAACGCGCTCCTCCCTACGCCACGGCGTGGCGCTCGTCCGCC 900
Qy      2322  GCTGGCGCCCGGGACACGCGCG 2345
Db      901  GCTGGCGCCCGGGACACGCGCG 924

RESULT 15
AAC58592
ID  AAC58592 standard; cDNA, 3112 BP.
XX
AC  AAC58592;
XX
DT
XX
XX  29-JAN-2001 (first entry)
XX
DE  Human PRO701 protein UNQ365 encoding cDNA SEQ ID NO:66.
XX
XX  Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW  dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW  haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW  antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW  antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW  osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW  idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW  systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW  autoimmune thrombocytopenia; immune-mediated renal disease;
KW  demyelinating disease; hepatobiliary disease; Whipple's disease;
KW  inflammatory bowel disease; gluten-sensitive enteropathy;
KW  autoimmune disease; immune-mediated skin disease; allergic disease;
KW  immunological disease; transplantation associated disease;
KW  graft rejection; graft-versus-host-disease; ss.
XX
OS  Homo sapiens.
XX
XX  WO200053758-A2.
XX
XX  14-SEP-2000.
XX
XX  02-MAR-2000; 200WO-US05841.
XX
XX  08-MAR-1999; 99WO-US05028.
XX  10-MAR-1999; 99US-0123618.
XX  12-MAR-1999; 99US-0123957.
XX  13-MAR-1999; 99US-0125775.
XX  12-APR-1999; 99US-0128849.
XX  20-APR-1999; 99WO-US08615.
XX  28-APR-1999; 99US-0131445.
XX  04-MAY-1999; 99US-0132371.
XX  02-JUN-1999; 99WO-US1252.
XX  23-JUN-1999; 99US-0141037.
XX  20-JUL-1999; 99US-0144758.
XX  26-JUL-1999; 99US-0145698.
XX  28-JUL-1999; 99US-0146222.
XX  01-SEP-1999; 99WO-US20111.
XX  08-SEP-1999; 99WO-US20594.
XX  13-SEP-1999; 99WO-US20944.
XX  15-SEP-1999; 99WO-US21090.
XX  15-SEP-1999; 99WO-US21547.
XX  05-OCT-1999; 99WO-US23089.
XX  29-OCT-1999; 99US-0162506.
XX  30-NOV-1999; 99WO-US28214.
XX  30-NOV-1999; 99WO-US28313.
XX  30-NOV-1999; 99WO-US28409.
XX  01-DEC-1999; 99WO-US28301.
XX  01-DEC-1999; 99WO-US28634.
XX  02-DEC-1999; 99WO-US28551.
XX  02-DEC-1999; 99WO-US28564.
XX  02-DEC-1999; 99WO-US28565.
XX  16-DEC-1999; 99WO-US30095.
XX  20-DEC-1999; 99WO-US30999.
XX  30-DEC-1999; 99WO-US31274.

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PR 05-JAN-2000; 200WO-US00219.
PR 06-JAN-2000; 200WO-US00277.
PR 06-JAN-2000; 200WO-US00376.
PR 11-FEB-2000; 200WO-US03565.
PR 18-FEB-2000; 200WO-US04341.
PR 18-FEB-2000; 200WO-US04342.
PR 22-FEB-2000; 200WO-US04414.
XX
XX (GETH ) GENENTECH INC.
PA
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
DR WPI; 2000-572271/53.
DR P-PSDB; AAB33427.
XX
XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
PS Claim 23; Fig 27; 309pp; English.
XX
XX The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC autoimmune or immune-mediated skin diseases, allergic diseases,
CC immunological diseases of the lung, and transplantation associated
CC diseases including graft rejection and graft-versus-host-disease.
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 3112 BP; 853 A; 867 C; 712 G; 680 T; 0 other;
Query Match 19.5%; Score 912.2; DB 21; Length 3112;
Best Local Similarity 64.7%; Pred. No. 1.2e-152;
Matches 1503; Conservative 0; Mismatches 748; Indels 72; Gaps 7;
Qy 527 CGCGGAGGAGCGCTTCCCGGTGGTGAACACGCGCTACGGGCGAGTGGCGGTGGCGCG 586
Db 112 CAGCCAAGCACAGTATCCAGTTGTCAACACAAATATGCAAAATCCGGGGGCTAAGAAC 171
Qy 587 CGAGCTCAACAAACGAGATCCTGGGCGCCCGTGTGAGTTCCTGGGCGTCCCTAGCCAC 646
Db 172 ACCGTTACCAATGAGATCTTGGTCCAGTGAGAGAGTACTTAGGGTCCCTATGCCTC 231
Qy 647 GCGCGCCCTGGGCGCCCGCTTTCAGCGGCTGAGGCGCCCGCTCTGTGCGCGCGCT 706
Db 232 ACCCCCACTGAGAGAGAGCGGCTTTCAGCCCGCAGAACCCCGCTCTCTGAGATGGCAT 291
Qy 707 GCGCAACGCCACACCCCTGCGCGCCCGTGGCGGAGACCTGACG---GGCGGTGCG 763
Db 292 CGGAAATACTACTAGTTTGTGCTGTGTGTCGTCGAGACCTGGATGAGATCTTACT 351
Qy 764 CGCCATCATGCTGCTGTGTGTGTTACCGACAACCTTGGAGGGCGCGCCACCTAGCTGCA 823
Db 352 GCATGACATGCTGCCCATCTGTGTTTACCGCAATTTGGATCTTTGATGACCTATTCA 411
Qy 824 GAAACGAGCGAGGAGTGGCTGTACTCTCACTTACCTGTCGTCGCCACCGAGAGCGGTCCGCT 883
Db 412 AGATCAAAATAGAGACTGCTTCTTACTTAAACATCTACGTGGCCCGAGAGATGGAGCCAA 471

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884 CACAAAAAAGCTGACAGGCG-----ACGCTCAATCGCCAGACACAGATATCCG 934
472 CACAAAAAAGCGAGATATACAGATATACCGTGTGAGACGAGATATCA 531
935 TGACCCCTG---GGAAGAACCTGTGATGCTGTTCTCCATGCGGCTCTACATGGAGG 991
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2762 TCTCTTGGCGCGCGGCGGCTGACCTGCTGCGCGCGGCTG 2804
2365 ACTTATGAGCGCAACACCATCATGATTCACAAACACTG 2407

Search completed: February 19, 2004, 00:51:30
Job time : 1135.58 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2004, 16:45:36 ; Search time 243.269 Seconds
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8467.711 Million cell updates/sec

Title: US-09-934-323-1

Perfect score: 4667

Sequence: 1 ggcacggaggaacttggtct.....ttgcctcttgactgtccctc 4667

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
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- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1092	23.4	1446	4	US-09-149-476-139
2	1011.2	21.7	4233	4	US-09-491-356C-5
3	871	18.7	4436	4	US-09-491-356C-6
4	724.6	15.5	1764	4	US-09-491-356C-3
5	700.4	15.0	2818	4	US-09-491-356C-4
6	494.8	10.6	5298	4	US-09-491-356C-1
7	145.6	3.1	1905	4	US-09-347-878-33
8	145.6	3.1	1907	1	US-08-462-884A-2
9	145.6	3.1	1908	1	US-08-461-881B-2
10	145.6	3.1	1908	2	US-09-123-960-2
11	132.4	2.8	2184	1	US-08-445-050-8
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13	132.4	2.8	2344	1	US-09-347-878-31
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18	132.4	2.8	3018	1	US-08-347-718B-3
19	132.4	2.8	3018	1	US-08-482-262-3
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26	100.2	2.1	2256	2	US-08-370-156-1
27	100.2	2.1	2256	3	US-08-814-095-1

ALIGNMENTS

RESULT 1

US-09-149-476-139
; Sequence 139, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
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; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
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; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
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; Sequence 4, Application US/09491356C
; Patent No. 6566061
; GENERAL INFORMATION:
; APPLICANT: Philibert, Robert A.
; APPLICANT: Ginns, Edward I.
; APPLICANT: Delisi, Lynn
; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
; FILE REFERENCE: 9465.6US11
; CURRENT APPLICATION NUMBER: US/09/491.356C
; CURRENT FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: PCT/US99/09365
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/083,465
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2818
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-491-356C-4

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Matches 1079; Conservative 0; Mismatches 491; Indels 54; Gaps 3;

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QY 1989 TCCAAATGAGCTCATGCTCAGTCCCTGCTGCTAGCTGACCTACTGACCACTTCCCAAG 2048
DB 782 TCCAAATGATGTTTATGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 841
QY 2049 ACTGGGAGCCCAACCGCGCTGCGGAGGATCAAGTTCATCCACCAAGGCCAAT 2108
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QY 2109 CGCTTCGAGGAGTGTGTGGAGCAAAATTCACAGCAAGGAGAGTATCTGCACATA 2168
DB 902 CGCTTTGAGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
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DB 962 GGCCTGAAGCCACGGTGGTGCACAACTATCCCGGCGCACTAAGGTGGCTTCTTGGAAACAT 1021
QY 2229 CTGCTGCCCACTGCACAACTGCACAGCGAGCTC-----TTCAACCAACCAACG 2279
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DB 1082 GTGCGGCTTCCGATACCAACCCACAGCTCCACATCAACCGGAGGCGCAATGGCAAGAC 1141
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QY 2391 -----GGCGCAAGGCTTATGACGCTTCCCGGAGCTACGCGGACTCTCCAG 2441
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QY 2442 GAGCTGAGCGTCAAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2501
DB 1262 GAATTAAGTGTCAACATCGCGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
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DB 1382 CAGCGGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1414

100

TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2184 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: 82..2088
OTHER INFORMATION: /label= Variant_T
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 151..2085
FEATURE:
NAME/KEY: repeat_region
LOCATION: 1756..2052
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1756..1788
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1789..1821
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 1822..1854
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LOCATION: 1888..1920
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NAME/KEY: repeat_unit
LOCATION: 1921..1953
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NAME/KEY: repeat_unit
LOCATION: 1954..1986
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NAME/KEY: repeat_unit
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NAME/KEY: repeat_unit
LOCATION: 2020..2052

US-08-445-050-8
Query Match 2.8%; Score 132.4; DB 1; Length 2184;
Best Local Similarity 48.8%; Pred. No. 4.4e-17;
Matches 528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;
QY 1000 ACATGTCGATGGCTCAGTCCTGGCTGCTATGGCAAGTCATTTAGCCACGCTCAACT 1059
DB 518 ACCTGATGACGGGAGGAGATCGCCACACGGGAAAGTCATCGTGTGACCTTCACT 577
QY 1060 ACCGTGTTGGGTGCTCGGTTTCTCAGCACCGGGGACAGGCTGCAAAAGGCACTATG 1119
DB 578 ACCGTGTCGGCCCTTGGTTTCTCAGCACCTGGGGAGCCCAATCTGCCAGGTAACTATG 637
QY 1120 GGTCCTGACGATCCAGGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1179
DB 638 GCTTCGGGATCAGACATCGGCAATGCTTGGGTGAAGAGATATCGGCGCTTCGGGG 697
QY 1180 GCGACCCCGGATGACCATCTTTTGGTTCCGGGGCAGGGGCTCTCTGGTCAACCTTC 1239
DB 698 GGGACCCCGACACATCAGCTCTTCGGGGAGTCTGCTGGAGTCCAGGCTCTCTCTGC 757
QY 1240 TGATCTCTCCCAACCATTCAGAAAGGCTCTTCAGAAAGGCCATCGCCCGAGGTGCAACG 1299

DB 758 AGACCTCTCCCTCAACAAAGGGCTCTATCCGGGAGCCATACGCCAGAGCGGCTGG 817
QY 1300 CCATTTCCAGCTGCTGTCAACTTACCAGCGGCTCAAGTACACGGGCTCTCTGCAACCA 1359
DB 818 CCCTGAGTCCCTGGTCAATCCAGAAACCACTCTTCTGGGCAAAAGGTGGCTGAGA 877
QY 1360 AGTGGGCTGTGACCGAGAGACAGTCTGAAGCTGTGGAGTCTCTGCGCCGAGGACCT 1419
DB 878 AGTGGGTTGGCTGTGGGTGATCCCGCCAGGATGGCCCTGCTGCTGAAGTTACTGATC 937
QY 1420 CCCGGAGCT---GGTGACCGAGCAGTGCAGCCTGCCGCTACACATGCTCCTTTGGGC 1476
DB 938 CCCGAGCCCTGACGCTGGCTATAGGTGCGCTGGCAGGCTGGAGTACCCCATGCTGC 997
QY 1477 CCGTGGTGGATGGGACGTGGTCCCGATGACCTGAGATCCCTGATGCTCATGACGAGGAGAT 1536
DB 998 ACTATGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1057
QY 1537 TCCTCACTAGCATGCTCATCGCGCTCAACAGGAGAGGGGCTCAAGTTCTGTGGAGG 1596
DB 1058 TGTAGCCCAACGCCCGGACATGCACTATATAGCAGGCAACCAACATGGACGCGCACA 1117
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QY 1711 TCAAGTTTATGACACAGACTGGGCGGACCGGCAATGGGCAATGGCGCAAAACCC 1770
DB 1238 CTTTGTGATGCTACACCGAGTCTGCGGCGCCAGGACCCATCCAGGAGAAATAGAGAGA 1297
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DB 1298 CTGTGTGAGCTTTGAGACCGGATGCTCTTCTGCTGGTCCCAACCGAGATTTGCCCTAGCCC 1357
QY 1825 AGCTGACGCGGACTTACGAGTCTCTCC---GTCTACTTTTACACCTTCTACCACTGCTGCC 1881
DB 1358 AGCAGAGCCATGTCAGAGATGCGAGACTACGCTACCTGTTTCCCATCTCTCTC 1417
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DB 1418 GGATGCGCGCTTACCCCAATGGGTGGGCGGCGACCATGCGATGACATTCAGTACGTTT 1477
QY 1942 TTGGCGTGGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2001
DB 1478 TCGGGAAGGCGCTTCGCGCACCCCGGCTACCGGCGGCTACCGGCGGCTACCGGCGGCT 1537
QY 2002 TCATGCTCAGTGGCTGGTTCATGACCTACTGACCAACTTCCCAAGACTGGGGAGCCCA 2061
DB 1538 CCATGATCG-----CCTACTGACCAACTTTTGCACAAACAGGGGAGCCCA 1582
QY 2062 AC 2063
DB 1583 AC 1584

RESULT 12
US-08-204-691-8
; Sequence 8, Application US/08204691
; Patent No. 5827683
; GENERAL INFORMATION:
; APPLICANT: Blaeckberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Hennell, Olle
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stroemqvist, Mats
; APPLICANT: Toernell, Jan
; TITLE OF INVENTION: No. 5827683el Polypeptides

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; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204.691
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 930686-4
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 930722-7
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner Ph.D., Richard J
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2184 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: mammary gland
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 82..2088
; OTHER INFORMATION: /label= Variant_T
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 151..2085
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 1756..2052
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 1756..1788
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; LOCATION: 1789..1821
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; NAME/KEY: repeat_unit
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; LOCATION: 1855..1887
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 1888..1920
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 1921..1953
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 1954..1986

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Db 1478 TCGGGAAGCCCTTTCGCCACCCCCACCGGCTACCGGCCCAAGACAGGACATCTCTTAAG 1537
QY 2002 TCATGCTCAGTCCGTGGTTCATGACTACTGACCAACTTTCGCCAAGACTGGGACCCCA 2061
Db 1538 CCATGATCG-----CCTACTGACCAACTTTTGGCCAAACAGGGGACCCCA 1582
QY 2062 AC 2063
Db 1583 AC 1584

RESULT 13
US-09-347-878-31
; Sequence 31, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25865-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 2344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(2252)
; FEATURE:
; OTHER INFORMATION: Human cholesterol esterase cDNA
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M85201/GenBank
US-09-347-878-31

Query Match 2.8%; Score 132.4; DB 4; Length 2344;
Best Local Similarity 48.8%; Pred. No. 4.5e-17;
Matches 528; Conservative 0; Mismatches 521; Indels 33; Gaps 5;

QY 1000 ACATGTTTCGATGCTCAGTCCCTGGCTGCTATGGCAACGTCAATGTAGCAGCTCAACT 1059
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QY 1180 GCGACCCGAGCGTATCACCATCTTTGGTTCGGGCGAGGGCCCTCTGGTCAACTTC 1239
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QY 1360 AGTGGGCTGTGACCGAGGACAGTGTGAGTGTGGAGTGTCTCGCGCGGAAGCCCT 1419
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QY 1420 CCGCGAGCT---GGTGAACAGAGAGTGCAGCCTGCCCGCTACCATCGCCTTTGGGC 1476
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QY 1477 CCGTGTGATGCGAGCTGGTCCCGATGACCCCTGAGATCCTCATGACAGGAGAAAT 1536
Db 925 ACTATGTGGCTTCGTCCTCTGTCATTGATGGAGACTTCACTCCCGCTGACCCGATCAAC 984
QY 1537 TCCTCAACTACGATGCTCATCGGCGTCAACGAGGAGAGGCTCAAGTTGTTGGAGG 1596
Db 985 TGTACGCCAACGCCGCCGACATCGACTATATAGCAGGCAACCAACATGGAGCGGCCACA 1044
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QY 1825 AGCTGACGCGGACTACAGTCTCCC---GTCTACTTTTACACCTTCTACCACTGCTCC 1881
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QY 1882 AGCGGAGGCGCGCTGAGTGGGCGAGATCGCGCGACCGGGAGTAACTGCCCCATGTCT 1941
Db 1345 GGATGCCGCTTACCCCAATGGTGGGCGCCAGCATGCAGATGACATTCAGTACGTTT 1404
QY 1942 TTGGCGTGGCCATGGTGGTGGCCACCGACCTCTTTCCTGTAATCTTCTCAAAGATGACG 2001
Db 1405 TCGGGAAGCGCTTTCGCCACCCCAACCGGCTACCGGCGCCCAAGACAGGACAGTCTTAAGG 1464
QY 2002 TCATGCTCAGTGGCGTGTATGACCTACTGACCAACTTCGCCAAGACTTGGGGACCCCA 2061
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QY 2062 AC 2063
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RESULT 14
US-08-445-050-1
; Sequence 1, Application US/08445050
; Patent No. 5763739
; GENERAL INFORMATION:
; APPLICANT: Blaeckberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Hernell, Oile
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stroomqvist, Mats
; APPLICANT: Toernell, Jan
; TITLE OF INVENTION: No. 5763739el Polypeptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

[REDACTED]

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Db 938 CCCGAGCCCTGACGCTGSCCTATAAGGTGCGCTGGCAGGCGCTGGAGTACCCCATGCTGC 997
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QY 1882 AGCGGAGGCGCGGCTCAGTGGGCGAGATGGCGGCGGAGTGAAGTCTCCCTATGTCT 1941
Db 1418 GATCCCGTCTACCCCAATGGGTGGGCGGACCATGAGATGACATTCAGTACGTTT 1477
QY 1942 TTGGCGTCCCAATGGGTGGGCGGACCGGACTCTTCTCCCTGTAACTTCTCCAAAGATGAGC 2001
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QY 2062 AC 2063
Db 1583 AC 1584

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RESULT 15
US-08-204-691-1
; Sequence 1, Application US/08204691
; Patent No. 5827683
; GENERAL INFORMATION:
; APPLICANT: Blaeckberg, Lars
; APPLICANT: Edlund, Michael
; APPLICANT: Hansson, Lennart
; APPLICANT: Harnell, Olle
; APPLICANT: Lundberg, Lennart
; APPLICANT: Stromqvist, Mats
; APPLICANT: Toernell, Jan
; TITLE OF INVENTION: No. 5827683el Polypeptides
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,691
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300686-4
; FILING DATE: 01-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300722-7
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner P.D., Richard J
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: mammary gland
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 82..2319
; OTHER INFORMATION: /product= "bile-salt-stimulated"
; OTHER INFORMATION: lipase"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 985..1173
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; NAME/KEY: exon
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FEATURE:
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US-08-204-691-1

Query Match 2.8%; Score 132.4; DB 1; Length 2428;

Best Local Similarity 48.8%; Fred. No. 4.5e-17; Indels 33; Gaps 5;

Matches 528; Conservative 0; Mismatches 521;

QY 1000 ACATGTTTCATGGCTCAGTCTGGTGGCTATGGAACGTCATTTGATGAGAGACTTCAATCCCGCTGACCGATCAACC 1059
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DB 998 ACTATGTGGGCTTCGTCCCTGTGTCATTTGATGAGAGACTTCAATCCCGCTGACCGATCAACC 1057
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DB 1058 TGTACGCCAAACCGCGGCACATCGACTATATAGCAGGACCAACACATGGACGCGCACCA 1117
QY 1597 ACTCTGACAGAGCGAGGAGCGGTGTCTGCGAGCGCTTTGACTTCACTGTCTTCAACT 1656
DB 1118 TCTTCGCCAGCATCGACATGCTGCTCATCAACAGGGCAACAGAAAGTCAACGAGGAG 1177
QY 1657 TTGTGGACACCTGTATGGCTACCGGAGGCAAGATGTGCTTCGGG-----AGACCA 1710
DB 1178 ACTTCTACAGCTGTGTCAGTGTTCACATCAACAGGGGTTCAGAGCGCCACAGACCA 1237
QY 1711 TCAAGTTTATGTACACAGACTGGGCGGACCGGCAATGGCGAAATGGCCCGCAAAACCC 1770
DB 1238 CCTTTGATGTCTACACCGAGTCTCTGGGCCAGGACCCATCCCGAGGAGATAAGAGAAGA 1297
QY 1771 TGGTGGCGCTCTT-----ACTGACCAACATGGGTGGCACACAGCTGTGGCCACTGCCA 1824
DB 1298 CTGTGGTGGACTTTGAGACCGATGCTCTTCTCTGTGCTCCACCGAGATGGCCCTAGCCC 1357
QY 1825 AGCTGCACCGCGACTACCAAGTCTCCC---GTCTACTTTTACACCTTCTACCACTGCT 1881
DB 1358 AGCACAGAGCCATGCGCAAGAGTGGCAAGACCTACGCTTACCTGTTTCCCATCCCTCTC 1417
QY 1882 AGCGGAGGGCGGCTGTAGTGGGCGAGATGCGGCGGACCGGGATGAACTGCCCTATGTCT 1941
DB 1418 GGATGCCCGTCTACCCCAATGGGTGGGGGCCGACCATGCGATGACATTCAGTACGTTT 1477
QY 1942 TTGGCGTGGCCATGGTGGGTGGCCACCGACCTCTTCCCTGTAACTTCTCCAAGAAATGAG 2001
DB 1478 TCGGGAAGCCCTTCGCCACCCCGGCTACCGGCCCAAGACAGGACAGTCTCTAAGG 1537
QY 2002 TCATGTCTCAGTGGCGTGTGATGACCTACTGACCAACTTTCGCCAAGACTGGGGACCCCA 2061
DB 1538 CCATGATCG-----CCTACTGGACCAACTTTCGCCAAACAGGGGACCCCA 1582
QY 2062 AC 2063
DB 1583 AC 1584

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